Genetic diversity and connectivity within *Mytilus* spp. in the subarctic and Arctic

Climate changes in the Arctic are predicted to alter distributions of marine species. However, such changes are difficult to quantify because information on present species distribution and the genetic variation within species is lacking or poorly examined. Blue mussels, *Mytilus* spp., are ecosystem engineers in the coastal zone globally. To improve knowledge of distribution and genetic structure of the *Mytilus edulis* complex in the Arctic, we analyzed 81 SNPs in 534 *Mytilus* spp. individuals sampled at 13 sites to provide baseline data for distribution and genetic variation of *Mytilus* mussels in the European Arctic. *Mytilus edulis* was the most abundant species found with a clear genetic split between populations in Greenland and the Eastern Atlantic. Surprisingly, analyses revealed the presence of *Mytilus trossulus* in high Arctic NW Greenland (77°N) and *Mytilus galloprovincialis* or their hybrids in SW Greenland, Svalbard, and the Pechora Sea. Furthermore, a high degree of hybridization and introgression between species was observed. Our study highlights the importance of distinguishing between congener species, which can display local adaptation and suggests that information on dispersal routes and barriers is essential for accurate predictions of regional susceptibility to range expansions or invasions of boreal species in the Arctic.

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University, University of Tromsø, Russian Academy of Sciences, University of Stirling
Authors: Mathiesen, S. S. (Intern), Thyrring, J. (Ekstern), Hansen, J. H. (Intern), Berge, J. (Ekstern), Sukhotin, A. (Ekstern), Leopold, P. (Ekstern), Bekaert, M. (Ekstern), Sejr, M. K. (Ekstern), Eg Nielsen, E. (Intern)
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Genome architecture enables local adaptation of Atlantic cod despite high connectivity

Adaptation to local conditions is a fundamental process in evolution; however, mechanisms maintaining local adaptation despite high gene flow are still poorly understood. Marine ecosystems provide a wide array of diverse habitats that frequently promote ecological adaptation even in species characterized by strong levels of gene flow. As one example, populations of the marine fish Atlantic cod (Gadus morhua) are highly connected due to immense dispersal capabilities but nevertheless show local adaptation in several key traits. By combining population genomic analyses based on 12K single-nucleotide polymorphisms with larval dispersal patterns inferred using a biophysical ocean model, we show that Atlantic cod individuals residing in sheltered estuarine habitats of Scandinavian fjords mainly belong to offshore oceanic populations with considerable connectivity between these diverse ecosystems. Nevertheless, we also find evidence for discrete fjord populations that are genetically differentiated from offshore populations, indicative of local adaptation, the degree of which appears to be influenced by connectivity. Analyses of the genomic architecture reveal a significant overrepresentation of a large ~5 Mb chromosomal rearrangement in fjord cod, previously proposed to comprise genes critical for the survival at low salinities. This suggests that despite considerable connectivity with offshore populations, local adaptation to fjord environments may be enabled by suppression of recombination in the rearranged region. Our study provides new insights into the potential of local adaptation in high gene flow species within fine geographical scales and highlights the importance of genome architecture in analyses of ecological adaptation. This article is protected by copyright. All rights reserved.

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Conserved structure and expression of hsp70 paralogs in teleost fishes

The cytosolic 70 KDa heat shock proteins (Hsp70s) are widely used as biomarkers of environmental stress in ecological and toxicological studies in fish. Here we analyze teleost genome sequences to show that two genes encoding inducible hsp70s (hsp70-1 and hsp70-2) are likely present in all teleost fish. Phylogenetic and synteny analyses indicate that hsp70-1 and hsp70-2 are distinct paralogs that originated prior to the diversification of the teleosts. The promoters of both genes contain a TATA box and conserved heat shock elements (HSEs), but unlike mammalian HSP70s, both genes contain an intron in the 5′ UTR. The hsp70-2 gene has undergone tandem duplication in several species. In addition, many other teleost genome assemblies have multiple copies of hsp70-2 present on separate, small, genomic scaffolds. To verify that these represent poorly assembled tandem duplicates, we cloned the genomic region surrounding hsp70-2 in Fundulus heteroclitus and showed that the hsp70-2 gene copies that are on separate scaffolds in the genome assembly are arranged as tandem duplicates. Real-time quantitative PCR of F. heteroclitus genomic DNA indicates that four copies of the hsp70-2 gene are likely present in the F. heteroclitus genome. Comparison of expression patterns in F. heteroclitus and Gasterosteus aculeatus demonstrates that hsp70-2 has a higher fold increase than hsp70-1 following heat shock in gill but not in muscle tissue, revealing a conserved difference in expression patterns between isoforms and tissues. These data indicate that ecological and toxicological studies using hsp70 as a biomarker in teleosts should take this complexity into account.
Evaluation of otolith shape as a tool for stock discrimination in marine fishes using Baltic Sea cod as a case study

In the Western Baltic Sea two genetically distinct cod stocks "Eastern Baltic cod" and "Western Baltic cod" occur with considerable mixing of stocks. In this study we evaluated the applicability of otolith shape analysis for classification of individuals caught in the mixed stock cod fishery, using SNP (single nucleotide polymorphism) based genetic assignment of otolith shape baselines. We further developed a management approach for mixed stock assignment by robust stochastic baseline selection and posterior bias correction by individual reassignment of the least likely classifications into the alternative stock. Classification criteria selected by Monte Carlo runs of Linear Discriminant Analysis were captured by otolith area and 20 Elliptic Fourier Descriptors of primarily low frequency harmonics. Classification success was considerably lower when using a baseline of spawning individuals only, compared to the better spatial coverage of a combined baseline also including genotyped individuals from the mixed stock area. Furthermore, the inclusion of genotyped individuals balanced the baseline size composition and to a large extent removed a strong size related bias in classification success. These results demonstrate the interplay of environmental, ontogenetic and genetic influences on otolith shape, which complicates the application of otolith shape for stock discrimination in mixed-stock scenarios. Rigorous genetic validation and further studies on the temporal dynamics of shape formation are necessary.

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Authors: Hüssy, K. (Intern), Mosegaard, H. (Intern), Albertsen, C. M. (Intern), Eg Nielsen, E. (Intern), Hansen, J. H. (Intern), Eero, M. (Intern)
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Scopus rating (2014): SJR 1.105 SNIP 1.312 CiteScore 2.17
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Historical DNA documents long distance natal homing in marine fish

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Greenland Climate Research Centre, Stanford University, Greenland Institute of Natural Resources, Aarhus University
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Spatio-temporal trends in stock mixing of eastern and western Baltic cod in the Arkona Basin and the implications for recruitment

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Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Ecosystem based Marine Management, Section for Marine Living Resources, GEOMAR - Helmholtz Centre for Ocean Research Kiel
Authors: Hüssy, K. (Intern), Hinrichsen, H. (Ekstern), Eero, M. (Intern), Mosegaard, H. (Intern), Hansen, J. H. (Intern), Lehmann, A. (Ekstern), Lundgaard, L. S. (Intern)
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Web of Science (2010): Indexed yes
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Variability and connectivity of plaice populations from the Eastern North Sea to the Baltic Sea, part II. Biological evidence of population mixing

A multi-disciplinary study was conducted to clarify stock identity and connectivity patterns in the populations of European plaice (Pleuronectes platessa) in the Skagerrak-Kattegat transition area between the Eastern North Sea and the Baltic Sea. Five independent biological studies were carried out in parallel. Genetic markers suggested the existence of different genetic populations in the transition area. Growth backcalculation with otoliths resulted in significant although limited differences in growth rates between North Sea and Skagerrak, indicating weak differentiation or important mixing. Hydrogeographical drift modelling suggested that some North Sea juveniles could settle along the coast line of the Skagerrak and the Kattegat. Tagging data suggested that both juveniles and adult fish from the North Sea perform feeding migrations into Skagerrak in summer/autumn. Finally, survey data suggested that Skagerrak also belongs to the area distribution of North Sea plaice. The outcomes of the individual studies were then combined into an overall synthesis. The existence of some resident components was evidenced, but it was also demonstrated that North Sea plaice migrate for feeding into Skagerrak and might constitute a large share of the catches in this area. The mixing of different populations within a management area has implications for stock assessment and management. Choice must be made to either lump or split the populations, and the feasibility and constraints of both options are discussed. The outcomes of this work have directly influenced the management decisions in 2015.
Fishing and climate change impact the demography of marine fishes, but it is generally ignored that many species are made up of genetically distinct locally adapted populations that may show idiosyncratic responses to environmental and anthropogenic pressures. Here, we track 80 years of Atlantic cod (Gadus morhua) population dynamics in West Greenland using DNA from archived otoliths in combination with fish population and niche based modeling. We document how the interacting effects of climate change and high fishing pressure lead to dramatic spatiotemporal changes in the proportions and abundance of different genetic populations, and eventually drove the cod fishery to a collapse in the early 1970s. Our results highlight the relevance of fisheries management at the level of genetic populations under future scenarios of climate change.
From regionally predictable to locally complex population structure in a freshwater top predator: River systems are not always the unit of connectivity in Northern Pike Esox lucius

Contemporary genetic diversity is the product of both historical and contemporary forces, such as climatic and geological processes affecting range distribution and continuously moulded by evolutionary forces selection, gene flow and genetic drift. Predatory freshwater fishes, such as Northern Pike Esox lucius, commonly exhibit small population sizes, and several local populations are considered endangered. Pike inhabit diverse habitat types, including lakes, rivers and brackish marine waters, thus spanning from small isolated patches to large open marine systems. However, pike population structure from local to regional scales is relatively poorly described, in spite of its significance to developing conservation measures. We analysed microsatellite variation in a total of 1185 North European pike from 46 samples collected across both local and regional scales, as well as over time, to address two overarching questions: Is pike population structure associated with local and/or regional connectivity patterns, and which factors likely have the main influence on the contemporary distribution of genetic diversity? To answer this, we combined estimators of population diversity and structure to assess evidence of whether populations within (i) habitats, (ii) drainage systems and (iii) geographical regions are closer related than among these ranges, and whether patterns are temporally stable. Contrasting previous predictions that genetic drift obscures signals of postglacial colonisation history, we identified clear regional differences in population genetic signatures, suggesting a major effect of drainage divides on colonisation history and connectivity. However, several populations deviated from the general pattern, showing that local processes may be complex and need to be examined case-by-case.
Gene-associated markers can assign origin in a weakly structured fish, Atlantic herring

Regulations on the exploitation of populations of commercially important fish species and the ensuing consumer interest in sustainable products have increased the need to accurately identify the population of origin of fish and fish products. Although genomics-based tools have proven highly useful, there are relatively few examples in marine fish displaying accurate origin assignment. We synthesize data for 156 single-nucleotide polymorphisms typed in 1039 herring, Clupea harengus L., spanning the Northeast Atlantic to develop a tool that allows assignment of individual herring to their regional origin. We show the method's suitability to address specific biological questions, as well as management applications. We analyse temporally replicated collections from two areas, the Skagerrak (n = 81, 84, 66) and the western Baltic (n = 52, 52). Both areas harbour heavily fished mixed-origin stocks, complicating management issues. We report novel genetic evidence that herring from the Baltic Sea contribute to catches in the North Sea, and find support that western Baltic feeding aggregations mainly constitute herring from the western Baltic with contributions from the Eastern Baltic. Our study describes a general approach and outlines a database allowing individual assignment and traceability of herring across a large part of its East Atlantic distribution.
Managing population mixing; genetics supported stock splitting in Atlantic cod

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, Section for Ecosystem based Marine Management
Authors: Hansen, J. H. (Intern), Hüssy, K. (Intern), Huwer, B. (Intern), Mosegaard, H. (Intern), Eero, M. (Intern)
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MSC certification of plaice fisheries in area IIIa: Basic investigations and development of a management plan

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Authors: Hansen, J. H. (Intern), Ulrich, C. (Intern), Boje, J. (Intern), Christensen, A. (Intern), Degel, H. (Intern), Hüssy, K. (Intern), Worsøe Clausen, L. (Intern)
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Optimal bæredygtig udnyttelse af tilgængelige torskebestande for dansk fiskeri

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Authors: Eero, M. (Intern), Hansen, J. H. (Intern), Hüsey, K. (Intern), Huwer, B. (Intern), Berg, C. W. (Intern), Mariani, P. (Intern), Mosegaard, H. (Intern), Nielsen, A. (Intern), Nielsen, E. (Intern), Rindorf, A. (Intern), Ulrich, C. (Intern), Vinther, M. (Intern), Worsøe Clausen, L. (Intern)
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Oxygen minimum zone induced rapid temporal fluctuations of Eastern Baltic cod genetic diversity

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Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, Johann Heinrich von Thünen-Institute, Leibniz Institute of Marine Sciences
Authors: Dierking, J. (Ekstern), von Dewitz, B. (Ekstern), Elsbernd, L. (Ekstern), Schultz, H. (Ekstern), Bracamonte, S. (Ekstern), Hüsey, K. (Intern), Hansen, J. H. (Intern), Krumme, U. (Ekstern), Oeberst, R. (Ekstern), Hinrichsen, H. (Ekstern), Reusch, T. (Ekstern)
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Stock mixing of eastern and western Baltic cod in SD 24

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Authors: Hüsey, K. (Intern), Mosegaard, H. (Intern), Albertsen, C. M. (Intern), Hansen, J. H. (Intern), Eero, M. (Intern)
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The history of cod in Greenland: A major fishery collapse explained by archived DNA

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management, University of Fribourg
Conserving marine biodiversity: insights from life-history trait candidate genes in Atlantic cod (Gadus morhua)  
Recent technological developments have facilitated an increased focus on identifying genomic regions underlying adaptive trait variation in natural populations, and it has been advocated that this information should be important for designating population units for conservation. In marine fishes, phenotypic studies have suggested adaptation through divergence of life-history traits among natural populations, but the distribution of adaptive genetic variation in these species is still relatively poorly known. In this study, we extract information about the geographical distribution of genetic variation for 33 single nucleotide polymorphisms (SNPs) associated with life-history trait candidate genes, and compare this to variation in 70 putatively neutral SNPs in Atlantic cod (Gadus morhua). We analyse samples covering the major population complexes in the eastern Atlantic and find strong evidence for nonneutral levels and patterns of population structuring for several of the candidate gene-associated markers, including two SNPs in the growth hormone 1 gene. Thus, this study aligns with findings from phenotypic studies, providing molecular data strongly suggesting that these or closely linked genes are under selection in natural populations of Atlantic cod. Furthermore, we find that patterns of variation in outlier markers do not align with those observed at selectively neutral markers, and that outlier markers identify conservation units on finer geographical scales than those revealed when analysing only neutral markers. Accordingly, results also suggest that information about adaptive genetic variation will be useful for targeted conservation and management in this and other marine species.
Implications of stock recovery for a neighbouring management unit: experience from the Baltic cod

Cod in the Baltic Sea is assessed and managed as two separate stocks, i.e. eastern and western Baltic cod. The eastern Baltic cod has recently started to recover after several decades of severe depletion. In the present study, we suggest that the recovery of the eastern Baltic cod population has also substantially increased cod abundance in a specific area of the adjacent western Baltic management unit. This is investigated through long time-series of spatially resolved stock assessment data supplemented by genetic analyses of origin of the cod currently found in the transition area between the two populations. Due to immigrating cod from the east, there are currently large spatial differences in cod abundance and mean weight in the western Baltic management unit that raise new management concerns. First, the high abundance of cod of eastern origin found in the western Baltic management unit can mask the relatively poor state of the western Baltic cod population. Second, the current fishing mortality estimates for the entire western Baltic management unit, used as basis for fisheries management, are difficult to interpret as these are highly influenced by mixing of biological populations and the spatial distribution of fisheries.

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Web of Science (2015): Indexed yes
Learning from the past and stepping into the future: Population dynamics of Atlantic cod (Gadus morhua) revealed by historical DNA

Marine fish biodiversity is often highly variable in space and time, and the additional impacts of human exploitation and climate change might greatly affect the survival of many organisms within the ocean. Dramatic changes in the abundance of many fish populations have been widely observed over time together with shifting distributional range. However, it is known that population diversity or biocomplexity underpins ecosystem functioning and productivity, and stabilizes ecosystem processes and services. Thus, preserving intraspecific genetic diversity is of paramount importance for successful management and conservation of marine fish. The present thesis uses a spatiotemporal population genetic approach to examine historical dynamics of Atlantic cod populations (Gadus morhua) in Greenland and to elucidate how they have differentially responded to intense fishing pressure and environmental changes over the past century. Utilizing unique collections of archived fish samples, the overarching goals of this PhD project were to (1) examine the temporal stability of population structure of cod, (2) disentangle the population dynamics and how they have responded to intense fishing and environmental variability, and (3) understand important patterns of population connectivity. The thesis opens with a general introduction which briefly describes the historical and recent perception of world fisheries resources in human society (Chapter 1). The following chapters review relevant knowledge and methodological issues which have provided a critical rationale for addressing the research questions in this work. Chapter 2 emphasizes the importance of recognizing complex population structure in classical marine fish to reach effective management goals. Chapter 3 defines the most important drivers of genetic variation, and how these can generate detrimental demographic and evolutionary effects in marine fish populations. Chapter 4 presents the field of fisheries
genetics, giving particular emphasis on genetic stock identification and retrospective genetic monitoring. Subsequently, a collection of manuscripts is provided. The different studies have revealed (Paper 1) complex and dynamic interactions of four genetically distinct populations of cod, (Paper 2) that the different populations exhibited dramatic spatiotemporal changes in abundance and distribution and responded markedly different to historical commercial fishing and recent increases of ocean temperatures, (Paper 3) historical fish tags as a useful source of DNA for conducting retrospective genetic analysis, and (Paper 4) long-distance natal homing in cod. Overall, this thesis provides unprecedented insights into the population dynamics of Atlantic cod at the northern margin of its distribution. It illustrates how temporally spaced DNA samples offer a unique opportunity for disentangling the effects of primary forces shaping marine fish populations accumulated over decades or even a century. Of particular note, Paper 1, 2 and 4 represent some of the first concrete examples of how spatiotemporal data delivered by geneticists can be successfully applied in current fisheries management schemes.

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Authors: Bonanomi, S. (Intern), Eg Nielsen, E. (Intern), Hansen, J. H. (Intern)
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**Population genomics of marine fishes: next generation prospects and challenges**
Over the past few years, technological advances have facilitated giant leaps forward in our ability to generate genome-wide molecular data, offering exciting opportunities for gaining new insights into the ecology and evolution of species where genomic information is still limited. Marine fishes are valuable organisms for advancing our understanding of evolution on historical and contemporary time scales, and here we highlight areas in which research on these species is likely to be particularly important in the near future. These include possibilities for gaining insights into processes on ecological time scales, identifying genomic signatures associated with population divergence under gene flow, and determining the genetic basis of phenotypic traits. We also consider future challenges pertaining to the implementation of genome-wide coverage through next-generation sequencing and genotyping methods in marine fishes. Complications associated with fast decay of linkage disequilibrium, as expected for species with large effective population sizes, and the possibility that adaptation is associated with both soft selective sweeps and polygenic selection, leaving complex genomic signatures in natural populations, are likely to challenge future studies. However, the combination of high genome coverage and new statistical developments offers promising solutions. Thus, the next generation of studies is likely to truly facilitate the transition from population genetics to population genomics in marine fishes. This transition will advance our understanding of basic evolutionary processes and will offer new possibilities for conservation and management of valuable marine resources.

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University
Authors: Hansen, J. H. (Intern), Therkildsen, N. O. (Intern), Pujolar, J. (Ekstern)
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The Baltic cod: A case study for testing stock discrimination based on otolith shape analysis in a mixed stock fishery

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Authors: Hüsey, K. (Intern), Mosegaard, H. (Intern), Hansen, J. H. (Intern), Eero, M. (Intern)
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The use of archived tags in retrospective genetic analysis of fish
Collections of historical tissue samples from fish (e.g. scales and otoliths) stored in museums and fisheries institutions are precious sources of DNA for conducting retrospective genetic analysis. However, in some cases only external tags used for documentation of spatial dynamics of fish populations have been preserved. Here we test the usefulness of fish tags as a source of DNA for genetic analysis. We extract DNA from historical tags from cod collected in Greenlandic waters between 1950 and 1968. We show that the quantity and quality of DNA recovered from tags is comparable to DNA from archived otoliths from the same individuals. Surprisingly, levels of cross-contamination do not seem to be significantly
higher in DNA from external (tag) than internal (otolith) sources. Our study therefore demonstrates that historical tags can be a highly valuable source of DNA for retrospective genetic analysis of fish
A genomic island linked to ecotype divergence in Atlantic cod

The genomic architecture underlying ecological divergence and ecological speciation with gene flow is still largely unknown for most organisms. One central question is whether divergence is genome-wide or localized in ‘genomic mosaics’ during early stages when gene flow is still pronounced. Empirical work has so far been limited, and the relative impacts of gene flow and natural selection on genomic patterns have not been fully explored. Here, we use ecotypes of Atlantic cod to investigate genomic patterns of diversity and population differentiation in a natural system characterized by high gene flow and large effective population sizes, properties which theoretically could restrict divergence in local genomic regions. We identify a genomic region of strong population differentiation, extending over approximately 20 cM, between pairs of migratory and stationary ecotypes examined at two different localities. Furthermore, the region is characterized by markedly reduced levels of genetic diversity in migratory ecotype samples. The results highlight the genomic region, or ‘genomic island’, as potentially associated with ecological divergence and suggest the involvement of a selective sweep. Finally, we also confirm earlier findings of localized genomic differentiation in three other linkage groups associated with divergence among eastern Atlantic populations. Thus, although the underlying mechanisms are still unknown, the results suggest that ‘genomic mosaics’ of differentiation may even be found under high levels of gene flow and that marine fishes may provide insightful model systems for studying and identifying initial targets of selection during ecological divergence.
Cod recovery as a new challenge for fisheries management: experience from the Baltic Sea

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Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, Institute Management
Authors: Eero, M. (Intern), Hüussy, K. (Intern), Mosegaard, H. (Intern), Hansen, J. H. (Intern), Bastardie, F. (Intern), Köster, F. (Intern)
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Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2013
Improved management based on stock identification of eastern and western Baltic cod

The objective of this project was to establish an empirically founded knowledge base for the sustainable exploitation of the western Baltic cod stock by including the complex stock structure and migration patterns.

Stock mapping: Extensive immigration of “Eastern” cod into the Arkona Basin (SD 24) within the “Western” cod’s management unit was documented using high-powered genetic tools. The majority (91%) of all spawning fish caught in SD 24 in 2011 were “Eastern” cod and only 9% were from the “Western” stock. The results suggest that the stock structure in the Arkona Basin is highly influenced by mixing of genetically separate stocks.

Trends in mixing: Since the 1980’s where cod in SD 24 consisted primarily of “Western” type, the proportion of “Eastern” cod has increased, particularly since 2005. Throughout that period, the immigration of “Eastern” cod into SD 24 consisted primarily of adult, older fish. The changes in biological characteristics (mean size at age, condition and maturity) observed in that area since 2005 are thus a direct consequence of the extensive immigration of “Eastern” cod. As no seasonal signals in stock mixing were observed, the immigration is not associated with a change in “Eastern” cod’s spawning behaviour.

Management: The stock mixing proportions were successfully implemented in DTU Aqua’s modeling framework for management scenarios. “Eastern” immigrants into SD 24 lead the management procedure to advice for higher TACs that enhance the pressure on the fishing mortality level in SD 22. The fishing mortality level in SD 22 in this situation will need to be lowered i.e. by allocating more effort and catch from SD 22 to SD 24. Higher landings are expected if effort is re-directed/re-allocated to SD 24, profiting from the “Eastern” immigrants. By lowering the fishing mortality in SD 22, the SSB in SD 22 is also preserved, which is assumed to be the main source of recruits for the whole “western” stock (i.e. SD 22 + SD 24). In conclusion: Within the frame of this project we showed that substantial immigration “Eastern” cod into SD 24 has occurred and that these stock dynamics should be incorporated in evaluations of future management plans.
were temporal outliers in the different populations and outliers from the 1928 to 1960 period showed almost complete stability during later decades. The contrasting microevolutionary trajectories among populations resulted in sequential shifts in spatial outliers, with no locus maintaining elevated spatial differentiation throughout the study period. Simulations of migration coupled with observations of temporally stable spatial structure at neutral loci suggest that population replacement or gene flow alone could not explain all the observed allele frequency variation. Thus, the genetic changes are likely to at least partly be driven by highly dynamic temporally and spatially varying selection. These findings have important implications for our understanding of local adaptation and evolutionary potential in high gene flow organisms and underscore the need to carefully consider all dimensions of biocomplexity for evolutionarily sustainable management.
Spatiotemporal SNP analysis reveals cryptic distribution shifts and signs of ongoing adaptation at the northern range margin for Atlantic cod

Accurate prediction of species distribution shifts in the face of climate change requires a sound understanding of population diversity and local adaptations. Previous modeling has suggested that global warming will lead to increased abundance of Atlantic cod (Gadus morhua) in the ocean around Greenland, but the dynamics of earlier abundance fluctuations are not well understood. We applied a retrospective spatiotemporal population genomics approach to examine the temporal stability of cod population structure in this region and to search for signatures of divergent selection over a 78-year period spanning major demographic changes. Analyzing >900 gene-associated single nucleotide polymorphisms in 847 individuals, we identified four genetically distinct groups that exhibited varying spatial distributions with considerable overlap and mixture. The genetic composition had remained stable over decades at some spawning grounds, whereas complete population replacement was evident at others. Observations of elevated differentiation in certain genomic regions are consistent with adaptive divergence between the groups, indicating that they may respond differently to environmental variation. Significantly increased temporal changes at a subset of loci also suggest that adaptation may be ongoing. These findings illustrate the power of spatiotemporal population genomics for revealing biocomplexity in both space and time and for informing future fisheries management and conservation efforts.
Main Research Area: Technical/natural sciences

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Relations
Activities:
Populationsgenetiske undersøgelser af torsk fra Vestgrønland
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Tilbage til fremtiden; DNA analyse af historiske samlinger af torske-øresten fra Grønland

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Eg Nielsen, E. (Intern), Therkildsen, N. O. (Intern), Hansen, J. H. (Intern), Hedeholm, R. (Ekstern), Grønkjær, P. (Ekstern)
Publication date: 2013
Event: Abstract from 17. Danske havforskermøde, Roskilde, Denmark.
Variability and connectivity of plaice populations from the Eastern North Sea to the Western Baltic Sea, and implications for assessment and management

An essential prerequisite of sustainable fisheries is the match between biologically relevant processes and management action. Various populations may however co-occur on fishing grounds, although they might not belong to the same stock, leading to poor performance of stock assessment and management. Plaice in Kattegat and Skagerrak have traditionally been considered as one stock unit. Current understanding indicates that several plaice components may exist in the transition area between the North Sea and the Baltic Sea. A comprehensive review of all available biological knowledge on plaice in this area is performed, including published and unpublished literature together with the analyses of commercial and survey data and historical tagging data. The results suggest that plaice in Skagerrak is closely associated with plaice in the North Sea, although local populations are present in the area. Plaice in Kattegat, the Belts Sea and the Sound can be considered a stock unit, as is plaice in the Baltic Sea. The analyses revealed great heterogeneity in the dynamics and productivity of the various local components, and suggested for specific action to maintain biodiversity.
Gene-associated markers provide tools for tackling illegal fishing and false eco-certification

Illegal, Unreported and Unregulated fishing has had a major role in the overexploitation of global fish populations. In response, international regulations have been imposed and many fisheries have been ‘eco-certified’ by consumer organizations, but methods for independent control of catch certificates and eco-labels are urgently needed. Here we show that, by using gene-associated single nucleotide polymorphisms, individual marine fish can be assigned back to population of origin with unprecedented high levels of precision. By applying high differentiation single nucleotide polymorphism assays, in four commercial marine fish, on a pan-European scale, we find 93-100% of individuals could be correctly assigned to origin in policy-driven case studies. We show how case-targeted single nucleotide polymorphism assays can be created and forensically validated, using a centrally maintained and publicly available database. Our results demonstrate how application of gene-associated markers will likely revolutionize origin assignment and become highly valuable tools for fighting illegal fishing and mislabelling worldwide.
Improving the assessment and management of the plaice stock complex between the North Sea and the Baltic Sea

Plaice in Kattegat and Skagerrak have traditionally been considered as one stock unit. However the collected information on biology and fishery in areas between the North and Baltic Seas suggest changes are needed in assessment units as well as in management areas. Plaice in Skagerrak (Division 20) is now considered to be closely associated with plaice in the North Sea and is proposed to be included in the North Sea plaice stock assessment, although it is recognized that local populations are present in the area. Therefore, specific management of the Skagerrak plaice is suggested. Plaice in Kattegat (Division 21), the Belts (Division 22), and the Sound (Division 23) is considered a stock unit and is proposed to be assessed as such. However, separate management by area is also suggested to assure the preservation of the local populations. Plaice in the Baltic (Divisions 24–32) is considered a stock unit and is proposed to be assessed and managed as such. Pragmatic options are suggested for empirical harvest control rules accounting for the dynamic of local abundance, using a survey-based biomass indicator. For the future, new scientific analyses should be developed to better inform the origin of the catches, provided that additional resources are allocated to the annual monitoring of different stocks and components. Such information would provide on-going quantitative information on the degree of mixing of the various components, potentially allowing a more accurate assessment, management, and conservation of the status of these
Optimization of fisheries resource exploitation in the Skagerrak (Oskar)

General information
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Bibliographical note
Work package contributions from Bo S. Andersen, Jakob H. Hansen, Karin Hüsey, Kasper Kristensen, Niels Madsen, Patrizio Mariani and Bjarné Stage
In co-operation with the Danish Fishermen’s Association
Source: orbit
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Publication: Research › Report – Annual report year: 2012

Where does the cod come from? Panels of gene-associated markers provide vastly improved origin assignment in Atlantic cod (Gadus morhua)

Methods for determining the geographical origin of individual fish are in high demand for fighting illegal, unreported, and unregulated (IUU) fishing and for independent control of catch certificates and “eco-labels”. Hitherto, genetic origin assignment of marine fish has been hampered by the general low levels of genetic differentiation among populations. By using a new concept of studying gene-associated single nucleotide polymorphisms (SNPs), we show that individual cod can be assigned back to population of origin with unprecedented high levels of precision. We assessed pan-European variation in more than 1200 gene-associated SNPs in cod and found that levels of differentiation for a subset of 132 SNPs was best explained by a model including directional selection. These high-differentiation SNPs were used for designing “minimum panels with maximum power” for a number of case studies relevant for controlling illegal fishing, ecolabels, and fisheries management. Our results demonstrate how application of gene-associated markers will probably revolutionize origin assignment in cod by providing faster, cheaper, and more reliable tools for origin assignment

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Organisations: National Institute of Aquatic Resources, Section for Population Ecology and Genetics, FishPopTrace Consortium
Adaptive evolution in Atlantic cod: global and regional geographical scales

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hemmer-Hansen, J. (Intern), Eg Nielsen, E. (Intern), Poulsen, N. A. (Ekstern), Loeschcke, V. (Ekstern), Moen, T. (Ekstern), Johansen, T. (Ekstern), Mittelholzer, C. (Ekstern), Taranger, G. (Ekstern), Ogden, R. (Ekstern), Carvalho, G. (Ekstern)
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Publication: Research › Poster – Annual report year: 2011

Application of SNPs for population genetics of nonmodel organisms: new opportunities and challenges
Recent improvements in the speed, cost and accuracy of next generation sequencing are revolutionizing the discovery of single nucleotide polymorphisms (SNPs). SNPs are increasingly being used as an addition to the molecular ecology toolkit in nonmodel organisms, but their efficient use remains challenging. Here, we discuss common issues when employing SNP markers, including the high numbers of markers typically employed, the effects of ascertainment bias and the inclusion of nonneutral loci in a marker panel. We provide a critique of considerations specifically associated with the application and population genetic analysis of SNPs in nonmodel taxa, focusing specifically on some of the most commonly applied methods.

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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Marine Living Resources, Royal Zoological Society of Scotland, University of Bologna, Katholieke Universiteit, Bangor University
Authors: Helyar, S. (Ekstern), Hansen, J. H. (Intern), Bekkevold, D. (Intern), Taylor, M. I. (Ekstern), Ogden, R. (Ekstern), Limborg, M. (Intern), Cariani, A. (Ekstern), Maes, G. E. (Ekstern), Diopere, E. (Ekstern), Carvalho, G. R. (Ekstern), Eg Nielsen, E. (Intern)
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Historical changes in population distribution and micro-evolution in response to climate variability: Retrospective genomic analysis of archived fish tissue collection

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Bonanomi, S. (Intern), Hansen, J. H. (Intern), Eg Nielsen, E. (Intern)
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Historical DNA reveals signatures of recent fisheries- or climate-induced evolution in Atlantic cod, Gadus morhua

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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Therkildsen, N. O. (Intern), Hansen, J. H. (Intern), Eg Nielsen, E. (Intern)
Publication date: 2011
Event: Poster session presented at Gordon Research Conference on Ecological & Evolutionary Genomics, Biddeford, Maine, USA.
Identification of single nucleotide polymorphisms in candidate genes for growth and reproduction in a nonmodel organism; the Atlantic cod, Gadus morhua

Recent technological developments have facilitated intensified searches for genetic markers under selection in nonmodel species. Here, we present an approach for the identification of candidate gene variation in nonmodel organisms. We report on the characterization of 82 single nucleotide polymorphisms (SNPs) and on the development of a specific genotyping assay for 30 SNPs in 18 candidate genes for growth and reproduction in Atlantic cod (Gadus morhua). These markers can be used for scanning natural populations for signatures of selection in both contemporary and archived historical samples, for example in retrospective studies assessing the effects of environmental changes, such as increasing temperatures, and selection imposed by high fishing pressure. Furthermore, these gene markers may be of interest to aquaculture, serving as a starting point for linking phenotypic traits important for productivity with genotypes and potentially be of use for marker-assisted selection in the future. This study demonstrates that the candidate gene approach is a valuable and targeted complement to the more random approach for discovering genetic variation in the genome and transcriptome applied through high throughput methods in nonmodel species.
Microgeographical population structure and adaptation in Atlantic cod Gadus morhua: spatio-temporal insights from gene-associated DNA markers

Recent technical advances have stimulated studies on spatial scales of adaptive genetic variation in marine fishes. However, very few studies have combined spatial and temporal sampling to investigate adaptive genetic structuring at local and microgeographical scales, i.e. scales at which neutral genetic markers have typically revealed very limited levels of population structure. In the present study we analyzed 92 gene-associated single-nucleotide polymorphism (SNP) markers in Atlantic cod Gadus morhua from several sampling sites within the North Sea and adjacent areas. To test for temporal stability, we included long- and short-term (i.e. from 24 to 38 and from 8 to 11 yr, respectively) temporally replicated samples from a subset of populations. As expected, we found very low levels of neutral genetic population structure (FST = 0.003). Three specific loci, however, showed highly elevated levels of genetic differentiation. Interestingly, these loci were identical to loci previously found to display signals of adaptive evolution on larger spatial scales. Analysis of historical samples revealed long-term temporally stable patterns of both neutral and adaptive divergence between some populations, indicating long-term temporal adaptive stability driven by strong local selection. In an environmentally dynamic area, on the other hand, patterns of genetic structuring were more variable. Overall, our results not only suggest separation of populations under both evolutionary and ecological paradigms, but also illustrate the usefulness of the spatio-temporal approach for making inferences about the dynamics and geographical distribution of adaptive genetic variation in natural populations.
Of fish and SNPs: The potential of genetics for traceability in European fisheries management

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Authors: Helyar, S. (Ekstern), Bekkevold, D. (Intern), Hansen, J. H. (Intern), Limborg, M. (Intern), Eg Nielsen, E. (Intern), Carvalho, G. R. (Ekstern)
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Using historical DNA to study fisheries-induced genetic change in Atlantic cod (Gadus morhua)

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Using historical DNA to study fisheries - induced genetic change in commercial fish stocks

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Authors: Therkildsen, N. O. (Intern), Hansen, J. H. (Intern), Eg Nielsen, E. (Intern)
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Using the candidate gene approach to study fisheries-induced evolution

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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Therkildsen, N. O. (Intern), Hansen, J. H. (Intern), Eg Nielsen, E. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
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Publication: Research › Poster – Annual report year: 2010
Genetic population structure of European sprat (Sprattus sprattus L.): differentiation across a steep environmental gradient in a small pelagic fish

Factors such as oceanographic retention, isolation by distance and secondary contact zones have, among others, been suggested to explain the low, but statistically significant, neutral population structure observed in many marine fishes. European sprat Sprattus sprattus is not known to display philopatric spawning behaviour or to exhibit local retention of eggs and larvae. It thus constitutes a good model for studying population structure in a characteristic small pelagic fish with high dispersal potential and an opportunistic life history. We analysed 931 specimens of sprat from nine spawning locations in and around the North- and Baltic Sea area and from a geographically distant population from the Adriatic Sea. Analyses of nine microsatellite loci revealed a sharp genetic division separating samples from the Northeastern Atlantic and the Baltic Sea (pairwise θ = 0.019–0.035), concurring with a steep salinity gradient. We found, at most, weak structure among samples within the Northeastern Atlantic region and within the Baltic Sea (pairwise θ = 0.001–0.009). The Adriatic Sea population was highly differentiated from all northern samples (pairwise θ = 0.071–0.092). Overall, the observed population structure resembles that of most other marine fishes studied in the North/Baltic Sea areas. Nevertheless, spatially explicit differences are observed among species, likely reflecting specific life-histories. Such fine-scale population structure should be taken into account, e.g. in ecosystem-based stock management.
Genomic signatures of local directional selection in a high gene flow marine organism, the Atlantic cod (Gadus morhua)

Background: Marine fishes have been shown to display low levels of genetic structuring and associated high levels of gene flow, suggesting shallow evolutionary trajectories and, possibly, limited or lacking adaptive divergence among local populations. We investigated variation in 98 gene-associated single nucleotide polymorphisms (SNPs) for evidence of selection in local populations of Atlantic cod (Gadus morhua L.) across the species distribution. Results: Our global genome scan analysis identified eight outlier gene loci with very high statistical support, likely to be subject to directional selection in local demes, or closely linked to loci under selection. Likewise, on a regional south/north transect of central and eastern Atlantic populations, seven loci displayed strongly elevated levels of genetic differentiation. Selection patterns among populations appeared to be relatively widespread and complex, i.e. outlier loci were generally not only associated with one of a few divergent local populations. Even on a limited geographical scale between the proximate North Sea and Baltic Sea populations four loci displayed evidence of adaptive evolution. Temporal genome scan analysis applied to DNA from archived otoliths from a Faeroese population demonstrated stability of the intra-population variation over 24 years. An exploratory landscape genetic analysis was used to elucidate potential effects of the most likely environmental factors responsible for the signatures of local adaptation. We found that genetic variation at several of the outlier loci was better correlated with temperature and/or salinity conditions at spawning grounds at spawning time than with geographic distance per se. Conclusion: These findings illustrate that adaptive population divergence may indeed be prevalent despite seemingly high levels of gene flow, as found in most marine fishes. Thus, results have important implications for our understanding of the interplay of evolutionary forces in general, and for the conservation of marine biodiversity under rapidly increasing evolutionary pressure from climate and fisheries induced changes in local environments.
Micro geographical population structure of cod Gadus morhua in the North Sea and west of Scotland: the role of sampling loci and individuals

We investigated potential microgeographical population structure among spatial and temporal samples of cod Gadus morhua L., collected in the northern North Sea and around Scotland, using microsatellite genetic markers. Results were highly dependent on the samples and microsatellite loci included. Analysis of molecular variance (AMOVA) revealed significant spatial (p = 0.04) and temporal (p = 0.02) variance when including samples of juveniles and the microsatellite Gmo 132, which is known to be subject to selection. However, neither spatial nor temporal variance components were significant (p = 0.15 and 0.23, respectively) after exclusion of juvenile samples and Gmo 132. Patterns of genetic differentiation showed a similar sensitivity to the sampling of loci. No apparent pattern was identified when only using suspected neutral microsatellites. In contrast, analysis of Gmo132 alone revealed a clear isolation of 2 samples collected at Viking and pairwise grouping of temporal adult samples from the same location. On a northeast Atlantic regional scale, inferences on local populations and patterns of population structuring were more robust to the inclusion of the microsatellite under selection. Our results demonstrate that, without cautious consideration of biased samples of individuals and loci, apparent microgeographical patterns of spatial genetic differentiation could be caused by sampling non-randomly distributed individuals of hitch-hiking selection at presumed neutral marker loci. However, while loci subject to selection may provide biased results in relation to identifying populations based on an evolutionary paradigm, they may prove valuable for separating populations on ecological time scales.
Population genomics of marine fishes: identifying adaptive variation in space and time

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Scopus rating (2011): SJR 3.469 SNIP 1.823 CiteScore 5.56
ISI indexed (2011): ISI indexed yes
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Web of Science (2010): Indexed yes
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Scopus rating (2009): SJR 3.455 SNIP 2.024
Web of Science (2009): Indexed yes
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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
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Adaptive differences in gene expression in European flounder (Platichthys flesus)

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Organisations: National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Larsen, P. F. (Intern), Eg Nielsen, E. (Intern), Williams, T. (Ekstern), Hansen, J. H. (Intern), Chipman, J. (Ekstern), Kruhoff, M. (Ekstern), Grønkjær, P. (Ekstern), George, S. (Ekstern), Dyrskjøt, L. (Ekstern), Loeschcke, V. (Ekstern)
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Adaptive divergence in a high gene flow environment: Hsc70 variation in the European flounder (Platichthys flesus L.)
Application of SNP's (Single Nucleotide Polymorphisms) for genetic stock identification in Atlantic cod (Gadus morhua L.)

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State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Hansen, J. H. (Intern), Moen, T. (Ekstern), Meldrup, D. (Intern)
Pages: ICES CM 2007/L:14
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES Council Meeting
ISSN (Print): 1015-4744
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Web of Science (2003): Indexed yes
Original language: English
Links:
Source: orbit
Source-ID: 226817
Publication: Research › Conference article – Annual report year: 2007

Evolutionary mechanisms shaping the genetic population structure of marine fishes; lessons from the European flounder (Platichthys flesus L.)

A number of evolutionary mechanisms have been suggested for generating low but significant genetic structuring among marine fish populations. We used nine microsatellite loci and recently developed methods in landscape genetics and coalescence-based estimation of historical gene flow and effective population sizes to assess temporal and spatial dynamics of the population structure in European flounder (Platichthys flesus L.). We collected 1062 flounders from 13 localities in the northeast Atlantic and Baltic Seas and found temporally stable and highly significant genetic differentiation among samples covering a large part of the species’ range (global F-ST = 0.024, P <0.0001). In addition to historical processes, a number of contemporary acting evolutionary mechanisms were associated with genetic structuring. Physical forces, such as oceanographic and bathymetric barriers, were most likely related with the extreme isolation of the island population at the Faroe Islands. A sharp genetic break was associated with a change in life history from pelagic to benthic spawners in the Baltic Sea. Partial Mantel tests showed that geographical distance per se was not related with genetic...
structuring among Atlantic and western Baltic Sea samples. Alternative factors, such as dispersal potential and/or environmental gradients, could be important for generating genetic divergence in this region. The results show that the magnitude and scale of structuring generated by a specific mechanism depend critically on its interplay with other evolutionary mechanisms, highlighting the importance of investigating species with wide geographical and ecological distributions to increase our understanding of evolution in the marine environment.

**General information**

State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, J. H. (Intern), Eg Nielsen, E. (Intern), Grønkjær, P. (Ekstern), Loeschcke, V. (Ekstern)
Pages: 3104-3118
Publication date: 2007
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Molecular Ecology
Volume: 16
Issue number: 15
ISSN (Print): 0962-1083
Ratings:
BFI (2018): BFI-level 2
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
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
Scopus rating (2004): SJR 2.827 SNIP 2.115
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 3.115 SNIP 2.131
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 2.813 SNIP 2.108
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.784 SNIP 2.099
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 2.664 SNIP 2.111
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 2.569 SNIP 2.102
Web of Science (1999): Indexed yes
Scopus rating (1998): SJR 2.462 SNIP 2.091
Web of Science (1998): Indexed yes
Scopus rating (1997): SJR 2.291 SNIP 2.091
Web of Science (1997): Indexed yes
Scopus rating (1996): SJR 2.182 SNIP 2.085
Web of Science (1996): Indexed yes
Scopus rating (1995): SJR 2.091 SNIP 2.079
Web of Science (1995): Indexed yes
Landscape genetics goes to sea

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Hansen, J. H. (Intern)
Pages: 6
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Biology
Volume: 6
Issue number: 3
ISSN (Print): 1478-5854
Ratings:
BFI (2018): BFI-level 2
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.61 SJR 3.425 SNIP 1.377
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.865 SNIP 1.566 CiteScore 4.46
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 4.026 SNIP 1.606 CiteScore 4.11
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.638 SNIP 2 CiteScore 4.07
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.387 SNIP 0.99 CiteScore 4.33
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.893 SNIP 1.207 CiteScore 4.66
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.197 SNIP 1.14
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.894 SNIP 1.333
What role for genomics in fisheries management and aquaculture?

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Wenne, R. (Ekstern), Boudry, P. (Ekstern), Hansen, J. H. (Intern), Lubieniecki, K. (Ekstern), Was, A. (Ekstern), Kause, A. (Ekstern)
Pages: 241-255
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Aquatic Living Resources
Volume: 20
Issue number: 3
ISSN (Print): 0990-7440
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.41 SJR 0.59 SNIP 0.743
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.747 SNIP 0.848 CiteScore 1.39
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.641 SNIP 0.905 CiteScore 1.25
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.547 SNIP 0.68 CiteScore 1.15
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.554 SNIP 0.618 CiteScore 1.19
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.628 SNIP 0.697 CiteScore 1.17
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.589 SNIP 0.545
Population structure and local adaptations in marine fishes

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, J. H. (Intern)
Number of pages: 173
Publication date: 2006

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Thesis_final_Jacob_HemmerHansen.pdf

Bibliographical note
Marine Ecology & Ecology and Genetics Department of Biological Sciences University of Aarhus and Department of Inland Fisheries Danish Institute for Fisheries Research

Population differentiation, local adaptation and speciation in marine fishes

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, J. H. (Intern)
Publication date: 2003

Publication information
Publisher: University of Aarhus and Danish Institute for Fisheries Research
Original language: English
Main Research Area: Technical/natural sciences
Projects:

Genomic analysis of DNA from archived shark jaws

National Institute of Aquatic Resources
Period: 15/12/2016 → 14/12/2019
Number of participants: 4
Phd Student:
Manuzzi, Alice (Intern)
Supervisor:
Hansen, Jakob Hemmer (Intern)
Ovenden, Jennifer (Ekstern)
Main Supervisor:
Eg Nielsen, Einar (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Forskningsrådsfinansiering
Project: PhD

Eastern Baltic cod - New knowledge of growth and mortality is the way to improved management advice (39366)
The aim of the project is to improve the knowledge and data basis for stock assessment and management for cod in the eastern Baltic Sea.

In later years, changes in growth and natural mortality of cod have presumably taken place and new knowledge on these parameters is essential for restoring analytical stock assessment for Eastern Baltic cod that is currently lacking. Improved knowledge on cod growth and mortality is therefore a prerequisite for being able to evaluate the stock status in relation to management targets and implement management plans that are built on quantitative stock assessment.

Ecological situation in the Baltic Sea has changed in later years, which requires updated biological information. This is done in the project using different approaches, bringing together expertise of different research areas. The approaches applied include molecular-genetic analyses of cod growth, bioenergetic modelling, and analyses of monitoring data on predation and condition/growth of cod. An important component of the project is cooperation with fishing industry to support tagging experiments of Baltic cod, to obtain updated estimates of cod growth.

Finally, the project combines the new knowledge on cod that becomes available from this and other relevant projects to ensure that the assessment of stocks status and management advice is based on best available scientific information.

This project is coordinated by DTU Aqua.

The project is funded by the Ministry of Environment and Food of Denmark and the European Maritime and Fisheries Fund (EMFF).

National Institute of Aquatic Resources
Section for Ecosystem based Marine Management
Danish Fishermen's Association

University of Copenhagen
Period: 15/08/2016 → 15/08/2018
Number of participants: 8
Research areas: Ecosystem based Marine Management & Fish Biology & Marine Populations and Ecosystem Dynamics & Population Genetics & Marine Living Resources & Fisheries Management
Project participant:
Storr-Paulsen, Marie (Intern)
Tomkiewicz, Jonna (Intern)
Genomic patterns and processes of population divergence in marine fishes
National Institute of Aquatic Resources
Period: 01/03/2016 → 28/02/2019
Number of participants: 3
Phd Student:
Le Moan, Alan (Intern)

Supervisor:
Bekkevold, Dorte (Intern)

Main Supervisor:
Hansen, Jakob Hemmer (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
Project: PhD

Sustainable management of Kattegat cod; Improved knowledge about stock components and migration (39346)
The Kattegat cod has been categorized as a data limited stock, mainly due to a large unallocated mortality, which may be
cauised by migration between Kattegat and neighbouring areas. In this project, we aim to improve our understanding of
migration patterns and mixing of different stock components within the Kattegat through a novel combination of genetic
and micro-chemical signatures for individual fish. Results from the project will feed directly into the ICES advisory process,
including a scheduled benchmark meeting in early 2017 where new procedures for stock assessment will be discussed.
As cod are also caught as bycatch in other fisheries, a more robust stock assessment for cod will also be important to
fisheries for other species under the landing obligation, which is scheduled for implementation in the Kattegat in 2017.

This project is coordinated by DTU Aqua.

The project is funded by the Ministry of Environment and Food of Denmark and the European Maritime and Fisheries
Fund (EMFF).

National Institute of Aquatic Resources
Section for Marine Living Resources

Danish Fishermen's Association
Period: 01/03/2016 → 28/02/2018
Number of participants: 7
Research areas: Population Genetics & Marine Living Resources & Fisheries Management
Project participant:
Hüssy, Karin (Intern)
Eero, Margit (Intern)
Thygesen, Uffe Høgsbro (Intern)
Storr-Paulsen, Marie (Intern)
Meldrup, Dorte (Intern)
Levinsky, Svend-Erik (Intern)
Project Coordinator:
Hansen, Jakob Hemmer (Intern)

Expertise in marine and aquatic ecology and genomics for sustainable management of fish and shellfish in Skagerrak-
Kattegat-Øresund (MarGen) (39301)
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.

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
Norwegian Institute for Water Research
University of Agder
Period: 01/07/2015 → 30/06/2018
Number of participants: 8
Research areas: Population Genetics & Freshwater Fisheries and Ecology
Project participant:
Bekkevold, Dorte (Intern)
Aarestrup, Kim (Intern)
Mensberg, Karen-Lise Dons (Intern)
Meldrup, Dorte (Intern)
Mikkelsen, Jørgen Skole (Intern)
Phd Student:
Kristensen, Martin Lykke (Intern)
Le Moan, Alan (Intern)
Project Manager, academic:
Hansen, Jakob Hemmer (Intern)
Project CodStory (39308)
The main objective of this project is to examine spatiotemporal genetic and trophic change of North Atlantic cod populations over the last millennium, a period of significant temperature fluctuations. This project addresses several important issues in current conservation and resource management, for example, population size fluctuations, migrations and distribution shifts of Atlantic cod in relation to climate change. The project will provide long term data (approximately 1100 years) on the genetic population structure, adaptive genetic change and trophic ecology of a single species, the Atlantic cod, expanding the application of cod as a model species in historical eco-genetics.

Specific research questions include:
- How have climate fluctuations effected migration, gene flow, distributional shifts and interactions of Atlantic cod populations in the North Atlantic?
- How have climate fluctuations affected the trophic niche of Atlantic cod through ecological regime shifts and change in Atlantic cod feeding migrations?
- How have climate fluctuation effected the trophic niche and trophic position of seabirds and do directional changes in seabird isotope values, together with isotope values from Atlantic cod, indicate specific ecosystem effects?
- How has climate change affected the adaptive evolution of Atlantic cod at centennial scales as revealed by spatiotemporal SNP analysis with broad genomic coverage?
This project is coordinated by the University of Iceland.

The project is funded by the Icelandic Research Council.

National Institute of Aquatic Resources
Section for Marine Living Resources
University of Iceland
University of Saskatchewan
City University of New York
National Museum of the Faroe Islands

Period: 01/03/2015 → 28/01/2018
Number of participants: 2
Research area: Population Genetics

Project participant:
Hansen, Jakob Hemmer (Intern)
Eg Nielsen, Einar (Intern)

Tracing the dynamics of mixed stocks in a transition area: Herring in Skagerrak-Kattegat and Western Baltic

National Institute of Aquatic Resources
Period: 01/12/2013 → 04/06/2014
Number of participants: 6
Phd Student:
Worsøe Clausen, Lotte (Intern)
Supervisor:
Bekkevold, Dorte (Intern)
Main Supervisor:
Mosegaard, Henrik (Intern)
Examiner:
Hansen, Jakob Hemmer (Intern)
Grønkjær, Peter (Ekstern)
Hammer, Cornelius (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: §15 Re-enrolment
Project: PhD

Adaptive differences between wild and farmed trout: linking traits with genomic variation

National Institute of Aquatic Resources
Period: 01/11/2013 → 15/10/2017
Number of participants: 6
Phd Student:
Frank-Gopolos, Thomas (Intern)
Supervisor:
Eg Nielsen, Einar (Intern)
Main Supervisor:
Bekkevold, Dorte (Intern)
Examiner:
Hansen, Jakob Hemmer (Intern)
Helyar, Sarah J. (Ekstern)
Jensen, Lasse Fast (Ekstern)

Financing sources
Source: Internal funding (public)
Optimal sustainable use of cod stocks accessible for Danish fisheries (DEL-TORSK) (39147)
Optimal sustainable utilization of cod stocks that contain several biological sub-populations requires taking population structure into account in stock assessment and management. The aim of this project was to develop scientific basis for cod management decisions in the North Sea and the Baltic that takes biological units of cod and their dynamics into account.

Methodological challenges concerning advising on stocks that contain sub-populations with differences in dynamics and biological parameters are common for North Sea and the Baltic. Therefore, the project considered both seas, in terms of developing methodological basis for addressing population structure in management advice. The results were presented at ICES benchmarks for North Sea and Baltic Sea cod in 2015, and used to developing further the management basis for optimal use of cod stocks.

The project included mapping of distribution of sub-populations using genetic analyses and modelling of transport of early life stages. These results were combined with existing knowledge on cod population structure both in the Baltic and North Sea, to identify distribution areas of sub populations. This information was then incorporated in area-specific stock assessment analyses.

This project was coordinated by DTU Aqua.

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 Ecosystem based Marine Management
Period: 17/07/2013 → 30/04/2015
Number of participants: 8
Research areas: Ecosystem based Marine Management & Marine Populations and Ecosystem Dynamics & Population Genetics & Fish Biology & Marine Living Resources & Fisheries Management
Project participant:
Hansen, Jakob Hemmer (Intern)
Mariani, Patrizio (Intern)
Berg, Casper Willestofte (Intern)
Hüssy, Karin (Intern)
Huwer, Bastian (Intern)
Nielsen, Anders (Intern)
Eg Nielsen, Einar (Intern)
Project Coordinator:
Eero, Margit (Intern)

MSC certification of the plaice fishery in area IIIa – basic investigations and development of a management model (39025)
A management plan is an important requirement for MSC certification of specific fisheries. However, prior to this project, reliable stock assessments, which are necessary for a management plan for plaice (Pleuronectes platessa) in area IIIa (Kattegat/Skagerrak), had not been available. These problems most likely originated from insufficient knowledge about the geographical distribution of populations as well as the interactions between populations in Kattegat/Skagerrak and neighbouring areas. Through a mapping of the distribution and dynamics of populations, this project aimed at providing the missing data that would ultimately allow for the development of a management plan for the plaice fishery in area IIIa. The work included information from genetics, tagging, otolith based growth estimation, oceanographic modelling and analyses of survey and fisheries data.

Results from the project showed evidence of both local population components in the Kattegat/Skagerrak as well as substantial mixing between North Sea population and these local components, and consequences of lumping or splitting the populations for stock assessment and management were discussed.

The outcomes of the work directly influenced the policy decisions since 2015. Decision was finally made to proceed with the lumping option, thus allowing a quantitative analytical assessment and management advice for the area. However, because of the differences in size between the two populations, there is a risk of depletion of the local Skagerrak population if the fisheries on it increase as a consequence of the increase in the North Sea stock. In terms of management, some mechanisms already exist for reducing the fishing pressure in the Skagerrak if deemed necessary, as plaice in the North Sea and in the Skagerrak are managed by two different Total Allowable Catches (TACs). It has therefore been suggested that routine monitoring of the survey and fisheries patterns would allow detecting any departures from the current situation, i.e., a decoupling of trends in the different areas and the different seasons that could indicate a reduced productivity of the local stock.
In the longer-term, the current progresses on the biological knowledge of the stock in Skagerrak should be sustained. Additional genetic allocation of individual fish to the different populations should be performed to obtain a better quantification of the mixing in different areas and seasons, and the survey coverage should be improved in the Skagerrak. The project was coordinated by DTU Aqua. 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 Living Resources

Danish Fishermen's Association

Danish Fishermen's Producers' Organization
Period: 01/07/2012 → 31/12/2014
Number of participants: 9
Research areas: Population Genetics & Fisheries Management & Marine Living Resources

Project participant:
Christensen, Asbjørn (Intern)
Ulrich, Clara (Intern)
Boje, Jesper (Intern)
Hüsey, Karin (Intern)
Geitner, Kerstin (Intern)
Worsøe Clausen, Lotte (Intern)
Meldrup, Dorte (Intern)
Hansen, Frank Ivan (Intern)
Project Coordinator:
Hansen, Jakob Hemmer (Intern)

Restoration and management of cod in the Skagerrak/Kattegat (CodS) (38969)
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)
Meldrup, Dorte (Intern)
Mensberg, Karen-Lise Dons (Intern)
Phd Student:
Bonanomi, Sara (Intern)

Reproduction capacity of European eel in captivity: Fecundity, follicular maturation and developmental competence of embryos and larvae

National Institute of Aquatic Resources
Period: 01/05/2012 → 30/09/2017
Number of participants: 7
Phd Student:
da Silva, Filipa (Intern)
Supervisor:
Kjørsvik, Elin (Ekstern)
Støttrup, Josianne Gatt (Intern)
Main Supervisor:
Tomkiewicz, Jonna (Intern)
Examiner:
Hansen, Jakob Hemmer (Intern)
Hamre, Kristin (Ekstern)
Rosenfeld, Hanna (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)
Project: PhD

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, 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

Project participant:
Hansen, Jakob Hemmer (Intern)
Huwer, Bastian (Intern)
Bastardie, Francois (Intern)
Eero, Margit (Intern)
Nielsen, J. Rasmus (Intern)
Worsøe Clausen, Lotte (Intern)
Mosegaard, Henrik (Intern)
Storr-Paulsen, Marie (Intern)
Olesen, Hans Jakob (Intern)
Kirkegaard, Eskild (Intern)
Larsen, Peter Vingaard (Intern)
Hansen, Frank Ivan (Intern)
Lundgaard, Louise Scherffenberg (Intern)
Willandsen, Maj-Britt (Intern)
de Jong, Noortje (Intern)
Mensberg, Karen-Lise Dons (Intern)
Meldrup, Dorthe (Intern)

Project Coordinator:
Hüssy, Karin (Intern)

**Analysis of historical and contemporary salmon samples in the world’s northernmost salmon population (38835)**
The project investigates potential genetic changes in the world’s northernmost population of Atlantic salmon (*Salmo salar*) from the Kapisillit river in Greenland. The aims are to elucidate whether geographical isolation in concert with overexploitation and habitat degradation has led to loss of genetic diversity and associated loss of evolutionary adaptive potential. By comparing genetic diversity in DNA extracted from historical scale collections from the 1950’s and contemporary samples, migration from other populations, loss of allelic diversity as well as genetically effective population sizes can be estimated. The research will contribute to setting management priorities for this unique and extremely vulnerable Atlantic salmon population.

The project is coordinated by DTU Aqua.

National Institute of Aquatic Resources
Section for Marine Living Resources

Greenland Institute of Natural Resources
Period: 01/01/2011 → 31/12/2012
Number of participants: 2
Research area: Population Genetics

Project Manager, academic:
Eg Nielsen, Einar (Intern)
Hansen, Jakob Hemmer (Intern)

Project
Population genetics of flounder in Danish waters (38819)

Knowledge about population structure and local adaptation is central for successful management of both freshwater and marine fisheries. For instance, recently accumulated knowledge about the geographical scale and extent of local adaptation in anadromous fishes has resulted in the abandonment of fish transplants and releases of foreign fish into natural populations, because such activities threaten the survival of natural populations. In coastal habitats, local fishermen have expressed interests in moving marine fish between geographically distant areas, but until now a lack of scientific knowledge about the scale and extent of local adaptation has prevented any detailed advice on the scale that such movements may be possible. In one particular case, it was proposed to move European flounder from the western parts of the Limfjord to the Bay of Aarhus in order to support a fishery in the bay where the species had reached very low abundances. Since these two areas are both geographically distant and environmentally different, it is possible that fish are also adapted to local environmental conditions. However, although earlier work has strongly suggested that populations of European flounder may be locally adapted, no study had directly compared samples from these areas.

In this project, we aimed to use a combination of genetic markers previously found not to be affected by selection (so-called “neutral markers”) and markers situated in or close to genes which may be important for local adaption. The application of such a combination of genetic markers may allow the assessment of geographical patterns and scales of both population structure and local adaptation in natural populations. The first stage of the project was the development of new genetic markers through screening candidate genes, identified as differentially expressed in relation to various stressors in laboratory experiments, for the presence of suitable genetic markers. Genetic markers were subsequently analyzed in individuals collected from the target as well as reference populations in 2011 and in additional reference samples available from 2003/2004. Results showed markedly different levels of genetic variation in putatively neutral and candidate gene associated markers throughout the species’ distribution. Furthermore, different frequencies of genetic variants near the stress response candidate gene, Hsc70, were observed between the Limfjord and the Bay of Aarhus, suggesting local adaptation to the two areas. Consequently, it was advised that fish were not moved between these two regions. In addition to providing information about the specific case, these results could also be important for guiding future research on finer geographical scales in this and other marine fishes.

The project was coordinated by DTU Aqua.

The project was funded by the Danish Rod and Net Fishing License Funds.

National Institute of Aquatic Resources

Section for Ecosystem based Marine Management

Northwest Jutland Recreational Fishermen’s Association
Period: 01/01/2011 → 31/12/2012
Number of participants: 5
Research areas: Population Genetics & Coastal Ecology
Project participant:
Meldrup, Dorte (Intern)
Støttrup, Josianne Gatt (Intern)
Sparrevohn, Claus Reedtz (Intern)
Nicolajsen, Hanne (Intern)
Project Manager, academic:
Hansen, Jakob Hemmer (Intern)

Predicting the consequences of global change for fish populations using genomic methods

National Institute of Aquatic Resources
Period: 01/06/2009 → 19/09/2012
Number of participants: 6
Phd Student:
Therkildsen, Nina Overgaard (Intern)
Supervisor:
Hansen, Jakob Hemmer (Intern)
Main Supervisor:
Eg Nielsen, Einar (Intern)
Examiner:
Bekkevold, Dorte (Intern)
Hansen, Michael Møller (Intern)
Waples, Robin S. (Ekstern)
Financing sources
Source: Internal funding (public)
Name of research programme: 1/3 DTU-stip, 2/3 FUR/andet
Project: PhD

Fish populations and traceability (FishPopTrace) (38283)
The underlying rationale of FishPopTrace was to assess and address challenges arising from the development of traceability tools within a forensic framework for four judiciously chosen target species: cod (Gadus morhua), hake (Merluccius merluccius), herring (Clupea harengus) and sole (Solea solea). Previous information on levels of population structuring in traits such as life histories, morphometrics, genetics and physiology was used to inform sample choice. Thenew data was restricted to markers at two levels:
- Routine screening: selection of markers that exhibit maximal discriminatory power to identify populations, though with discrete and controlled variance enabling validation (single nucleotide polymorphisms (SNPs) and otolith microchemistry and morphometrics). Data from DNA-based methods provided a mechanism for traceability throughout the food supply chain (“fish to fork”) and indicated discrete spawning populations, whereas otoliths aimed at providing an independent onboard traceability system of fish provenance.
- Testing of novel tools: additional tools were tested on a selection of populations to assess validity and potential for traceability and validation, including fatty acid analysis, proteomics, gene expression analysis and the generation of high-throughput microarray platforms for SNP genotyping.

Thus, FishPopTrace provided information relating to geography (“population tag”), as well as regional signatures that indicate biological differentiation in relation to spawning identity.
The project was coordinated by University of Wales Bangor, UK.
The project was funded by EU, Framework Programme 7.
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National Institute of Aquatic Resources
Section for Marine Living Resources
Bangor University
University of Padua
Universidad Complutense de Madrid
Katholieke Universiteit
University of Bologna
University of Bergen
European Commission - Joint Research Center
University of Bremen
Département Sciences & Techniques Alimentaires Marines
National Agricultural Research Foundation
Spanish National Foundation of Fish and Seafood Processors
Aarhus University
The Centre of Molecular Genetic Identification, VNIRO
Period: 01/01/2008 → 31/12/2011
Number of participants: 3
Research area: Population Genetics
Project participant:
Hansen, Jakob Hemmer (Intern)
Project Manager, academic:
Eg Nielsen, Einar (Intern)
Bekkevold, Dorte (Intern)

Fisheries induced evolution (FinE) (38279)
The project is set up to investigate the prevalence of fisheries-induced evolutionary changes in life-history traits of exploited fish stocks in European and North American waters. The aims are to unravel the underlying mechanisms of change ranging from the phenotypic to the genetic level, to evaluate their consequences on population and fisheries
dynamics, and to provide recommendations for evolutionarily enlightened management. This objective necessitates the development and application of novel methodological tools for investigating field data both at phenotypic and genetic levels, together with the setup of relevant experiments on model species and the careful construction of theoretical models suitable for complementing field data analyses and for evaluating managerial options. Earlier investigations have focused on specific aspects such as the analysis of long-term trends in phenotypic data, the investigation of temporal changes in neutral genetic markers, artificial fishing experiments, or the modeling of fisheries-induced evolutionary changes in life-history traits and their demographic consequences for exploited stocks. However, a comprehensive investigation of fisheries-induced evolution at the phenotypic and genetic level and of consequences on fish stocks dynamics are still largely missing, mostly because of the wide range of scientific expertises and approaches required for tackling these challenges. This project aims at combining fields of expertise as diverse as population genetics and quantitative genetics, life-history theory, population dynamics, evolutionary theory, and fisheries science.

The project is coordinated by International Institute for Applied Systems Analysis, Austria.

National Institute of Aquatic Resources
Section for Marine Living Resources
International Institute for Applied Systems Analysis
Institute of Marine Research
IFREMER
Catholic University of Leuven
University of Wales
Marine Scotland
University of Tromsø
Netherlands Institute for Fisheries Research
University of Oslo
Spanish National Research Council
Finnish Game and Fisheries Research Institute
Federal Research Centre for Fisheries
Period: 01/01/2007 → 31/12/2010
Number of participants: 3
Research area: Population Genetics
Project participant:
Hansen, Jakob Hemmer (Intern)
Therkildsen, Nina Overgaard (Intern)
Project Manager, academic:
Eg Nielsen, Einar (Intern)

Activities:

ICES - Benchmark Workshop for North Sea Stocks - WKNSEA (External organisation)
Period: 2015
Jakob Hemmer Hansen (Participant)
National Institute of Aquatic Resources
Section for Marine Living Resources

Related external organisation

ICES - Benchmark Workshop for North Sea Stocks - WKNSEA
Activity: Membership › Membership of commitees, commissions, boards, councils, associations, organisations, or similar

ICES - Data Compilation for Benchmark Workshop on North Sea stocks - DCWKNSEA (External organisation)
Period: 2014
Jakob Hemmer Hansen (Participant)
National Institute of Aquatic Resources
Section for Marine Living Resources
Degree of recognition: International

Related external organisation
ICES - Data Compilation for Benchmark Workshop on North Sea stocks - DCWKNSEA
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar