Dorte Meldrup - DTU Orbit (26/02/2018)

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Organisations

Section for Population Ecology and Genetics
25/02/2012 → 18/01/2013 Former
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Section for Marine Living Resources
23/01/2013 → present
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Publications:

Historical DNA documents long distance natal homing in marine fish

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Greenland Climate Research Centre, Stanford University, Greenland Institute of Natural Resources, Aarhus University
Pages: 2727-2734
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
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Scopus rating (2016): CiteScore 5.9 SJR 3.508 SNIP 1.651
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.862 SNIP 1.606 CiteScore 5.73
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.068 SNIP 1.705 CiteScore 5.36
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Archived DNA reveals fisheries and climate induced collapse of a major fishery

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.
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.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Hansen, J. H. (Intern), Therkildsen, N. O. (Intern), Meldrup, D. (Intern), Eg Nielsen, E. (Intern)
Pages: 213-228
Publication date: 2014
Microevolution in time and space: SNP analysis of historical DNA reveals dynamic signatures of selection in Atlantic cod

Little is known about how quickly natural populations adapt to changes in their environment and how temporal and spatial variation in selection pressures interact to shape patterns of genetic diversity. We here address these issues with a series of genome scans in four overfished populations of Atlantic cod (Gadus morhua) studied over an 80-year period. Screening of >1000 gene-associated single-nucleotide polymorphisms (SNPs) identified 77 loci that showed highly elevated levels of differentiation, likely as an effect of directional selection, in either time, space or both. Exploratory analysis suggested that temporal allele frequency shifts at certain loci may correlate with local temperature variation.
and with life history changes suggested to be fisheries induced. Interestingly, however, largely nonoverlapping sets of loci 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

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Publication date: 2013
Event: Abstract from Evolution meeting, Little Cottonwood Canyon, United States.
Main Research Area: Technical/natural sciences

Relations
Activities:

Spatiotemporal SNP analysis reveals pronounced biocomplexity at the northern range margin of Atlantic cod Gadus morhua

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

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Greenland Institute of Natural Resources, Marine Research Institute, Greenland Climate Research Centre, Aarhus University
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.
Microsatellite standardization and evaluation of genotyping error in a large multi-partner research programme for conservation of Atlantic salmon (Salmo salar L.)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Pages: 353-367
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information
Journal: Genetica
Volume: 139
Issue number: 3
ISSN (Print): 0016-6707
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.658 SNIP 0.638 CiteScore 1.38
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.638 SNIP 0.635 CiteScore 1.33
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.951 SNIP 0.878 CiteScore 1.85
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.94 SNIP 0.732 CiteScore 1.84
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.042 SNIP 0.853 CiteScore 2.02
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.996 SNIP 0.962 CiteScore 2.15
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.173 SNIP 1.09
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.906 SNIP 0.913
Does DNA extraction affect the physical and chemical composition of historical cod (Gadus morhua) otoliths?

Archived otoliths constitute an important source of historical DNA for use in temporal genetic studies, but such otoliths are also valuable for other research applications, e.g. growth or microchemistry studies, where information about the past is of relevance. Consequently, there are potentially conflicting interests regarding how the limited and irreplaceable otolith collections should be used. To resolve this, it is important to find out whether DNA extraction damages otoliths such that they can no longer be used for other research purposes or whether individual otoliths can be used in multiple applications.

We examined the effects of three different DNA extraction methods on the elemental composition, the morphology, and the clarity of annual growth increments for successful age estimation of Atlantic cod (Gadus morhua) otoliths that had been archived for 0–31 years. The three extraction methods yielded DNA of comparable quality, and none of the methods caused major damage to the otoliths. Of the element concentrations measured, only Mg and Rb showed considerable changes resulting from DNA extraction. The physical properties of the otolith (morphology and clarity of annual growth increments) were not affected. Hence, cod otoliths can be used for several research purposes after DNA extraction.

General information

State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Therkildsen, N. O. (Intern), Eg Nielsen, E. (Intern), Hüssy, K. (Intern), Meldrup, D. (Intern), Geffen, A. J. (Ekstern)
Pages: 1251-1259
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information

Journal: ICES Journal of Marine Science
Volume: 67
Issue number: 6
ISSN (Print): 1054-3139
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.63
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.18
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.62
Web of Science (2014): Indexed yes
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.

**Micro geographical population structure of cod Gadus morhua in the North Sea and west of Scotland: the role of sampling loci and individuals**

State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Wright, P. J. (Ekstern), Hansen, J. H. (Intern), Poulsen, N. A. (Intern), Gibb, L. M. (Ekstern), Meldrup, D. (Intern)
Pages: 213-225
Publication date: 2009
Main Research Area: Technical/natural sciences
Application of SNP's (Single Nucleotide Polymorphisms) for genetic stock identification in Atlantic cod (Gadus morhua L.)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Historical analysis of Pan I in Atlantic cod (Gadus morhua): temporal stability of allele frequencies in the southeastern part of the species distribution

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Population- and Ecosystem Dynamics
Authors: Eg Nielsen, E. (Intern), MacKenzie, B. (Intern), Magnussen, E. (Ekstern), Meldrup, D. (Intern)
Pages: 1448-1455
Publication date: 2007
Main Research Area: Technical/natural sciences
Molecular methods for assessing temporal adaptive changes in fish populations, a case study employing historical analysis of Pan I in cod (Gadus morhua)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Population- and Ecosystem Dynamics
Authors: E. Nielsen, B. MacKenzie, E. Magnussen, D. Meldrup
Pages: 1-3
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES Council Meeting
Volume: E:16
ISSN (Print): 1015-4744
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
Evidence of microsatellite hitch-hiking selection in Atlantic cod (Gadus morhua L.): implications for inferring population structure in nonmodel organisms

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Hansen, M. M. (Intern), Meldrup, D. (Intern)
Pages: 3219-3229
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology
Volume: 15
Issue number: 11
ISSN (Print): 0962-1083
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.9 SJR 3.508 SNIP 1.651
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.862 SNIP 1.606 CiteScore 5.73
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.068 SNIP 1.705 CiteScore 5.36
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
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
Retention of juveniles within a hybrid zone between North Sea and Baltic Sea Atlantic cod (Gadus morhua)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Aquaculture
Authors: Nielsen, E. (Intern), Grønkjær, P. (Ekstern), Meldrup, D. (Intern), Paulsen, H. (Intern)
Pages: 2219-2225
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Canadian Journal of Fisheries and Aquatic Sciences
Volume: 62
Issue number: 10
ISSN (Print): 0706-652X
Ratings:
BFI (2018): BFI-level 2
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BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.56 SJR 1.322 SNIP 1.163
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.256 SNIP 1.051 CiteScore 2.22
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.443 SNIP 1.379 CiteScore 2.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.421 SNIP 1.081 CiteScore 2.25
ISI indexed (2013): ISI indexed yes
Genetic population structure of turbot (Scophthalmus maximus L.) supports the presence of multiple hybrid zones for marine fishes in the transition zone between the Baltic Sea and the North Sea

Genetic population structure of turbot (Scophthalmus maximus L.) in the Northeast Atlantic was investigated using eight highly variable microsatellite loci. In total 706 individuals from eight locations with temporal replicates were assayed, covering an area from the French Bay of Biscay to the Aaland archipelago in the Baltic Sea. In contrast to previous genetic studies of turbot, we found significant genetic differentiation among samples with a maximum pairwise F-ST of 0.032. Limited or no genetic differentiation was found among samples within the Atlantic/North Sea area and within the Baltic Sea, suggesting high gene flow among populations in these areas. In contrast, there was a sharp cline in genetic differentiation going from the low saline Baltic Sea to the high saline North Sea. The data were explained best by two divergent populations connected by a hybrid zone; however, a mechanical mixing model could not be ruled out. A significant part of the genetic variance could be ascribed to variation among years within locality. Nevertheless, the population structure was relatively stable over time, suggesting that the observed pattern of genetic differentiation is biologically significant. This study suggests that hybrid zones are a common phenomenon for marine fishes in the transition area between the North Sea and the Baltic Sea and highlights the importance of using interspecific comparisons for inferring population structure in high gene flow species such as most marine fishes.
Stocking impact and migration pattern in an anadromous brown trout (Salmo trutta) complex: where have all the stocked spawning sea trout gone?

We examined polymorphism at seven microsatellite loci among sea trout (Salmo trutta) (n = 846) collected from three areas in the Limfjord (Denmark). We then assessed their potential population source by comparing, using a mixed stock analysis (MSA) Bayesian framework, their genetic composition to that of brown trout collected from 32 tributaries pooled into nine geographical regions (n = 3801) and two hatcheries (n = 222) used for stocking. For each of the three regional sea trout groups (western, central and eastern Limfjord, n = 91, n = 426, n = 329, respectively), MSA was conducted with (i) all individuals in the group, (ii) with the subset of spawning sea trout only and (iii) with the subset of foraging, nonspawning individuals only, a subset that consisted primarily of sea trout caught during their first year at sea. For all three regional sea trout groups, a higher proportion of individuals (regardless of whether they were foraging or spawning) appear to have originated from the rivers that drain locally, than from the rivers that drain in other parts of the Limfjord. This suggests (1) that sea trout, at least during their first year at sea, undertake limited migrations within the Limfjord system and (2) that sea trout on their spawning run were caught close to their natal rivers. The proportion of sea trout of hatchery origin varied widely among all three Limfjord areas and broadly reflected regional stocking histories, with high proportions of sea trout of domestic origin in the east (39.3%), where stocking with domestic trout was practised intensely at the time of sampling, and in the west (57.2%), where a programme of coastal stocking of post smolts took place over several years in the early 1990s. In contrast, in the central Limfjord, where stocking with domestic trout was largely abandoned in the early 1990s, the proportion of sea trout of domestic origin was only 8.5%. Interestingly, for all three regional sea trout groups, virtually no sea trout of hatchery origin were found among the spawning individuals, which were on average larger than the nonspawning sea trout. These results suggest that stocked domestic brown trout that become anadromous experience high mortality at sea and are therefore largely absent among the larger, spawning individuals. We conclude that sea trout of domestic origin exhibit much reduced ability to reproduce and are unlikely to contribute significantly to the local gene pool largely because of a relatively high mortality at sea before the onset of maturity.
Evidence of a hybrid-zone in Atlantic cod (Gadus morhua) in the Baltic and the Danish Belt Sea, revealed by individual admixture analysis

General information
State: Published
A hybrid zone in Atlantic cod (Gadus morhua) in the Baltic and the Danish Belt Sea revealed by individual admixture analysis

Distribution of individual inbreeding coefficients, relatedness and influence of stocking on native anadromous brown trout (Salmo trutta) population structure
Publication information
Journal: Molecular Ecology
Volume: 10
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.9 SJR 3.508 SNIP 1.651
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.862 SNIP 1.606 CiteScore 5.73
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.13 SNIP 1.564 CiteScore 5.6
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.068 SNIP 1.705 CiteScore 5.36
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.469 SNIP 1.823 CiteScore 5.56
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.513 SNIP 1.915
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.455 SNIP 2.024
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.326 SNIP 2.086
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.937 SNIP 1.918
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.932 SNIP 2.111
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.756 SNIP 2.099
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.544 SNIP 1.731
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.148 SNIP 1.564
Web of Science (2001): Indexed yes
Population of origin of Atlantic cod

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Hansen, M. M. (Intern), Schmidt, C. (Ekstern), Meldrup, D. (Intern), Grønkjær, P. (Ekstern)
Pages: 272-272
Publication date: 2001
Main Research Area: Technical/natural sciences

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Journal: Nature
Volume: 413
Issue number: 6853
ISSN (Print): 0028-0836
Ratings:
BFI (2018): BFI-level 3
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 13.33
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 14.38
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 14.22
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 14.96
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 14.01
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 13.96
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Development of new VNTR markers for pike and assessment of variability at di- and tetranucleotide repeat microsatellite loci

Levels of variation at six VNTR (variable number of tandem repeats) loci, one minisatellite and five microsatellite loci, isolated from tri- and tetranucleotide enriched DNA libraries for northern pike were generally low in two Danish populations (1-4 alleles; expected heterozygosity 0-0.57), though one highly variable microsatellite (13 alleles; expected heterozygosity 0.79) was identified. In combination with previously published microsatellites a set consisting of nine polymorphic loci appeared to be useful for discriminating populations, as determined by assignment tests. (C) 1999 The Fisheries Society of the British Isles.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Taggart, J. (Ekstern), Meldrup, D. (Intern)
Pages: 183-188
Publication date: 1999
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Biology
Volume: 55
Issue number: 1
ISSN (Print): 0022-1112
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.57 SJR 0.741 SNIP 0.882
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.951 SNIP 0.935 CiteScore 1.64
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.944 SNIP 0.934 CiteScore 1.76
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.049 SNIP 1.118 CiteScore 1.98
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.93 SNIP 1.035 CiteScore 1.88
The Kattegat cod has been categorized as a data limited stock, mainly due to a large unallocated mortality, which may be caused 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
Expertise in marine and aquatic ecology and genomics for sustainable management of fish and shellfish in Skagerrak-Kattegat-Öresund (MarGen) (39301)

The marine and freshwater regions encompassing Skagerrak, Kattegat, Öresund and the North Sea are biologically highly productive and contain plentiful living aquatic resources that are important for the region. At the same time the coastal areas are densely populated and industrialized, fish and shellfish resources are heavily harvested, and waters are subject to pollution and eutrophication. The region is also markedly affected by the ongoing global warming, with sea temperature rising nearly 2 degrees C during the last 40 years. These environmental pressures call for investigations into the consequences for aquatic organisms, their potential for adapting to environmental changes, and for identifying management strategies that could mitigate deteriorating environmental conditions, using state-of-the-art methodology. Here, we will capitalize on the revolutionizing developments in genomics, electronic tagging and computer modelling to obtain insights on the ecology, evolution and management of aquatic biodiversity in the region.

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

This project is coordinated by DTU Aqua.

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

National Institute of Aquatic Resources
Section for Marine Living Resources
Institute of Marine Research
University of Gothenburg
Aarhus University
University of Oslo
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)
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 populations 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)
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Boje, Jesper (Intern)
Hüssy, Karin (Intern)
Geitner, Kerstin (Intern)
Worsøe Clausen, Lotte (Intern)
Meldrup, Dorte (Intern)
Hansen, Frank Ivan (Intern)
Project Coordinator:
Hansen, Jakob Hemmer (Intern)
Project

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)

**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, 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 Minestry 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 Vinggaard (Intern)
Hansen, Frank Ivan (Intern)
Lundgaard, Louise Scherffenberg (Intern)
Willandsen, Maj-Britt (Intern)
de Jong, Noortje (Intern)
Mensberg, Karen-Lise Dons (Intern)
Meldrup, Dorte (Intern)
Project Coordinator:
Hüssy, Karin (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:
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Støtrup, Josianne Gatt (Intern)
Sparrevoeh, Claus Reedtz (Intern)
Nicolajsen, Hanne (Intern)

Project Manager, academic:
Hansen, Jakob Hemmer (Intern)