Local adaptation at the transcriptome level in brown trout: Evidence from early life history temperature genomic reaction norms

Local adaptation and its underlying molecular basis has long been a key focus in evolutionary biology. There has recently been increased interest in the evolutionary role of plasticity and the molecular mechanisms underlying local adaptation. Using transcriptome analysis, we assessed differences in gene expression profiles for three brown trout (Salmo trutta) populations, one resident and two anadromous, experiencing different temperature regimes in the wild. The study was based on an F2 generation raised in a common garden setting. A previous study of the F1 generation revealed different reaction norms and significantly higher Q_{ST} than F_{ST} among populations for two early life-history traits. In the present study we investigated if genomic reaction norm patterns were also present at the transcriptome level. Eggs from the three populations were incubated at two temperatures (5 and 8 degrees C) representing conditions encountered in the local environments. Global gene expression for fry at the stage of first feeding was analysed using a 32k cDNA microarray. The results revealed differences in gene expression between populations and temperatures and population × temperature interactions, the latter indicating locally adapted reaction norms. Moreover, the reaction norms paralleled those observed previously at early life-history traits. We identified 90 cDNA clones among the genes with an interaction effect that were differently expressed between the ecologically divergent populations. These included genes involved in immune- and stress response. We observed less plasticity in the resident as compared to the anadromous populations, possibly reflecting that the degree of environmental heterogeneity encountered by individuals throughout their life cycle will select for variable level of phenotypic plasticity at the transcriptome level. Our study demonstrates the usefulness of transcriptome approaches to identify genes with different temperature reaction norms. The responses observed suggest that populations may vary in their susceptibility to climate change.
An assessment of the spatial scale of local adaptation in brown trout (Salmo trutta L.): footprints of selection at microsatellite DNA loci

Local adaptation is considered a paradigm in studies of salmonid fish populations. Yet, little is known about the geographical scale of local adaptation. Is adaptive divergence primarily evident at the scale of regions or individual populations? Also, many salmonid populations are subject to spawning intrusion by farmed conspecifics that experience selection regimes fundamentally different from wild populations. This prompts the question if adaptive differences between wild populations and hatchery strains are more pronounced than between different wild populations? We addressed these issues by analyzing variation at 74 microsatellite loci (including anonymous and expressed sequence tag- and quantitative trait locus-linked markers) in 15 anadromous wild brown trout (Salmo trutta L.) populations, representing five geographical regions, along with two lake populations and two hatchery strains used for stocking some of the populations. FST-based outlier tests revealed more outlier loci between different geographical regions separated by 522±228 km (mean±s.d.) than between populations within regions separated by 117±79 km (mean±s.d.). A significant association between geographical distance and number of outliers between regions was evident. There was no evidence for more outliers in comparisons involving hatchery trout, but the loci under putative selection generally were not the same as those found to be outliers between wild populations. Our study supports the notion of local adaption being increasingly important at the scale of regions as compared with individual populations, and suggests that loci involved in adaptation to captive environments are not necessarily the same as those involved in adaptive divergence among wild populations.
Identifying footprints of selection in stocked brown trout populations: a spatio-temporal approach

Studies of interactions between farmed and wild salmonid fishes have suggested reduced fitness of farmed strains in the wild, but evidence for selection at the genic level is lacking. We studied three brown trout populations in Denmark which have been significantly admixed with stocked hatchery trout (19–64%), along with two hatchery strains used for stocking. The wild populations were represented by contemporary samples (2000–2006) and two of them by historical samples (1943–1956). We analysed 61 microsatellite loci, nine of which showed putative functional relationships [expressed sequence tag (EST)-linked or quantitative trait loci]. FST-based outlier tests provided support for diversifying selection at chromosome regions marked by three loci, two anonymous and one EST-linked. Patterns of differentiation suggested that the loci were candidates for being under diversifying hitch-hiking selection in hatchery vs. wild environments. Analysis of hatchery strain admixture proportions showed that in one wild population, two of the loci showed significantly lower admixture proportions than the putatively neutral loci, implying contemporary selection against alleles introduced by hatchery strain trout. In the most strongly admixed population, however, there was no evidence for selection, possibly because of immigration by stocked trout overcoming selection against hatchery-derived alleles or supportive breeding practices allowing hatchery strain trout to escape natural selection. To our knowledge, this is the first study demonstrating footprints of selection in wild salmonid populations subject to spawning intrusion by farmed fish.
Admixture analysis of stocked brown trout populations using mapped microsatellite DNA markers: indigenous trout persist in introgressed populations

Admixture between wild and captive populations is an increasing concern in conservation biology. Understanding the extent of admixture and the processes involved requires identification of admixed and non-admixed individuals. This can be achieved by statistical methods employing Bayesian clustering, but resolution is low if genetic differentiation is weak. Here, we analyse stocked brown trout populations represented by historical (1943-1956) and contemporary (2000s) samples, where genetic differentiation between wild populations and stocked trout is weak (pair-wise F-ST of 0.047 and 0.053). By analysing a high number of microsatellite DNA markers (50) and making use of linkage map information, we achieve clear identification of admixed and non-admixed trout. Moreover, despite strong population-level admixture by hatchery strain trout in one of the populations (70.8%), non-admixed individuals nevertheless persist (7 out of 53 individuals). These remnants of the indigenous population are characterized by later spawning time than the majority of the admixed individuals. We hypothesize that isolation by time mediated by spawning time differences between wild and hatchery strain trout is a major factor rescuing a part of the indigenous population from introgression.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Mensberg, K. D. (Intern)
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Publication date: 2009
Main Research Area: Technical/natural sciences
Molecular basis of local adaptation in brown trout (Salmo trutta L.)

General information
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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Meier, K. (Intern), Hansen, M. M. (Intern), Jensen, L. F. (Ekstern), Loeschske, V. (Ekstern), Pertoldi, C. (Ekstern) , Mensberg, K. D. (Intern), Holdensgaard, G. (Ekstern)
Publication date: 2009
Event: Poster session presented at ESEB conference, Torino, Italy, .
Sixty years of anthropogenic pressure: a spatio-temporal genetic analysis of brown trout populations subject to stocking and population declines

Analyses of historical samples can provide invaluable information on changes to the genetic composition of natural populations resulting from human activities. Here, we analyse 21 microsatellite loci in historical (archived scales from 1927 to 1956) and contemporary samples of brown trout (Salmo trutta) from six neighbouring rivers in Denmark, to compare the genetic structure of wild populations before and after population declines and stocking with nonlocal strains of hatchery trout. We show that all populations have been strongly affected by stocking, with admixture proportions ranging from 14 to 64%. Historical population genetic structure was characterized by isolation by distance and by positive correlations between historical effective population sizes and habitat area within river systems. Contemporary population genetic structure still showed isolation by distance, but also reflected differences among populations in hatchery trout admixture proportions. Despite significant changes to the genetic composition within populations over time, dispersal rates among populations were roughly similar before and after stocking. We also assessed whether population declines or introgression by hatchery strain trout should be the most significant conservation concern in this system. Based on theoretical considerations, we argue that population declines have had limited negative effects for the persistence of adaptive variation, but admixture with hatchery trout may have resulted in reduced local adaptation. Collectively, our study demonstrates the usefulness of analysing historical samples for identifying the most important consequences of human activities on the genetic structure of wild populations.
Local adaptation in brown trout early life-history traits: implications for climate change adaptability

General information
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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Jensen, L. (Ekstern), Hansen, M. M. (Intern), Pertoldi, C. (Ekstern), Holdensgaard, G. (Ekstern), Mensberg, K. D. (Intern), Loeschcke, V. (Ekstern)
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BFI (2018): BFI-level 2
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.89 SJR 2.541 SNIP 1.474
Reproductive isolation, evolutionary distinctiveness and setting conservation priorities: The case of European lake whitefish and the endangered North Sea houting (Coregonus spp.)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Fraser, D. (Ekstern), Als, T. D. (Intern), Mensberg, K. D. (Intern)
Pages: 137
Spatially and temporally fluctuating selection at non-MHC immune genes: evidence from TAP polymorphism in populations of brown trout (Salmo trutta, L.)

Temporal samples of Danish brown trout (Salmo trutta) from populations representing varying geographical scales were analysed using eight putatively neutral microsatellite loci and two microsatellite loci embedded in TAP genes (Transporter associated with Antigen Processing). These genes encode molecules that are central to the major histocompatibility complex (MHC) class I restricted antigen presentation and thus integral components in the adaptive immune system. As such, they could be influenced by selection, driven by pathogens and parasites in a manner similar to MHC genes.

Analysis of allele frequencies at presumably neutral microsatellite loci revealed a temporally unstable population structure within regions, while the population structure was stable over time among regions. Analyses of the two TAP markers indicated an effect of selection at both a regional and micro-geographical spatial scale. Moreover, signals of divergent selection among temporal samples within localities suggest that selection also might fluctuate at a temporal scale. These results suggest that immune genes other than the classical MHC class I and II might be subject to selection and warrant further studies of functional polymorphism of such genes in natural populations.

General information
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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Jensen, L. (Ekstern), Hansen, M. M. (Intern), Mensberg, K. D. (Intern), Loeschcke, V. (Ekstern)
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Journal: Heredity
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.56 SJR 2.03 SNIP 1.243
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.094 SNIP 1.298 CiteScore 3.47
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.162 SNIP 1.304 CiteScore 3.42
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.029 SNIP 1.149 CiteScore 3.44
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.088 SNIP 1.356 CiteScore 3.5
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.279 SNIP 1.289 CiteScore 3.58
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.376 SNIP 1.253
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.244 SNIP 1.268
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.985 SNIP 1.242
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.747 SNIP 1.218
Gene flow, effective population size and selection at major histocompatibility complex genes: brown trout in the Hardanger Fjord, Norway

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Skaala, Ø. (Ekstern), Jensen, L. (Ekstern), Bekkevold, D. (Intern), Mensberg, K. D. (Intern)
Pages: 1413-1425
Publication date: 2007
Main Research Area: Technical/natural sciences

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Journal: Molecular Ecology
Volume: 16
Issue number: 7
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Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.9 SJR 3.508 SNIP 1.651
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.862 SNIP 1.606 CiteScore 5.73
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.068 SNIP 1.705 CiteScore 5.36
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Genetic restoration of a stocked brown trout Salmo trutta population using microsatellite DNA analysis of historical and contemporary samples

1. Gene flow from domesticated to wild populations is a major threat to wild salmonid fish. However, few studies have addressed how populations could be restored after admixture has occurred. We analysed the prospects for restoring the previously intensively stocked brown trout population of the Skjern River, Denmark, by identifying remaining non-admixed individuals to be used for supportive breeding.

2. We analysed microsatellite DNA markers in historical (1940-50s) and contemporary (1992-2004) samples from the Skjern River system, from the strain of domesticated trout previously used for stocking, and from the neighbouring Stora River. We analysed admixture proportions to estimate the genetic contribution by domesticated trout. We identified non-admixed trout using assignment tests, and further analysed the possible sources of indigenous trout by estimating contemporary migration among populations.

3. Genetic differentiation between the historical Stora and Skjern river populations was low (\( \theta_{ST} = 0.004 \)), suggesting considerable gene flow in the past. The contemporary Skjern and Stora river populations and a supportive breeding brood stock were strongly admixed, but some non-admixed individuals nevertheless remained in the wild-caught samples. In addition, two resident populations in isolated tributaries were found to be indigenous. The indigenous anadromous individuals from the Skjern River were unlikely to have been recruited from either the isolated tributary populations or the neighbouring Stora River and were presumably derived from unidentified spawning sites in the river system.

4. All but one non-admixed anadromous Skjern River trout were females, which we ascribed to sampling bias. Moreover, all non-admixed fish were late-spawning (January-February) whereas the majority of all trout caught for the study were ripe by November-December. The difference in spawning time could be an important factor delaying complete admixture of domesticated and indigenous trout.

5. Synthesis and applications. This study demonstrates the feasibility of restoring populations that have been admixed with exogenous individuals, by identifying non-admixed individuals using genetic markers. However, the results also highlight the problem that numbers of identified non-admixed individuals may be small, necessitating
identification of nearby, closely related populations that can be incorporated into breeding programmes.

**General information**

**State:** Published  
**Organisations:** Section for Population Ecology and Genetics, National Institute of Aquatic Resources  
**Authors:** Hansen, M. M. (Intern), Bekkevold, D. (Intern), Jensen, L. (Ekstern), Mensberg, K. D. (Intern), Eg Nielsen, E. (Intern)  
**Pages:** 669-679  
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BFI (2018): BFI-level 2  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 2  
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BFI (2016): BFI-level 2  
Scopus rating (2016): CiteScore 5.5 SJR 2.869 SNIP 2.008  
Web of Science (2016): Indexed yes  
BFI (2015): BFI-level 2  
Scopus rating (2015): SJR 3.242 SNIP 1.96 CiteScore 5.38  
BFI (2014): BFI-level 2  
Scopus rating (2014): SJR 2.998 SNIP 2.171 CiteScore 5.25  
Web of Science (2014): Indexed yes  
BFI (2013): BFI-level 2  
Scopus rating (2013): SJR 3.031 SNIP 2.225 CiteScore 5.45  
ISI indexed (2013): ISI indexed yes  
Web of Science (2013): Indexed yes  
BFI (2012): BFI-level 2  
Scopus rating (2012): SJR 3.122 SNIP 2.089 CiteScore 5.18  
ISI indexed (2012): ISI indexed yes  
BFI (2011): BFI-level 2  
Scopus rating (2011): SJR 3.665 SNIP 2.294 CiteScore 5.23  
ISI indexed (2011): ISI indexed yes  
BFI (2010): BFI-level 2  
Scopus rating (2010): SJR 3.091 SNIP 2.014  
BFI (2009): BFI-level 2  
Scopus rating (2009): SJR 3.22 SNIP 2.112  
BFI (2008): BFI-level 2  
Scopus rating (2008): SJR 3.08 SNIP 2.252  
Web of Science (2008): Indexed yes  
Scopus rating (2007): SJR 3.494 SNIP 2.592  
Web of Science (2007): Indexed yes  
Scopus rating (2006): SJR 3.095 SNIP 2.385  
Web of Science (2006): Indexed yes  
Scopus rating (2005): SJR 3.124 SNIP 2.257  
Scopus rating (2004): SJR 2.709 SNIP 2.134  
Scopus rating (2003): SJR 3.09 SNIP 2.121  
Scopus rating (2002): SJR 2.682 SNIP 1.744  
Scopus rating (2001): SJR 2.128 SNIP 1.69  
Scopus rating (2000): SJR 1.935 SNIP 1.523
Loss of genetic variation in hatchery-reared Indian major carps, *Catla catla*

**General information**
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Simonsen, V. (Ekstern), Mensberg, K. D. (Intern), Sarder, R. (Ekstern), Alam, S. (Ekstern)
Pages: 229-241
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Main Research Area: Technical/natural sciences

**Publication Information**
Journal: Journal of Fish Biology
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.57 SJR 0.741 SNIP 0.882
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.951 SNIP 0.935 CiteScore 1.64
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.944 SNIP 0.934 CiteScore 1.76
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.049 SNIP 1.118 CiteScore 1.98
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.93 SNIP 1.035 CiteScore 1.88
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.895 SNIP 0.946 CiteScore 1.66
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.774 SNIP 0.834
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.773 SNIP 0.891
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.883 SNIP 0.968
Web of Science (2008): Indexed yes
Underwater but not out of sight: genetic monitoring of effective population size in the endangered North Sea houting (Coregonus oxyrhynchus)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Mensberg, K. D. (Intern)
Pages: 780-787
Publication date: 2006
Main Research Area: Technical/natural sciences

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Journal: Canadian Journal of Fisheries and Aquatic Sciences
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Web of Science (2018): Indexed yes
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Scopus rating (2016): CiteScore 2.56 SJR 1.322 SNIP 1.163
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.256 SNIP 1.051 CiteScore 2.22
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.443 SNIP 1.379 CiteScore 2.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.421 SNIP 1.081 CiteScore 2.25
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Spatial and temporal genetic differentiation and effective population size of brown trout (Salmo trutta L.) in small Danish rivers

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Jensen, L. F. (Ekstern), Hansen, M. M. (Intern), Carlsson, J. (Ekstern), Loeschcke, V. (Ekstern), Mensberg, K. D. (Intern)
Pages: 615-621
Publication date: 2005
Main Research Area: Technical/natural sciences

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Journal: Conservation Genetics
Volume: 6
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Widespread hybridization among species of Indian major carps in hatcheries, but not in the wild

Twenty-one allozyme loci in samples of wild-caught and hatchery-reared Indian major carps from Bangladesh were analysed. Bayesian model-based clustering analysis revealed the presence of four taxa, corresponding to the three known species along with a fourth unknown taxon present in two hatchery samples. Individual admixture coefficients showed that 24% of all hatchery-reared fishes were hybrids, whereas a single hybrid was observed in the wild-caught samples. Only catla Catla catla x rohu Labeo rohita and mrigal Cirrhinus cirrhosus x rohu hybrids were observed, the vast majority of which were F₁ hybrids, though five individuals represented putative backcrosses. Mitochondrial DNA analysis revealed that catla x rohu hybridization primarily involved catla males and rohu females, whereas mrigal x rohu hybrids primarily resulted from rohu males and mrigal females. Despite the high percentage of F₁-hybrids in hatchery samples, reproductive barriers among species have so far precluded widespread introgression. Continued hybridization may eventually lead to a breakdown of species barriers, thereby compromising the genetic integrity of the species in the wild, and leading to production losses in aquaculture. (c) 2005 The Fisheries Society of the British Isles.
Genetic detection of sex-specific dispersal in historical and contemporary populations of anadromous brown trout Salmo trutta

The study of sex-biased dispersal has attracted considerable attention in birds and mammals, but less in other taxa, including fishes. We analysed sex-specific dispersal in historical (1910s and 1950s) and contemporary (1990s) samples of anadromous brown trout Salmo trutta. We tested the hypothesis that dispersal is unbiased using information from microsatellite DNA and applying an assignment index for 11 temporally and spatially separated samples. Our results are most consistent with brown trout dispersal being male biased, and provide no evidence of female bias. We found no evidence that dispersal patterns changed over time, indicating that stocking with hatchery strains did not affect sex-specific dispersal.

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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Bekkevold, D. (Intern), Hansen, M. M. (Intern), Mensberg, K. D. (Intern)
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Web of Science (2018): Indexed yes
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Web of Science (2017): Indexed Yes
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Scopus rating (2016): CiteScore 5.9 SJR 3.508 SNIP 1.651
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.862 SNIP 1.606 CiteScore 5.73
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Long-term effective population sizes, temporal stability of genetic composition and potential for local adaptation in anadromous brown trout (Salmo trutta) populations

We examined the long-term temporal (1910s to 1990s) genetic variation at eight microsatellite DNA loci in brown trout (Salmo trutta L) collected from five anadromous populations in Denmark to assess the long-term stability of genetic composition and to estimate effective population sizes (N-e). Contemporary and historical samples consisted of tissue and archived scales, respectively. Pairwise Theta(ST) estimates, a hierarchical analysis of molecular variance (AMOVA) and multidimensional scaling analysis of pairwise genetic distances between samples revealed much closer genetic relationships among temporal samples from the same populations than among samples from different populations. Estimates of N-e, using a likelihood-based implementation of the temporal method, revealed N-e greater than or equal to 500 in two of three populations for which we have historical data. A third population in a small (3 km) river showed N-e greater than or equal to 300. Assuming a stepping-stone model of gene flow we considered the relative roles of gene flow, random genetic drift and selection to assess the possibilities for local adaptation. The requirements for local adaptation were fulfilled, but only adaptations resulting from strong selection were expected to occur at the level of individual populations. Adaptations resulting from weak selection were more likely to occur on a regional basis, i.e. encompassing several populations. N-e appears to have declined recently in at least one of the studied populations, and the documented recent declines of many other anadromous brown trout populations may affect the persistence of local adaptation.
Admixture analysis and stocking impact assessment in brown trout (Salmo trutta), estimated with incomplete baseline data

Studies of genetic interactions between wild and domesticated fish are often hampered by unavailability of samples from wild populations prior to population admixture. We assessed the utility of a new Bayesian method, which can estimate individual admixture coefficients even with data missing from the populations contributing to admixture. We applied the method to analyse the genetic contribution of domesticated brown trout (Salmo trutta) in samples of anadromous trout from two stocked populations with no genetic data available before stocking. Further, we estimated population level admixture proportions by the mean of individual admixture coefficients. This method proved more informative than a multidimensional scaling analysis of individual-based genetic distances and assignment tests. The results showed almost complete absence of stocked, domesticated trout in samples of trout from the rivers. Consequently, stocking had little effect on improving fisheries. In one population, the genetic contribution by domesticated trout was small, whereas in the other population, some genetic impact was suggested. Admixture in this sample of anadromous trout despite absence of stocked domesticated trout could be because of introgression by domesticated trout adopting a resident life history.

General information

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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Bekkevold, D. (Intern), Mensberg, K. D. (Intern)
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  - Web of Science (2017): Indexed yes
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  - Scopus rating (2016): CiteScore 2.56 SJR 1.322 SNIP 1.163
  - Web of Science (2016): Indexed yes
  - BFI (2015): BFI-level 2
  - Scopus rating (2015): SJR 1.256 SNIP 1.051 CiteScore 2.22
  - Web of Science (2015): Indexed yes
  - BFI (2014): BFI-level 2
  - Scopus rating (2014): SJR 1.443 SNIP 1.379 CiteScore 2.6
  - Web of Science (2014): Indexed yes
  - BFI (2013): BFI-level 2
  - Scopus rating (2013): SJR 1.421 SNIP 1.081 CiteScore 2.25
  - ISI indexed (2013): ISI indexed yes
  - Web of Science (2013): Indexed yes
Brown trout (Salmo trutta) stocking impact assessment using microsatellite DNA markers

The genetic integrity of many salmonid fish populations is threatened by stocking of domesticated conspecifics. The purpose of this study was to assess the utility of microsatellite DNA markers for detecting loss of genetic diversity in hatchery strains, for estimating their genetic relationships, and for monitoring the genetic impact of stocking activity on wild populations of salmonid fishes. Brown trout from ten hatchery strains, one supportive breeding "strain," and five wild populations were screened for variation at eight loci. In most hatchery strains, genetic variation was comparable to that of wild populations, but three strains showed loss of allelic variation. In six of the hatchery strains, significant differentiation was observed between age classes. Genetic differentiation among all populations was moderate (F-ST = 0.065, p(ST) = 0.076), and only a minor part of genetic diversity was distributed between the wild and hatchery populations. We assessed whether wild populations were introgressed by stocked hatchery trout by performing assignment tests to determine population of origin and estimating maximum potential introgression rates. The results suggested that genetic introgression by hatchery trout had occurred for only two of the five populations potentially influenced by stocking. In one of these two rivers, microsatellite data obtained from a limited number of old scale samples indicated that individuals from the original population were genetically divergent from those of the present population, suggesting that extinction of the original population had taken place. The study demonstrates that microsatellite analysis provides a useful tool for distinguishing heavily introgressed populations from those unaffected by stocking. The information can be used to assist in (1) prioritizing populations for conservation and (2) the choice of wild populations to be used as sources for the reintroduction of salmonids in areas where local, indigenous gene pools have been extirpated.
Genetic monitoring of supportive breeding in brown trout (Salmo trutta L.), using microsatellite DNA markers

Stocking with offspring of local wild fish, so-called supportive breeding, is often advocated as an alternative to stocking domesticated fish. However, it is important to ensure that supportive breeding does not result in inbreeding and loss of genetic variability. We analysed eight microsatellite loci in samples of wild and hatchery-reared brown trout (Salmo trutta) from three populations subject to supportive breeding. For calibrating statistical procedures, we included two test samples of reared offspring for which the precise number of parent fish was known and a sample from a further wild reference population. Three different statistical procedures were used to detect population bottlenecks and loss of variability: (i) a randomization test for comparing allelic diversity between samples; (ii) estimates of effective number of breeders from gametic-phase disequilibrium; and (iii) a test for assessing population bottlenecks based on detecting deviations from mutation-drift equilibrium. All three procedures were useful but they also exhibited different strengths and limitations, with the test for population bottlenecks probably being the single most useful procedure for routine monitoring. In two populations subject to supportive breeding, there were strong indications of reduced effective population sizes, and significant genetic differentiation was observed between different samples from the same population.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Ruzzante, D. (Ekstern), Bouza, C. (Ekstern), Mensberg, K. D. (Intern)
Pages: 2130-2139
Publication date: 2000
Main Research Area: Technical/natural sciences
Microsatellite and mitochondrial DNA polymorphism reveals life history dependent interbreeding between hatchery and wild brown trout (Salmo trutta L.)

The effects of stocking hatchery trout into wild populations were studied in a Danish river, using microsatellite and mitochondrial DNA (mtDNA) markers. Baseline samples were taken from hatchery trout and wild trout assumed to be unaffected by previous stocking. Also, samples were taken from resident and sea trout from a stocked section of the river. Genetic differentiation between the hatchery strain and the local wild population was modest (microsatellite $F_{ST} = 0.06$).

Using assignment tests, more than 90% of individuals from the baseline samples were classified correctly. Assignment tests involving samples from the stocked river section suggested that the contribution by hatchery trout was low among sea trout (<7%), but high (46%) among resident trout. Hybrid index analysis and a high percentage of mtDNA haplotypes specific to indigenous trout observed among resident trout that were assigned to the hatchery strain suggested that interbreeding took place between hatchery and wild trout. The latter result also indicated that male hatchery trout contributed more to interbreeding than females. We suggest that stronger selection acts against stocked hatchery trout that become anadromous compared to hatchery trout that become resident. As most resident trout are males this could also explain why gene flow from hatchery to wild trout appeared to be male biased. The results show that even despite modest differentiation at neutral loci domesticated trout may still perform worse than local populations and it is important to be aware of differential survival and reproductive success both between life-history types and between sexes.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Ruzzante, D. (Ekstern), Eg Nielsen, E. (Intern), Mensberg, K. D. (Intern)
Pages: 583-594
Publication date: 2000
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology
Volume: 9
Postglacial recolonization patterns and genetic relationships among whitefish (Coregonus sp.) populations in Denmark, inferred from mitochondrial DNA and microsatellite markers

The genetic relationships among morphologically and geographically divergent populations of whitefish (genus: Coregonus) from Denmark and the Baltic Sea region were studied by analysis of microsatellites and polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) analysis of mitochondrial DNA (mtDNA) segments. The endangered North Sea houting (classified as C. oxyrhynchus) differs morphologically and physiologically from other Danish whitefish (C. lavaretus). However, limited divergence of North Sea houting was observed both at the level of mtDNA and microsatellites. The implications of these results for the conservation status of North Sea houting are discussed in the light of current definitions of evolutionary significant units. Both mtDNA and microsatellite data indicated that postglacial recolonization by C. lavaretus in Denmark was less likely to have taken place from the Baltic Sea. Instead, the data suggested a recent common origin of all Danish whitefish populations, including North Sea houting, probably by recolonization via the postglacial Elbe River system. Estimates of genetic differentiation among populations based on mtDNA and microsatellites were qualitatively different. In addition, for both classes of markers analyses of genetic differentiation yielded different results, depending on whether molecular distances between alleles or haplotypes were included.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology
Authors: Hansen, M. M. (Intern), Mensberg, K. D. (Intern), Berg, S. (Intern)
Pages: 239-252
Publication date: 1999
Main Research Area: Technical/natural sciences

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Journal: Molecular Ecology
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Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
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BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.068 SNIP 1.705 CiteScore 5.36
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.469 SNIP 1.823 CiteScore 5.56
ISI indexed (2011): ISI indexed yes
Genetic differentiation and relationship between genetic and geographical distance in Danish sea trout (Salmo trutta L.) populations

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Mensberg, K. D. (Intern)
Pages: 493-504
Publication date: 1998
Main Research Area: Technical/natural sciences

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Journal: Heredity
Volume: 81
Issue number: 5
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Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.56 SJR 2.03 SNIP 1.243
Improved primer sequences for the mitochondrial ND1, ND3/4 and ND5/6 segments in salmonid fishes: application to RFLP analysis of Atlantic salmon

New specific primers for the mtDNA segments ND1, ND3/4 and ND5/6 designed from the rainbow trout sequence, improved PCR amplification for salmonid fishes. RFLP analysis revealed restriction site variation for all three segments in Atlantic salmon. Eleven haplotypes were detected in a screening of 30 individuals from four European populations. (C) 1998 The Fisheries society of the British Isles.
Genetic variation within and among Danish brown trout (Salmo trutta L) hatchery strains, assessed by PCR-RFLP analysis of mitochondrial DNA segments

Eleven Danish brown trout hatchery strains were studied by PCR-RFLP analysis of the ND-I and ND-5/6 segments of the mitochondrial genome. For comparison, data from wild trout representing three Danish river systems also were included. Reduced variability in terms of nucleon diversity and number of haplotypes was observed in most hatchery strains. However, computer simulations showed that even with relatively large numbers of female spawners considerable loss of haplotypes could take place over time. Therefore, reduced variability in some of the strains did not necessarily indicate a critical loss of allelic Variation at nuclear loci. The genetic relationships among the strains were compared with information from hatchery managers on the origin of the strains. In one case, a strain supposed to be recently founded from wild trout appeared to be of a mixed wild and hatchery origin. Genetic differentiation among strains (Phi(ST) = 0.23) was of the same order of magnitude as that observed among wild Danish trout populations. However, minimal differentiation (Phi(ST) = 0.01) was observed among the four quantitatively most important strains, supplying 80% of all hatchery trout stocked in Denmark. (C) 1997 Elsevier Science B.V.

General information

State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Institute Management
Authors: Hansen, M. M. (Intern), Mensberg, K. D. (Intern), Rasmussen, G. (Intern), Simonsen, V. (Ekstern)
Pages: 15-29
Publication date: 1997
Main Research Area: Technical/natural sciences

Publication information

Journal: Aquaculture
Volume: 153
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Ratings:
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BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.75 SJR 1.101 SNIP 1.524
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.103 SNIP 1.254 CiteScore 2.12
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.002 SNIP 1.34 CiteScore 2.16
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.136 SNIP 1.3 CiteScore 2.18
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.212 SNIP 1.487 CiteScore 2.32
ISI indexed (2012): ISI indexed yes
The problem of sampling families rather than populations: Relatedness among individuals in samples of juvenile brown trout Salmo trutta L.  
In species exhibiting a nonrandom distribution of closely related individuals, sampling of a few families may lead to biased estimates of allele frequencies in populations. This problem was studied in two brown trout populations, based on analysis of mtDNA and microsatellites. In both samples mtDNA haplotype frequencies differed significantly between age classes, and in one sample 17 out of 18 individuals less than 1 year of age shared one particular mtDNA haplotype. Estimates of relatedness showed that these individuals most likely represented only three full-sib families. Older trout exhibiting the same haplotypes generally were not closely related.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Mensberg, K. D. (Intern)
Pages: 469-474
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Main Research Area: Technical/natural sciences

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BFI (2018): BFI-level 2
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Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
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BFI (2014): BFI-level 2
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BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
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Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.469 SNIP 1.823 CiteScore 5.56
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.513 SNIP 1.915
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.455 SNIP 2.024
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.326 SNIP 2.086
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.937 SNIP 1.918
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.932 SNIP 2.111
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.756 SNIP 2.099
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.544 SNIP 1.731
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.148 SNIP 1.564
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.964 SNIP 1.677
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 2.417 SNIP 1.816
Original language: English
Source: orbit
Source-ID: 225688
Founder effects and genetic population structure of brown trout (Salmo trutta) in a Danish river system
The influence of founder effects on the genetic population structure of brown trout (Salmo trutta) was studied in a small Danish river system. Samples of trout from seven locations were analysed by allozyme electrophoresis and mitochondrial DNA restriction fragment length polymorphism analysis. For comparison, allozyme data from other Danish trout populations and mtDNA data from two hatchery strains were included. Genetic differentiation among populations was found to be small but significant. Pairwise tests for homogeneity of allele and haplotype frequencies between samples showed that significance was predominantly due to a single population. In two of the locations studied, extinction-recolonization events had taken place. In one of the populations, founding had not resulted in divergence, while the other founded population was the one that had diverged significantly from the remaining populations. Computer simulations of the influence of founder effects on mitochondrial DNA differentiation and variability showed that the observed divergence could be due either to natural founder effects or to a genetic contribution by hatchery trout. However, the allozyme results pointed towards natural founder effects as the most likely explanation.
The marine and freshwater regions encompassing Skagerrak, Kattegat, Øresund and the North Sea are biologically highly productive and contain plentiful living aquatic resources that are important for the region. At the same time the coastal areas are densely populated and industrialized, fish and shellfish resources are heavily harvested, and waters are subject to pollution and eutrophication. The region is also markedly affected by the ongoing global warming, with sea temperature rising nearly 2 degrees C during the last 40 years. These environmental pressures call for investigations into the consequences for aquatic organisms, their potential for adapting to environmental changes, and for identifying management strategies that could mitigate deteriorating environmental conditions, using state-of-the-art methodology. Here, we will capitalize on the revolutionizing developments in genomics, electronic tagging and computer modelling to obtain insights on the ecology, evolution and management of aquatic biodiversity in the region.

The ØKS region harbours leading scientific environments within the aquatic, marine and genomic sciences that are complementary with respect to research and education and that would strongly benefit from better integration and networking. This proposal also aims to establish a research cluster and expand the number of active PhDs, postdocs and senior researchers within the region, thereby fostering an innovative research and educational network in the ØKS region.

This project is coordinated by DTU Aqua.

The project is funded by EU, InterReg (regional collaboration).

National Institute of Aquatic Resources
Section for Marine Living Resources
Institute of Marine Research
University of Gothenburg
Aarhus University
University of Oslo
The development of tools for tracing and evaluating the genetic impact of fish from aquaculture (AquaTrace) (38948)
The genetic changes associated with domestication in aquaculture pose an increasing threat to the integrity of native fish gene pools. Consequently, there is a bourgeoning need for the development of molecular tools to assess and monitor the genetic impact of escaped or released farmed fish. In addition, exploration of basic links between genetic differences among farmed and wild fish and differences in important life-history traits with fitness consequences are crucial prerequisites for designing biologically informed management strategies.

The project “AquaTrace” will establish an overview of current knowledge on aquaculture breeding, genomic resources and previous research projects for the marine species seabass, seabream and turbot. The project will apply cutting-edge genomic methods for the development of high-powered, cost-efficient, forensically validated and transferable DNA based tools for identifying and tracing the impact of farmed fish in the wild. Controlled experiments with wild and farmed fish and their hybrids will be conducted with salmon and brown trout as model organisms using advanced “common garden” facilities. These experiments will elucidate the fundamental consequences of introgression by pinpointing and assessing the effects on fitness of specific genomic regions.

Generated insights will form the basis of a risk assessment and management recommendations including suggestions for mitigation and associated costs. This information and the developed molecular tools will be available as open-access support to project participants and external stakeholders including the aquaculture industry. The project is expected to facilitate technology transfer to the aquaculture sector by promoting better tailored breeding practices and traceability throughout production chain. Overall this initiative will support the development of sustainable European aquaculture and provide “Good Environmental Status” in line with the Marine Strategy Framework Directive.

This project involved 21 partners and was coordinated by DTU Aqua.

The project is funded by EU, Framework Programme 7.

National Institute of Aquatic Resources
Section for Marine Living Resources
Havforskningsinstituttet
Università degli Studi di Padova
Universidad de Santiago de Compostela
Katholieke Universiteit
TRACE Wildlife Forensics Network Limited
European Commission - Joint Research Center
INRA Institut National de La Recherche Agronomique
Bangor University

Period: 01/11/2012 → 31/10/2016
Number of participants: 5
Research area: Population Genetics
The project had two main aims:
- To develop plans for ecosystem based and sustainable management of coastal stocks of cod in Skagerrak/Kattegat.
- To develop necessary scientific knowledge needed for a first pilot restoration of a locally extinct stock of cod.

The work in the project was highly multi-disciplinary and included aspects of law, policies and institutional rules, socio economy, genetics, ecology, physiology and behavioural ecology. The work was divided into 10 work packages and one work package responsible for coordination.

The different WPs addressed the following tasks:
- WP1: Genetic mapping of potential donor stocks of cod.
- WP2: Genetic characterization of extinct cod stocks in fjord areas of Skagerrak.
- WP3: Ecological inventory of fjords with and without cod, to establish the effect of local cod stocks on fjord ecosystems.
- WP4: Risk assessment in particular focusing on the risk of contamination of released cod larvae or juveniles that migrate into nearby stocks.
- WP5: Legal and institutional aspects of restoring fjord stocks of fish.
- WP6: Societal costs and values of cod restoration.
- WP7: Establishing production of cod juveniles, for tests of feeding and migration behaviours in relation to individual genotype.
- WP8: Developing a step-by-step plan for starting a pilot restoration, including applications for necessary permissions.
- WP9: Development of suggestions of management plans for existing or restored fjord stocks of cod.
- WP10: Synthesis and final report to stakeholders. (Scientific reports will be submitted for publication in scientific journals, in addition).
- WP11: Coordination, internal and external communication including project meetings.

The main results of the project were:
- Cod was present in very small stocks in fjords in eastern Skagerrak, as found from trawling of fish eggs during spawning period. The eggs found were identified as cod from genetic markers. Thus restoration should wait and instead all possible protection should be applied so that these tiny small groups of local spawning cod can increase in numbers over the years to come.
- Several of the fjords in Skagerrak/Kattegat have cod that genetically is a mix of North Sea cod and Kattegat cod. Some fjords along the Norwegian coast have genetically unique elements in the cod stocks.
- The Kattegat spawning stock should be a very important source for eastern Skagerrak cod populations, according to our oceanographic models.

The project was coordinated by Department of Biological and Environmental Science, University of Gothenburg.

This project was funded by EU, InterReg (regional collaboration).

National Institute of Aquatic Resources
Section for Marine Living Resources
University of Gothenburg
Institute of Marine Research
Lund University

Period: 01/07/2012 → 31/12/2014
Number of participants: 5
Research areas: Population Genetics & Marine Living Resources & Fisheries Management
Project participant:
Hansen, Jakob Hemmer (Intern)
Eg Nielsen, Einar (Intern)
Eastern-western Baltic cod: Improved management based on stock discrimination of eastern and western Baltic cod (Øst-Vesttorsk) (38989)

The aim of this project was to improve the management of western Baltic cod by incorporating stock identification routines in order to discriminate between eastern and western Baltic cod stocks. In recent years evidence from fishery patterns and otolith structures have indicated an increasing degree of mixing between the two cod stocks which up until 2013 were managed as two separate stocks. Changes in fishing pressure and patterns would therefore result in a risk for local depletion of the smaller western stock.

Stock identification methods were based on established approaches using genetic discrimination and otolith shape analysis, and improved by linking these methods. This method provides a tool to estimate the degree of stock mixing using the existing otolith archives. This approach documented an increase of eastern Baltic cod from 30% to > 80% in the eastern part of the western Baltic Sea management area. As a consequence of this stock mixing, a new procedure incorporating stock mixing on an annual basis was set in place in 2016, with the aim to improve stock exploitation and reduce the risk of local depletion. The knowledge gained also influenced recent management regulations, particularly a prolongation of spawning closer of the fishery in 2016.

The project was coordinated by Centre for Environment, Fisheries & Aquaculture Science, UK. The project was funded by the Danish Ministry of Food, Agriculture and Fisheries and the European Fisheries Fund (EFF).

National Institute of Aquatic Resources
Section for Marine Ecology and Oceanography
Cefas
Period: 27/06/2011 → 29/03/2013
Number of participants: 18
Research areas: Marine Populations and Ecosystem Dynamics & Marine Living Resources & Population Genetics & Fisheries Management

Genetic and genomic approaches to the study of Atlantic eels: Speciation, genetic population structure and footprints of selection (38875)
Anguillid eels, including European (Anguilla anguilla) and American eel (A. rostrata) have fascinated scientists for centuries. At the same time, their geographical distribution and life cycle make them highly suitable study objects to address fundamental issues in evolutionary biology related to speciation and adaptation.

In this project, we made use of unique samples of eel larvae collected in the Sargasso Sea during the Galathea 3 expedition. Novel genomic resources generated by 454 massively parallel sequencing and novel statistical methods were used for:
- testing if the two species represent sympatric speciation.
- analysing the demographic history of the species, comparing present declines to historical population declines.
- testing whether or not European eel is panmictic, despite widespread geographical distribution of adult eels in continental Europe and North Africa.
- testing whether the distribution of both species across subarctic to subtropical environments reflects extreme phenotypic plasticity or if footprints of temperature-related selection is evident at the genomic level.

Scientific papers reporting results generated from this project include:
- Als, Thomas Damm; Hansen, Michael Møller; Maes, Gregory E.; Castonguay, Martin; Riemann, Lasse; Aarestrup, Kim; Munk, Peter; Sparholt, Henrik; Hanel, Reinhold; Bernatchez, Louis. 2011. All roads lead to home: panmixia of European eel in the Sargasso Sea. Molecular Ecology, Vol. 20, 1333-1346.

The project was coordinated by Department of Biological Sciences, Aarhus University.
The project was funded by the Danish Council for Independent Research.

National Institute of Aquatic Resources
Section for Marine Living Resources
Aarhus University
Period: 01/01/2010 → 31/12/2012
Number of participants: 3
Research area: Population Genetics
Project participant:
Bekkevold, Dorte (Intern)
Mensberg, Karen-Lise Dons (Intern)
Project Manager, academic:
Als, Thomas Damm (Intern)