Einar Eg Nielsen - DTU Orbit (10/02/2018)

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Organisations

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Publications:

Artsspecifik sporing og kvantificering af eDNA fra marine fisk i Østersøen

General information
State: Published
Authors: Knudsen, S. W. (Ekstern), Ebert, R. B. (Ekstern), Hesselsøe, M. (Ekstern), Kunike, F. (Ekstern), Hassingboe, J. (Ekstern), Mortensen, P. B. (Ekstern), Thomsen, P. F. (Forskerdatabase), Hansen, B. K. (Intern), Eg Nielsen, E. (Intern), Møller, P. R. (Ekstern)
Publication date: 2017
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Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2017

Den skeptiske optimist: Udfordringer og perspektiver i anvendelse af eDNA til marin monitering og fiskeriforvaltning

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Eg Nielsen, E. (Intern), Bekkevold, D. (Intern), Hansen, B. K. (Intern)
Publication date: 2017
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Publication: Research › Conference abstract for conference – Annual report year: 2017

Extracting DNA from 'jaws': High yield and quality from archived tiger shark (Galeocerdo cuvier) skeletal material

Archived specimens are highly valuable sources of DNA for retrospective genetic/genomic analysis. However, often limited effort has been made to evaluate and optimize extraction methods, which may be crucial for downstream applications. Here, we assessed and optimized the usefulness of abundant archived skeletal material from sharks as a source of DNA for temporal genomic studies. Six different methods for DNA extraction, encompassing two different commercial kits and three different protocols, were applied to material, so-called bio-swarf, from contemporary and archived jaws and vertebrae of tiger sharks (Galeocerdo cuvier). Protocols were compared for DNA yield and quality using a qPCR approach. For jaw swarf, all methods provided relatively high DNA yield and quality, while large differences in yield between protocols were observed for vertebrae. Similar results were obtained from samples of white shark (Carcharodon carcharias). Application of the optimized methods to 38 museum and private angler trophy specimens dating back to 1912 yielded sufficient DNA for downstream genomic analysis for 68% of the samples. No clear relationships between age of samples, DNA quality and quantity were observed, likely reflecting different preparation and storage methods for the trophies. Trial sequencing of DNA capture genomic libraries using 20 000 baits revealed that a significant proportion of captured sequences were derived from tiger sharks. This study demonstrates that archived shark jaws and vertebrae are potential high-yield sources of DNA for genomic-scale analysis. It also highlights that even for similar tissue types, a careful evaluation of extraction protocols can vastly improve DNA yield.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Queensland, Pepperell Research and Consulting Pty Ltd.
Authors: Eg Nielsen, E. (Intern), Morgan, J. A. T. (Ekstern), Maher, S. L. (Ekstern), Edson, J. (Ekstern), Gauthier, M. (Ekstern), Pepperell, J. (Ekstern), Holmes, B. J. (Ekstern), Bennett, M. B. (Ekstern), Ovenden, J. R. (Ekstern)
Pages: 431-442
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology Resources
Volume: 17
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ISSN (Print): 1755-098X
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 6.06 SJR 2.864 SNIP 2.176
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.305 SNIP 1.564 CiteScore 4.47
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.842 SNIP 2.217 CiteScore 5.04
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 3.472 SNIP 2.986 CiteScore 7.31
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.172 SNIP 1.87 CiteScore 4.26
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.395 SNIP 1.173 CiteScore 2.75
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.94 SNIP 0.814
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.277 SNIP 1.291
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.926 SNIP 0.938
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.042 SNIP 0.928
Scopus rating (2006): SJR 0.927 SNIP 0.958
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.057 SNIP 1.152
Scopus rating (2004): SJR 0.941 SNIP 0.95
Scopus rating (2003): SJR 0.698 SNIP 0.55
Scopus rating (2002): SJR 0.465 SNIP 0.373
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.
Geographic extent of introgression in Sebastes mentella and its effect on genetic population structure

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Institute of Marine Research, Greenland Institute of Natural Resources, University of Washington
Authors: Saha, A. (Ekstern), Johansen, T. (Ekstern), Hedeholm, R. (Ekstern), Eg Nielsen, E. (Intern), Westgaard, J. (Ekstern), Hauser, L. (Ekstern), Planque, B. (Ekstern), Cadrin, S. X. (Ekstern), Boje, J. (Intern)
Pages: 77–90
Publication date: 2017
Main Research Area: Technical/natural sciences

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Journal: Evolutionary Applications
Volume: 10
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.96 SJR 2.299 SNIP 1.478
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.666 SNIP 1.392 CiteScore 4.27
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.356 SNIP 1.402 CiteScore 4.23
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.478 SNIP 1.432 CiteScore 4.48
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.185 SNIP 1.179 CiteScore 3.82
ISI indexed (2012): ISI indexed yes
Scopus rating (2011): SJR 2.427 SNIP 1.216 CiteScore 4.5
Scopus rating (2010): SJR 1.633 SNIP 1.014
Scopus rating (2009): SJR 1.241 SNIP 0.87
Original language: English
Electronic versions:
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DOIs:
Population structure and connectivity of tiger sharks (Galeocerdo cuvier) across the Indo-Pacific Ocean basin

Population genetic structure using nine polymorphic nuclear microsatellite loci was assessed for the tiger shark (Galeocerdo cuvier) at seven locations across the Indo-Pacific, and one location in the southern Atlantic. Genetic analyses revealed considerable genetic structuring (FST > 0.14, p<0.001) between all Indo-Pacific locations and Brazil. By contrast, no significant genetic differences were observed between locations from within the Pacific or Indian Oceans, identifying an apparent large, single Indo-Pacific population. A lack of differentiation between tiger sharks sampled in Hawaii and other Indo-Pacific locations identified herein is in contrast to an earlier global tiger shark nDNA study. The results of our power analysis provide evidence to suggest that the larger sample sizes used here negated any weak population subdivision observed previously. These results further highlight the need for crossjurisdictional efforts to manage the sustainable exploitation of large migratory sharks like G. cuvier.
The development of tools for tracing and evaluating the genetic impact of fish from aquaculture

**General information**

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Padua
Authors: Bargelloni, L. (Ekstern), Nielsen, E. E. (Intern)
Pages: 87
Publication date: 2017
Conference: 12th International Symposium on Genetics in Aquaculture, Santiago de Compostella, Spain, 21/06/2015 - 21/06/2015
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- Web of Science (2018): Indexed yes
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- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 2
- Scopus rating (2016): CiteScore 2.75 SJR 1.101 SNIP 1.524
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 2
- Scopus rating (2015): SJR 1.103 SNIP 1.254 CiteScore 2.12
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 2
- Scopus rating (2014): SJR 1.002 SNIP 1.34 CiteScore 2.16
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 1.136 SNIP 1.3 CiteScore 2.18
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 1.212 SNIP 1.487 CiteScore 2.32
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 1.294 SNIP 1.542 CiteScore 2.39
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 1.151 SNIP 1.394
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 0.941 SNIP 1.263
- Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 2
- Scopus rating (2008): SJR 0.909 SNIP 1.173
- Web of Science (2008): Indexed yes
The use of selective breeding is still relatively limited in aquaculture species. Information on such activities is sparse, hindering an overall evaluation of their success. Here, we report on the results of an online survey of the major aquaculture breeding companies operating in Europe. Six main reared fish species were targeted. A total of 31 respondents contributed to the survey, representing 75 % of European breeding organizations. Family-based breeding schemes were predominant, but individual selection was more frequently applied in marine species. Artificial fertilization is the preferred means of reproduction; however, mass spawning is often used as a fallback method. The most frequently selected trait is growth performance, but the number of selected traits has been increasing over the years through the addition of traits such as disease resistance or product quality. The use of molecular tools is now common in all programs, mainly for pedigree traceability. An increasing number of programs use either genomic or marker-assisted selection.

Results related to the seed production market confirmed that for Atlantic salmon there are a few dominant players at the European level, with 30–50 % market share. Only part of the European fish aquaculture industry today fully exploits selective breeding to the best advantage. A larger impact assessment still needs to be made by the remainder, particularly on the market share of fish seed (eggs, larvae or juveniles) and its consequences for hatchery stability.
Er det genetik der bestemmer, hvor længe laks opholder sig i havet?

**General information**

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Freshwater Fisheries Ecology
Authors: Bekkevold, D. (Intern), Eg Nielsen, E. (Intern), Sivebæk, F. (Intern)
Publication date: 2016

**Publication information**

Source/Publisher: Fiskepleje.dk
Main Research Area: Technical/natural sciences
Links:
Evaluating genetic traceability methods for captive-bred marine fish and their applications in fisheries management and wildlife forensics

Growing demands for marine fish products is leading to increased pressure on already depleted wild populations and a rise in aquaculture production. Consequently, more captive-bred fish are released into the wild through accidental escape or deliberate releases. The increased mixing of captive-bred and wild fish may affect the ecological and/or genetic integrity of wild fish populations. Unambiguous identification tools for captive-bred fish will be highly valuable to manage risks (fisheries management) and tracing of escapees and seafood products (wildlife forensics). Using single nucleotide polymorphism (SNP) data from captive-bred and wild populations of Atlantic cod Gadus morhua L. and sole Solea solea L., we explored the efficiency of population and parentage assignment techniques for the identification and tracing of captive-bred fish. Simulated and empirical data were used to correct for stochastic genetic effects. Overall, parentage assignment performed well when a large effective population size characterized the broodstock and escapees originated from early generations of captive breeding. Consequently, parentage assignments are particularly useful from a fisheries management perspective to monitor the effects of deliberate releases of captive-bred fish on wild populations. Population assignment proved to be more efficient after several generations of captive breeding, which makes it a useful method in forensic applications for well-established aquaculture species. We suggest the implementation of a case-by-case strategy when choosing the best method.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, KU Leuven, University of Bologna, Royal Zoological Society of Scotland, University of East Anglia, University of Padua, Wageningen University & Research, European Commission - Joint Research Center, Bangor University, Queen's University Belfast
Authors: Bylemans, J. (Ekstern), Maes, G. E. (Ekstern), Diopere, E. (Ekstern), Cariani, A. (Ekstern), Senn, H. (Ekstern), Taylor, M. I. (Ekstern), Helyar, S. (Ekstern), Bargelloni, L. (Ekstern), Bonaldo, A. (Ekstern), Carvalho, G. (Ekstern), Guarniero, I. (Ekstern), Komen, H. (Ekstern), Martinsohn, J. T. (Ekstern), Eg Nielsen, E. (Intern), Tinti, F. (Ekstern), Volckaert, F. A. M. (Ekstern), Ogden, R. (Ekstern)
Pages: 131-145
Publication date: 2016
Main Research Area: Technical/natural sciences

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Journal: Aquaculture Environment Interactions
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.19 SJR 0.945 SNIP 1.051
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.867 SNIP 0.867 CiteScore 2.25
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.861 SNIP 1.047 CiteScore 2.25
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.253 SNIP 1.495 CiteScore 2.45
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.729 SNIP 1.108 CiteScore 1.19
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
Scopus rating (2011): SJR 1.144 SNIP 1.167
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 aimed approach for mixed stock assignment by robust stochastic baseline selection and posterior bias correction by individual reassignment of the least likely classifications into the alternate 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.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Ecology and Oceanography, Section for Marine Living Resources, Section for Ecosystem based Marine Management
Authors: Hüssy, K. (Intern), Mosegaard, H. (Intern), Albertsen, C. M. (Intern), Eg Nielsen, E. (Intern), Hansen, J. H. (Intern), Eero, M. (Intern)
Pages: 210-218
Publication date: 2016
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In this study, 11 microsatellite markers were used to determine the structure of West Greenlandic lumpfish Cyclopterus lumpus populations across six spawning locations spanning >1500 km and compared with neighbouring populations in Canada and Iceland. To evaluate whether data allow for identification of origin of C. lumpus in Greenlandic waters, genetic assignment analysis was performed for 86 C. lumpus sampled on a feeding migration. Significant structuring with isolation by distance was observed in the West Greenland samples and two major subpopulations, north and south, were suggested. Based on FST values, closer relationships were observed between Greenland and Canada, than Greenland and Iceland. Surprisingly, the North Greenland population showed more similarities with Canadian samples, than did the geographically closer south-west Greenland population. Origin could be assigned for a high proportion of non-spawning fish and demonstrated a marked east-west spatial separation of fish of Greenlandic and Icelandic genotypes.
Historical DNA documents long distance natal homing in marine fish

General information
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Volume: 25
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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
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General information
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Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine Living Resources
Authors: Sivebæk, F. (Intern), Eg Nielsen, E. (Intern)
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Publication information
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Main Research Area: Technical/natural sciences
Links: http://www.fiskepleje.dk/Fiskebiologi/laks/laksekvote/laksekvote-2016?utm_source=newsletter&utm_media=mail&utm_campaign=Nyhedsbrev%2023%20november%202015
Publication: Communication › Internet publication – Annual report year: 2016

Laksen i Storå skal fremover klare sig uden udsætninger

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Institute Management, Section for Marine Living Resources
Authors: Sivebæk, F. (Intern), Koed, A. (Intern), Eg Nielsen, E. (Intern), Jepsen, N. (Intern), Aarestrup, K. (Intern)
Publication date: 2016

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Source/Publisher: Fiskepleje.dk
Main Research Area: Technical/natural sciences
Publication: Communication › Internet publication – Annual report year: 2016

Learning from 'apparent consensus' in TAC disputes: Exploring knowledge overlaps in LEK and genetic categorization of Atlantic cod
The rapid development of genetic science has improved the methods for fisheries stock assessments with increasing implications for management. One key accomplishment has been the identification of different sub-populations of Atlantic cod. Recognizing that local coastal fishers in the North Atlantic have often held a local knowledge about local cod populations, this study examines the extent to which genetic analysis corroborates this local knowledge and vice versa. In Nuuk, capital of Greenland situated by the Nuuk fiord system, local fishers say that they and generations before them have been observing both inshore and offshore cod in the Nuuk fiord system. Fisher interviews were conducted in order to understand the construction as well as the content of this specific local ecological knowledge. Furthermore, fishers were invited to assign cod from their catches into categories based on their knowledge of inshore and offshore cod. These cod were subsequently analyzed and assigned to population using genetic methodologies. The comparison between visual and genetic assignment was not able to confirm any convincing consensus between fishers' understanding of offshore and inshore cod and the corresponding genetic categories. However, an examination of existing inshore and off-shore catch surveys confirmed the relevance of the morphological characteristics (liver condition and shape) of ecologically defined inshore and off-shore cod that provided the basis for fishers' categorizations. This opens a discussion of the fishers' way of knowing about inshore and offshore cod respectively and if and how the content of their knowledge could be made relevant in relation to scientific advice procedures

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Greenland Institute of Natural Resources, Aalborg University
Authors: Hedeholm, R. B. (Ekstern), Jacobsen, R. B. (Ekstern), Eg Nielsen, E. (Intern)
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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 2.7 SJR 1.335 SNIP 1.182
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.591 SNIP 1.397 CiteScore 3.07
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.438 SNIP 1.56 CiteScore 3.09
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.472 SNIP 1.635 CiteScore 2.71
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.339 SNIP 1.495 CiteScore 2.54
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.406 SNIP 1.263 CiteScore 2.07
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.289 SNIP 1.483
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.947 SNIP 1.142
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.838 SNIP 1.417
Scopus rating (2007): SJR 0.927 SNIP 1.377
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.961 SNIP 2.043
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.84 SNIP 1.229
Scopus rating (2004): SJR 0.793 SNIP 1.116
Scopus rating (2003): SJR 0.506 SNIP 1.11
Scopus rating (2002): SJR 0.444 SNIP 0.8
Scopus rating (2001): SJR 0.532 SNIP 0.639
Scopus rating (2000): SJR 0.391 SNIP 1.442
Scopus rating (1999): SJR 0.527 SNIP 1.141

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Relations
Activities:
Populationsgenetiske undersøgelser af torsk fra Vestgrønland
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Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine Living Resources
Authors: Sivebæk, F. (Intern), Eg Nielsen, E. (Intern)
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Main Research Area: Technical/natural sciences
Links:
http://www.fiskepleje.dk/Nyheder/2016/02/Laksebestande-status-2016-laksekvoter?id=808315d7-4c1d-404a-bd89-37052194b903&utm_source=newsletter&utm_media=mail&utm_campaign=2016_02_17_Nyhedsbrev
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Undgå indavl, hvis du udsætter ørreder i naturen

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Main Research Area: Technical/natural sciences
Links:
http://www.fiskepleje.dk/nyheder/2016/11/opdraet-af-oerred-til-udsaetning?id=1eb1a5b0-cad4-4b84-aefa-6353bc7b5821&utm_source=newsletter&utm_media=mail&utm_campaign=
Publication: Communication › Internet publication – Annual report year: 2016

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

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Ecosystem based Marine Management, Greenland Climate Research Centre, WSL Swiss Federal Research Institute, Stanford University, Greenland Institute of Natural Resources, Danish Meteorological Institute, Marine Research Institute, Aarhus University
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Main Research Area: Technical/natural sciences

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Ratings:
BFI (2018): BFI-level 1
Arctic warming will promote Atlantic-Pacific fish interchange

Throughout most of the Quaternary Period, inhospitable environmental conditions above the Arctic Circle have been a formidable barrier separating most marine organisms in the North Atlantic from those in the North Pacific. Rapid warming has begun to lift this barrier, potentially facilitating the interchange of marine biota between the two seas. Here, we forecast the potential northward progression of 515 fish species following climate change, and report the rate of potential species interchange between the Atlantic and the Pacific via the Northwest Passage and the Northeast Passage. For this, we projected niche-based models under climate change scenarios and simulated the spread of species through the passages when climatic conditions became suitable. Results reveal a complex range of responses during this century, and accelerated interchange after 2050. By 2100 up to 41 species could enter the Pacific and 44 species could enter the Atlantic, via one or both passages. Consistent with historical and recent biodiversity interchanges, this exchange of fish species may trigger changes for biodiversity and food webs in the North Atlantic and North Pacific, with ecological and economic consequences to ecosystems that at present contribute 39% to global marine fish landings

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Lausanne, Universite de Bordeaux, Greenland Climate Research Centre, Aarhus University, DHI Denmark, University of Copenhagen, Danish Meteorological Institute
Authors: Wisz, M. (Intern), Broennimann, O. (Ekstern), Grønkjær, P. (Ekstern), Møller, P. R. (Ekstern), Olsen, S. M. (Ekstern), Swingedouw, D. (Ekstern), Hedeholm, R. (Ekstern), Eg Nielsen, E. (Intern), Guisan, A. (Ekstern), Pellissier, L. (Ekstern)
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Publication information
Journal: Nature Climate Change
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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.
Hvad kan du gøre for laksen?

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine Living Resources, Institute Management
Authors: Sivebæk, F. (Intern), Eg Nielsen, E. (Intern), Koed, A. (Intern)
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Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Marine Living Resources, Institute Management
Authors: Sivebæk, F. (Intern), Eg Nielsen, E. (Intern), Koed, A. (Intern)
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http://www.fiskepleje.dk/Nyheder/2015/01/Laksekvoter-2015
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Mating success and sexual selection in a pelagic copepod, Temora longicornis: Evidence from paternity analyses
Knowledge about mating patterns is essential for understanding and explaining rates of reproduction and genetic potential of copepods populations. The aim of this study was to examine (1) the occurrence of multiple paternity in Temora longicornis, (2) the effect of multiple paternity (if present) on the females reproductive output, and (3) whether mating is random or some individuals have a higher than average chance of fertilizing or being fertilized (super individuals). We show that multiple paternity is common in this copepod species, that females benefit from multiple matings by increased offspring production, and that a relatively small fraction of the males and females in a population account for most of the offspring production. In both males and females, mating is nonrandom. Superior individuals with a higher than average matings success were identified both among females and among males.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Centre for Ocean Life, Section for Marine Living Resources
Authors: Sichlau, M. H. (Intern), Eg Nielsen, E. (Intern), Thygesen, U. H. (Intern), Kiørboe, T. (Intern)
Pages: 600-610
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Optimal bæredygtig udnyttelse af tilgængelige torskbestande for dansk fiskeri

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Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Section for Marine Living Resources, Section for Marine Ecology and Oceanography, Centre for Ocean Life
Authors: Eero, M. (Intern), Hansen, J. H. (Intern), Hüssy, K. (Intern), Huwer, B. (Intern), Berg, C. W. (Intern), Mariani, P. (Intern), Mosegaard, H. (Intern), Nielsen, A. (Intern), Eg Nielsen, E. (Intern), Rindorf, A. (Intern), Ulrich, C. (Intern), Vinther, M. (Intern), Worsøe Clausen, L. (Intern)
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Reply to 'Sources of uncertainties in cod distribution models'

General information
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Authors: Wisz, M. (Intern), Broennimann, O. (Ekstern), Grønkjær, P. (Ekstern), Møller, P. D. R. (Ekstern), Olsen, S. M. (Ekstern), Swingedouw, D. (Ekstern), Hedeholm, R. (Ekstern), Eg Nielsen, E. (Intern), Guisan, A. (Ekstern), Pellissier, L. (Ekstern)
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 10.06
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 9.64
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 7.38
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
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The history of cod in Greenland: A major fishery collapse explained by archived DNA

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Combination of genetics and spatial modelling highlights the sensitivity of cod (Gadus morhua) population diversity in the North Sea to distributions of fishing

Conserving genetic diversity in animal populations is important for sustaining their ability to respond to environmental change. However, the “between-population” component of genetic diversity (biocomplexity) is threatened in many exploited populations, particularly marine fish, where harvest management regions may be larger than the spatial extent of genetically distinct subpopulations. Using single-nucleotide polymorphism data, we delineated the geographic limits of three population units of Atlantic cod (Gadus morhua) in northwest European waters. Two of the populations cohabit the North Sea, and trawl survey data showed differing trends in their abundances. We developed a spatial model of these units to simulate population dynamics under spatial patterns of harvesting. Competition between units during the pelagic juvenile stages in the model led to suppression of the more localized northern North Sea (Viking) unit by the more widespread (Dogger) unit, and its premature extinction under some spatial patterns of fishing. Fishery catch limits for cod are set at the scale of the whole North Sea without regard to such subpopulation dynamics. Our model offers a method to quantify adjustments to regional fishing mortality rates to strike a balance between maximizing sustainable yield and conserving vulnerable populations.

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State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, University of Strathclyde, Agri-Food and Biosciences Institute, Scottish Association for Marine Science, University of Hull, Marine Scotland Science, Cefas, Bangor University
Authors: Heath, M. R. (Ekstern), Culling, M. A. (Ekstern), Crozier, W. W. (Ekstern), Fox, C. J. (Ekstern), Gurney, W. S. C. (Ekstern), Hutchinson, W. F. (Ekstern), Eg Nielsen, E. (Intern), O'Sullivan, M. (Ekstern), Preedy, K. F. (Ekstern), Righton, D. A. (Ekstern), Speirs, D. C. (Ekstern), Taylor, M. I. (Ekstern), Wright, P. J. (Ekstern), Carvalho, G. R. (Ekstern)
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Journal: ICES Journal of Marine Science
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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**
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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)
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Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.746 SNIP 0.803 CiteScore 1.62
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.837 SNIP 0.786 CiteScore 1.72
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.942 SNIP 0.993 CiteScore 1.98
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.871 SNIP 0.968 CiteScore 2.1
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.875 SNIP 0.962 CiteScore 1.7
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.824 SNIP 0.892 CiteScore 1.61
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.729 SNIP 0.808
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.041 SNIP 1.02
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.091 SNIP 1.189
Scopus rating (2007): SJR 1.2 SNIP 1.06
Scopus rating (2006): SJR 0.864 SNIP 0.857
Scopus rating (2005): SJR 1.124 SNIP 1.064
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.886 SNIP 0.905
Scopus rating (2003): SJR 0.909 SNIP 0.804
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.618 SNIP 0.659
Scopus rating (2001): SJR 0.513 SNIP 0.39
Web of Science (2001): Indexed yes
Original language: English
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 managements 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.
Outlier SNP markers reveal fine-scale genetic structuring across European hake populations (Merluccius merluccius)

Shallow population structure is generally reported for most marine fish and explained as a consequence of high dispersal, connectivity and large population size. Targeted gene analyses and more recently genome-wide studies have challenged such view, suggesting that adaptive divergence might occur even when neutral markers provide genetic homogeneity across populations. Here, 381 SNPs located in transcribed regions were used to assess large and fine-scale population structure in the European hake (Merluccius merluccius), a widely distributed demersal species of high priority for the European fishery. Analysis of 850 individuals from 19 locations across the entire distribution range showed evidence for several outlier loci, with significantly higher resolving power. While 299 putatively neutral SNPs confirmed the genetic break between basins (FCT = 0.016) and weak differentiation within basins, outlier loci revealed a dramatic divergence between Atlantic and Mediterranean populations (FCT range 0.275–0.705) and fine-scale significant population structure. Outlier loci separated North Sea and Northern Portugal populations from all other Atlantic samples and revealed a strong differentiation among Western, Central and Eastern Mediterranean geographical samples. Significant correlation of allele frequencies at outlier loci with seawater surface temperature and salinity supported the hypothesis that populations might be adapted to local conditions. Such evidence highlights the importance of integrating information from neutral and adaptive evolutionary patterns towards a better assessment of genetic diversity. Accordingly, the generated outlier SNP data could be used for tackling illegal practices in hake fishing and commercialization as well as to develop explicit spatial models for defining management units and stock boundaries.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Milano, I. (Ekstern), Babbucci, M. (Ekstern), Cariani, A. (Ekstern), Atanassova, M. (Ekstern), Bekkevold, D. (Intern), Carvalho, G. (Ekstern), Espiñeira, M. (Ekstern), Fiorentino, F. (Ekstern), Garofalo, G. (Ekstern), Geffen, A. (Ekstern), Hansen, J. (Ekstern), Helyar, S. (Ekstern), Nielsen, E. (Intern), Ogden, R. (Ekstern), Patarnello, T. (Ekstern), Stagioni, M. (Ekstern), Tinti, F. (Ekstern), Bargalloni, L. (Ekstern)
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BFI (2015): BFI-level 2
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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
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BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.068 SNIP 1.705 CiteScore 5.36
ISI indexed (2012): ISI indexed yes
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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

General information

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Biologisk institut
Authors: Bonanomi, S. (Intern), Therkildsen, N. O. (Intern), Hedeholm, R. B. (Forskerdatabase), Hansen, J. H. (Intern), Eg Nielsen, E. (Intern)
Pages: 616-621
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Publication information

Journal: Molecular Ecology Resources
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Issue number: 3
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.

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Icelandic Food Research, University of East Anglia, Royal Zoological Society of Scotland, Marine Research Institute, Institute of Marine Research, Bangor University, University of Bergen
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ISI indexed (2013): ISI indexed yes
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Web of Science (2012): Indexed yes
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Scopus rating (2011): SJR 3.469 SNIP 1.823 CiteScore 5.56
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
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Dansk fiskeris udnyttelse af discardforbuddet: En udredning

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Organisations: National Institute of Aquatic Resources, Section for Ecosystem based Marine Management, Public Sector Consultancy, Section for Marine Living Resources, Institute Management, AquaMind
Authors: Larsen, E. (Intern), Dalskov, J. (Intern), Eg Nielsen, E. (Intern), Kirkegaard, E. (Intern), Nielsen, J. W. (Ekstern), Tørring, P. (Ekstern), Schou, M. (Ekstern)
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http://www.aqua.dtu.dk/Publikationer/Forskningsrapporter/Forskningsrapporter_siden_2008
Publication: Commissioned › Report – Annual report year: 2014
Exploring geovisualization symbology for landscape genetics

Landscape genetics, which considers genetic population structure in the context of spatially referenced parameters in the surrounding landscape, has been shown to be extremely useful for wildlife management. Unfortunately its widespread uptake beyond the research community is hampered due to a lack of effective communication of usable information in a suitable format for application by stakeholders such as wildlife regulators or managers. To improve the communication of suitable information, geovisualization of results should be facilitated in a comprehensible format for stakeholders without GIS or genetic expertise. While specialist applications exist, alternative accessible solutions do not provide adequate support for the visualization of multi-attribute spatially referenced genetic population structure information. As a solution, we document our exploration for an appropriate symbology to communicate landscape genetic information through an accessible, web-based interface. A full problem description, review of available technologies, development rationale, and discussion of the symbology exploration are provided.
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.

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Web of Science (2017): Indexed Yes
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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
Seksuel selektion hos en pelagisk copepod, Temora longicornis

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Organisations: National Institute of Aquatic Resources, Centre for Ocean Life, Section for Marine Living Resources
Authors: Sichlau, M. H. (Intern), Eg Nielsen, E. (Intern), Kiørboe, T. (Intern)
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Event: Abstract from 17. Danske havforskermøde, Roskilde, Denmark.
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Publication: Research › Journal article – Annual report year: 2013

Spatiotemporal SNP analysis reveals cryptic distribution shifts and signs of ongoing adaptation at the northern range margin for Atlantic cod

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Spatiotemporal distribution and composition of mixed stock fishery of Atlantic cod (Gadus morhua) in West Greenlandic waters based on retrospective genetic analysis

Historical samples of fish are a unique source of DNA to investigate the temporal dynamics of fish population structure and distribution over time. During the last century Atlantic cod (Gadus morhua) stocks have declined dramatically in Greenlandic Waters. Recent genetic investigations have identified the presence of four genetically distinct spawning groups in the area. We used SNP (Single Nucleotide Polymorphism) analysis of DNA from archived historical cod otoliths (1946-2011) to conduct a retrospective spatiotemporal genetic analysis. The aim was to detect historical changes in the contribution from the different spawning groups in population mixtures of cod in West Greenland Waters in response to climate variability and fisheries. Performing genetic assignment test, we found stable genetic composition of feeding aggregations over decades in some areas, whereas shifts in composition were evident in others. Our findings are consistent with previous results demonstrating that the distribution of different spawning components has changed over time. We discuss how these results will allow a better prediction of future population structure and abundance of cod in a changing environment as in Greenlandic Waters and thus lead to more robust management plans.

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.
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Bibliographical note

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Relations

Activities:

Populationsgenetiske undersøgelser af torsk fra Vestgrønland
Publication: Research - peer-review › Journal article – Annual report year: 2013

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.
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2013
Tissue specific haemoglobin gene expression suggests adaptation to local marine conditions in North Sea flounder (Platichthys flesus L.)

Recent genetic analyses of candidate genes and gene expression in marine fishes have provided evidence of local adaptation in response to environmental differences, despite the lack of strong signals of population structure from conventional neutral genetic markers. In this study expression of the haemoglobin alpha and beta subunit genes was studied in reciprocally transplanted European flounder Platichthys flesus from the highly saline North Sea and the brackish Baltic Sea. Clear differences in expression patterns of haemoglobin alpha and beta subunit genes were found among different types of tissue in flounder. In gill tissue a plastic response to salinity treatments was observed with general up-regulation of these genes concomitant with higher salinity. For liver tissue a population specific expression differences was observed with lower expression at simulated non-native compared to native salinities. Finally, for kidney tissue a stress response was observed in one population, with gene up-regulation when North Sea flounders were transplanted to low salinity. This study underlines the importance of tissue specific gene expression and the significance of gene expression for evolution of local adaptation in high gene flow marine fishes. © 2013 The Genetics Society of Korea
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.
“AquaTrace” The development of tools for tracing and evaluating the genetic impact of fish from aquaculture

Aquaculture represents a key solution to meet the escalating demand for fish. Accordingly, development of appropriate legislation within the European Union aquaculture sector underpinned by cutting-edge research and technology is required. This necessitates implementation of breeding programmes and farming technologies which are economically viable, environmentally friendly, and perceived as socially acceptable. Here we present the objectives, implementation, and potential impact of a new EU FP7 project. The rationale behind AquaTrace is development of reliable and cost-effective molecular tools to identify the genetic origin of both wild and farmed fish (assignment and genetic traceability), as well as for the detection of interbreeding genetic introgression between farmed and wild stocks. This work will be carried out on three marine fish of economic significance: the European sea bass (Dicentrarchus labrax), gilthead sea bream (Sparus aurata), and turbot (Scophthalmus maximus). To address quantitative effects of farm introgression, the rationale is to examine links between key fitness and life-history traits and specific functional genetic variation between wild and farmed fish, using Atlantic salmon and brown trout as model species. Thus, the scientific objectives of AquaTrace are to address and assess the genetic impact of aquaculture escapees introducing genes to wild populations that have been undergoing adaptation to farmed conditions through breeding and domestication selection.

Nonetheless, the methods and aims also have implications for our general knowledge of local adaptation in wild populations, and thus also apply in a restocking context (e.g. when locally depleted wild populations are stocked with non-native strains that are potentially maladapted to local conditions).

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Population Ecology and Genetics, AquaTrace consortium
Authors: Eg Nielsen, E. (Intern), Bekkevold, D. (Intern), Svåsand, T. (Ekstern), Bargelloni, L. (Ekstern), Martinez, P. (Ekstern), Volckaert, F. (Ekstern), Ogden, R. (Ekstern), Martinsohn, J. (Ekstern), Carvalho, G. (Ekstern), Bernatchez, L. (Ekstern), Chavanne, H. (Ekstern), Glover, K. (Ekstern), Maes, G. (Ekstern), Taylor, M. (Ekstern), Webster, L. (Ekstern)
Publication date: 2012
Event: Main Research Area: Technical/natural sciences
Publication: Research - Conference abstract for conference – Annual report year: 2012

Differences in salinity tolerance and gene expression between two populations of Atlantic cod (Gadus morhua) in response to salinity stress

Populations of marine fish, even from contrasting habitats, generally show low genetic differentiation at neutral genetic markers. Nevertheless, there is increasing evidence for differences in gene expression among populations that may be ascribed to adaptive divergence. Studying variation in salinity tolerance and gene expression among Atlantic cod (Gadus morhua) from two populations distributed across a steep salinity gradient, we observed high mortality (45% North Sea cod and 80% Baltic Sea cod) in a reciprocal common garden setup. Quantitative RT-PCR assays for expression of hsp70 and Na/K-ATPase α genes demonstrated significant differences in gene regulation within and between populations and treatment groups despite low sample sizes. Most interesting are the significant differences observed in expression of the Na/K-ATPase α gene in gill tissue between North Sea and Baltic cod. The findings strongly suggest that Atlantic cod are adapted to local saline conditions, despite relatively low levels of neutral genetic divergence between populations.

General information
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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Larsen, P. F. (Ekstern), Eg Nielsen, E. (Intern), Meier, K. (Intern), Olsvik, P. (Ekstern), Hansen, M. (Ekstern), Loeschcke, V. (Ekstern)
Pages: 454-466
Environmental selection on transcriptome-derived SNPs in a high gene flow marine fish, the Atlantic herring (Clupea harengus)

High gene flow is considered the norm for most marine organisms and is expected to limit their ability to adapt to local environments. Few studies have directly compared the patterns of differentiation at neutral and selected gene loci in marine organisms. We analysed a transcriptome-derived panel of 281 SNPs in Atlantic herring (Clupea harengus), a
highly migratory small pelagic fish, for elucidating neutral and selected genetic variation among populations and to identify candidate genes for environmental adaptation. We analysed 607 individuals from 18 spawning locations in the northeast Atlantic, including two temperature clines (5–12 °C) and two salinity clines (5–35‰). By combining genome scan and landscape genetic analyses, four genetically distinct groups of herring were identified: Baltic Sea, Baltic–North Sea transition area, North Sea/British Isles and North Atlantic; notably, samples exhibited divergent clustering patterns for neutral and selected loci. We found statistically strong evidence for divergent selection at 16 outlier loci on a global scale, and significant correlations with temperature and salinity at nine loci. On regional scales, we identified two outlier loci with parallel patterns across temperature clines and five loci associated with temperature in the North Sea/North Atlantic. Likewise, we found seven replicated outliers, of which five were significantly associated with low salinity across both salinity clines. Our results reveal a complex pattern of varying spatial genetic variation among outlier loci, likely reflecting adaptations to local environments. In addition to disclosing the fine scale of local adaptation in a highly vagile species, our data emphasize the need to preserve functionally important biodiversity.

**General information**

State: Published

Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources

Authors: Limborg, M. (Intern), Helyar, S. (Ekstern), de Bruyn, M. (Ekstern), Taylor, M. (Ekstern), Eg Nielsen, E. (Intern), Ogden, R. (Ekstern), Carvalho, G. (Ekstern), Bekkevold, D. (Intern)

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- Web of Science (2016): Indexed yes
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- 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
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- 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
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 suggests 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.

**General information**

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Organisations: National Institute of Aquatic Resources, Section for Management Systems, Section for Public Sector Consultancy, Section for Population Ecology and Genetics
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Links: http://ices.dk/products/CMdocs/CM-2012/N/N0212.pdf
Publication: Research › Paper – Annual report year: 2012

**Insights from the past: Retrospective monitoring of genetic variation in Atlantic cod (Gadus morhua)**

Accelerated rates of climate change and other growing anthropogenic pressure challenge the persistence of many plant and animal populations. Faced with drastically altered environmental conditions, natural populations may either go extinct locally or respond by: 1) dispersing to areas with more favorable conditions; 2) modifying their trait expression to better fit with new local conditions through phenotypic plasticity; or 3) adapt genetically in response to selection. A better understanding of the relative importance of these different coping mechanisms and the interactions between them in different settings will be crucial for making reliable predictions about the future distribution of biodiversity. The present thesis uses genomic analysis of historical and contemporary DNA samples to retrospectively assess how populations of Atlantic cod, Gadus morhua, have responded to environmental and human-induced changes over the past century. Capitalizing on unique collections of archived samples and recently developed genomic resources, we study temporal and spatial variation at both microsatellite loci and up to 1047 gene-associated single nucleotide polymorphisms (SNPs) over a period of 80 years. The extensive sampling in time and the – for a non-model species – high genomic coverage provide unprecedented resolution for disentangling effects of drift, migration and selection. This elucidation generates novel insights about how cod previously have responded microevolutionarily to changed conditions. Focusing on two different cod population complexes, our overarching objectives have been to assess 1) whether levels of genetic diversity, population structure and distribution patterns have remained stable over time despite large demographic changes, 2) if we could detect molecular signatures of selection over decadal time scales and if so, how widespread such signatures would be, 3) if recent changes in selection pressures have been gradual or abrupt and what factors may have driven them, 4) how temporal and spatial variation in selection pressure have interacted, and 5) if signatures of recent selection are parallel between adjacent populations and across different geographic regions.

The thesis is divided into six chapters that report on different efforts to address these objectives. It opens with a general introduction and synopsis that lays out the context for the research, summarizes the main findings and discusses perspectives for future research (Chapter 1). Chapter 2 presents a baseline study demonstrating temporal stability at microsatellite loci over an 80-year period in a Canadian cod population. This result sets the stage for two SNP-based spatiotemporal population genomics studies that search for signatures of recent selection and examine the stability of population structure in Canadian (Chapter 3) and Greenlandic (Chapter 4) cod populations. The final two chapters elaborate on methodological developments that were implemented to reach the primary research goals: Chapter 5 evaluates the quality of SNP genotyping in our historical samples and demonstrates high reproducibility of our presented data while Chapter 6 proposes a new statistical approach to detecting loci under selection based on temporal variation in allele frequencies. Our results provide important insights about the recent dynamics at both study locations. In Canada, the population structure appears to have remained intact over the study period, whereas in Greenland the temporal analyses reveal large changes in the spatial distribution and mixing of different populations. Against this backdrop of contrasting neutral evolutionary patterns, we observe widespread signatures of selection in both systems, reflected in substantial locus-specific divergence in space and time. This suggests ongoing adaptation in response to temporally and
spatially varying selection pressures, and nonparallel patterns between adjacent areas indicate that populations may react differently to environmental variation. Both dispersal and adaptation hence appear to be important responses to environmental change in cod populations, depending on local conditions. 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 of biodiversity and natural resources.

**Monitoring adaptive genetic responses to environmental change**

Widespread environmental changes including climate change, selective harvesting and landscape alterations now greatly affect selection regimes for most organisms. How animals and plants can adapt to these altered environments via contemporary evolution is thus of strong interest. We discuss how to use genetic monitoring to study adaptive responses via repeated analysis of the same populations over time, distinguishing between phenotypic and molecular genetics approaches. After describing monitoring designs, we develop explicit criteria for demonstrating adaptive responses, which include testing for selection and establishing clear links between genetic and environmental change. We then review a few exemplary studies that explore adaptive responses to climate change in Drosophila, selective responses to hunting and fishing, and contemporary evolution in Daphnia using resurrected resting eggs. We further review a broader set of 44 studies to assess how well they meet the proposed criteria, and conclude that only 23% fulfill all criteria. Approximately half (43%) of these studies failed to rule out the alternative hypothesis of replacement by a different, better-adapted population. Likewise, 34% of the studies based on phenotypic variation did not test for selection as opposed to drift. These shortcomings can be addressed via improved experimental designs and statistical testing. We foresee monitoring of adaptive responses as a future valuable tool in conservation biology, for identifying populations unable to evolve at sufficiently high rates and for identifying possible donor populations for genetic rescue. Technological advances will further augment the realization of this potential, especially next-generation sequencing technologies that allow for monitoring at the level of whole genomes.

**General information**

State: Published
Organisations: National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Therkildsen, N. O. (Intern), Eg Nielsen, E. (Intern)
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**Relations**

Activities:
Populationsgenetiske undersøgelser af torsk fra Vestgrønland
Publication: Research › Ph.D. thesis – Annual report year: 2012
Retrospective genomic analysis of Atlantic cod in Greenlandic Waters
The memory remains: application of historical DNA for scaling biodiversity loss

Few species worldwide have attracted as much attention in relation to conservation and sustainable management as Pacific salmon. Most populations have suffered significant reductions, many have disappeared, and even entire evolutionary significant units (ESUs) are believed to have been lost. Until now, no ‘smoking gun’ in terms of direct genetic evidence of the loss of a salmon ESU has been produced. In this issue of Molecular Ecology, Iwamoto et al. (2012) use microsatellite analysis of historical scale samples of Columbia River sockeye salmon (Oncorhynchus nerka) from 1924 (Fig. 1) to ask the pertinent question: Do the historical samples contain salmon from extirpated populations or ESUs? They identified four genetic groups in the historical samples of which two were almost genetically identical to contemporary ESUs in the river, one showed genetic relationship with a third ESU, but one group was not related to any of the contemporary populations. In association with ecological data, the genetic results suggest that an early migrating Columbia River headwater sockeye salmon ESU has been extirpated. The study has significant importance for conservation and reestablishment of sockeye populations in the Columbia River, but also underpins the general significance of shifting baselines in conservation biology, and how to assess loss of genetic biodiversity. The results clearly illustrate the huge and versatile potential of using historical DNA in population and conservation genetics. Because of the extraordinarily plentiful historical samples and rapid advances in fish genomics, fishes are likely to spearhead future studies of temporal ecological and population genomics in non-model organisms.
Unraveling biocomplexity of Northeast Atlantic herring stocks using SNP markers

Atlantic herring (Clupea harengus) exhibit biocomplexity, with widespread, geographically explicit populations that perform long-range migration to common feeding and wintering areas, where they are exploited by fisheries. This means that exploited stocks do not describe discrete units, thereby complicating stock assessment and management. It is therefore of management interest to trace individual population migration patterns and contributions to fisheries. To underpin management and to develop a validated tool for traceability of individuals from mixed-stock samples we applied single nucleotide polymorphism (SNP) markers in Northeast Atlantic herring population samples. Marker panels were targeted to include gene-associated loci to maximize statistical resolution. Application of 281 SNP markers to samples representing different levels of stock complexity showed that the regional origin of individual fish and mixed fish samples could be successfully identified at high statistical power. Our results demonstrate the usefulness of genetic stock identification even in fish, such as herring, exhibiting weak neutral genetic structure, and that such methods allow unprecedented insights into temporal and spatial dynamics applicable to stock assessment methods, as well as presenting a traceability tool for certification of herring and herring products.

General information
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Organisations: National Institute of Aquatic Resources, Section for Population Ecology and Genetics, FishPopTrace Consortium
Authors: Bekkevold, D. (Intern), Limborg, M. (Intern), Helyar, S. (Ekstern), Taylor, M. (Ekstern), Eg Nielsen, E. (Intern), Carvalho, G. (Ekstern)
Publication date: 2012
Event:
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – 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.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Population Ecology and Genetics, FishPopTrace Consortium
Authors: Eg Nielsen, E. (Intern), Hansen, J. H. (Intern), Taylor, M. (Ekstern), Carvalho, G. (Ekstern)
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Adaptive evolution in Atlantic cod: global and regional geographical scales

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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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Event: Poster session presented at European Society for Evolutionary Biology Congress, Turin, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
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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.

General information
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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
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Web of Science (2015): Indexed yes
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Scopus rating (2013): SJR 3.472 SNIP 2.986 CiteScore 7.31
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Gene expression analysis for the identification of selection and local adaptation in fishes

In recent years, variation in gene expression has been recognized as an important component of environmental adaptation in multiple model species, including a few fish species. There is, however, still little known about the genetic basis of adaptation in gene expression resulting from variation in the aquatic environment (e.g., temperature, salinity and oxygen) and the physiological effect and costs of such differences in gene expression. This review presents and discusses progress and pitfalls of applying gene expression analyses to fishes and suggests simple frameworks to get started with gene expression analysis. It is emphasized that well-planned gene expression studies can serve as an important tool for the identification of selection in local populations of fishes, even for non-traditional model species where limited genomic information is available. Recent studies focusing on gene expression variation among natural fish populations are reviewed, highlighting the latest applications that combine genetic evidence from neutral markers and gene expression data.

**General information**
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- Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
- Authors: Larsen, P. F. (Ekstern), Schulte, P. (Ekstern), Eg Nielsen, E. (Intern)
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Scopus rating (2016): CiteScore 1.57 SJR 0.741 SNIP 0.882
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Scopus rating (2014): SJR 0.944 SNIP 0.934 CiteScore 1.76
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Scopus rating (2013): SJR 1.049 SNIP 1.118 CiteScore 1.98
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Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.895 SNIP 0.946 CiteScore 1.66
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.774 SNIP 0.834
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
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Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.883 SNIP 0.968
Web of Science (2008): Indexed yes
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Web of Science (2007): Indexed yes
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Web of Science (2006): Indexed yes
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Web of Science (2004): Indexed yes
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Web of Science (2003): Indexed yes
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Web of Science (2002): Indexed yes
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DOIs:
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.

**General information**

State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Poulsen, N. A. (Ekstern), Hemmer-Hansen, J. (Intern), Loeschcke, V. (Ekstern), Carvalho, G. (Ekstern), Eg Nielsen, E. (Intern)
Pages: 231-243
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Main Research Area: Technical/natural sciences

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Volume: 436
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- BFI (2017): BFI-level 2
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 2
- Scopus rating (2016): CiteScore 2.4
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 2
- Scopus rating (2015): CiteScore 2.56
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 2
- Scopus rating (2014): CiteScore 2.75
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 2
- Scopus rating (2013): CiteScore 2.79
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 2
- Scopus rating (2012): CiteScore 2.9
- ISI indexed (2012): ISI indexed yes
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- BFI (2011): BFI-level 2
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- 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
- Web of Science (2006): Indexed yes
- Web of Science (2005): Indexed yes
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
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.087 SNIP 0.972
Scopus rating (2007): SJR 0.868 SNIP 0.82
Scopus rating (2006): SJR 1.105 SNIP 0.724
Scopus rating (2005): SJR 1.329 SNIP 0.836
Scopus rating (2004): SJR 1.551 SNIP 1.074
Scopus rating (2003): SJR 1.304 SNIP 0.762
Scopus rating (2002): SJR 0.964 SNIP 0.585
Scopus rating (2001): SJR 1.177 SNIP 0.735
Scopus rating (2000): SJR 1.001 SNIP 0.626
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.074 SNIP 0.87
Original language: English
DOIs:
10.1007/s10709-011-9554-4
Source: orbit
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Publication: Research - peer-review › Journal article – Annual report year: 2011

Of fish and SNPs: The potential of genetics for traceability in European fisheries management

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Helyar, S. (Ekstern), Bekkevold, D. (Intern), Hansen, J. H. (Intern), Limborg, M. (Intern), Eg Nielsen, E. (Intern), Carvalho, G. R. (Ekstern)
Publication date: 2011
Main Research Area: Technical/natural sciences
Links:
Source: orbit
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Tracing fish and fish products from ocean to fork using advanced molecular technologies

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Martinsohn, J. (Ekstern), Geffen, A. (Ekstern), Maas, G. (Ekstern), Eg Nielsen, E. (Intern), Ogden, R. (Ekstern), Waples, R. (Ekstern), Carvalho, G. (Ekstern)
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Publication date: 2011

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Title of host publication: Food chain integrity: a holistic approach to food traceability, safety, quality and authenticity
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Publisher: Woodhead Publishing
Editors: Hoofar, J., Kieran, J., Butler, F., Prugger, R.
ISBN (Print): 9780857090683
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Number: 212
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 278705
Publication: Research - peer-review › Book chapter – Annual report year: 2011
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), Hüussy, 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
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.46
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.35
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.32
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Despite the enormous input into the worldwide development of fish and shellfish farming in the recent decades, in part as an attempt to minimize the impact of fishing on already overexploited natural populations, the application of genomics to aquaculture and fisheries remains poorly developed. Improving state-of-the-art genomics research in various aquaculture systems, as well as its industrial applications, remains one of the major challenges in this area and should be the focus of well developed strategies to be implemented in the next generation of projects. This chapter will first provide an overview of the genomic tools and resources available, then discuss the application of genomic approaches to the improvement of fish and shellfish farming (e.g. breeding, reproduction, growth, nutrition and product quality), including the evaluation of stock diversity and the use of selection procedures. The chapter will also discuss the use of genomic approaches to study and monitor natural fish and shellfish populations and to understand interactions within their ecosystems.
Influences of environmental cues, migration history and habitat familiarity on partial migration

The factors that drive partial migration in organisms are not fully understood. Roach (Rutilus rutilus), a freshwater fish, engage in partial migration where parts of populations switch between summer habitats in lakes and winter habitats in connected streams. To test if the partial migration trait is phenotypically plastic or has genetic components, we translocated roach from 2 populations with different opportunities for migration to a lake with migration opportunity, containing a local roach population. This enabled monitoring of partial migration of fish in 3 different situations: 1) previous opportunity for migration, migrating in a familiar environment (the local population); 2) previous opportunity for migration, migrating in an unfamiliar environment; and 3) no previous opportunity for seasonal migration, migrating in an unfamiliar environment. In addition, we evaluated the migration patterns of roach in the lake with migration opportunity where from group 2 fish were translocated. Directional migration in and out of the lakes was monitored using Passive Integrated Transponder technology. Translocated fish with previous migration opportunity showed migration patterns more similar to local fish than to their home lake population, and individuals translocated from the lake without migration opportunity migrated when given the opportunity, suggesting that partial migration is phenotypically plastic and triggered by lake-specific environmental cues. We found temperature to be a proximate cue for migration decisions. Individuals without previous migration opportunity migrated at a lower proportion and with different small-scale migration patterns, suggesting that also genetic components are involved in the expression of the partial migration trait.

General information
State: Published
Organisations: Section for Freshwater Fisheries Ecology, National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Skov, C. (Intern), Aarestrup, K. (Intern), Baktoft, H. (Ekstern), Brodersen, J. (Ekstern), Brönmark, C. (Ekstern), Hansson, L. (Ekstern), Eg Nielsen, E. (Intern), Nielsen, T. (Ekstern), Nilsson, A. (Ekstern)
Pages: 1140-1146
Publication date: 2010
Main Research Area: Technical/natural sciences

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Journal: Behavioral Ecology
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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 1.642 SNIP 1.252 CiteScore 2.71
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.699 SNIP 1.125 CiteScore 2.65
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.814 SNIP 1.311 CiteScore 2.92
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.78 SNIP 1.216 CiteScore 3.02
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.787 SNIP 1.249 CiteScore 3.06
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.958 SNIP 1.238 CiteScore 3.15
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.18 SNIP 1.261
Large effective population size and temporal genetic stability in Atlantic cod (Gadus morhua) in the southern Gulf of St. Lawrence

Worldwide, many commercial fish stocks have experienced dramatic declines due to overfishing. Such fisheries-induced population reductions could potentially erode the genetic diversity of marine fish populations. Based on analyses of DNA extracted from archived and contemporary samples, this paper compares the genetic variability at nine microsatellite loci in a Canadian population of Atlantic cod (Gadus morhua) over 80 years, spanning from before the fishery intensified to now when the population is at historically low abundance. Extensively validated genetic data from the temporally spaced samples were used to estimate the effective population size. Over the period, we observed no loss of either heterozygosity or allelic diversity. Several of the estimation methods applied could not distinguish the effective population size from infinity, and the lower 95% confidence limit on estimates was generally >500, suggesting that the effective population size is probably considerably larger than this. Hence, it appears that the southern Gulf of St. Lawrence cod stock has maintained genetic variability to sustain future evolution despite a dramatic population decline

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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Therkildsen, N. O. (Intern), Eg Nielsen, E. (Intern), Swain, D. P. (Ekstern), Pedersen, J. S. (Ekstern)
Pages: 1585-1595
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Main Research Area: Technical/natural sciences

Publication information
Journal: Canadian Journal of Fisheries and Aquatic Sciences
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BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
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Scopus rating (2016): CiteScore 2.56 SJR 1.322 SNIP 1.163
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.256 SNIP 1.051 CiteScore 2.22
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Using historical DNA to study fisheries-induced genetic change in Atlantic cod (Gadus morhua)

**General information**

State: Published
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)
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Main Research Area: Technical/natural sciences
Links:
Using historical DNA to study fisheries - induced genetic change in commercial fish stocks

General information
State: Published
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
Event: Abstract from Oceans Past III Stories from the sea - history of marine animal populations and their exploitation, November 18-20, Trinity College, Dublin, Ireland.
Main Research Area: Technical/natural sciences
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http://www.hmapcoml.org/oceanspast/
Source: orbit
Source-ID: 269274
Publication: Research › Conference abstract for conference – Annual report year: 2010

Using the candidate gene approach to study fisheries-induced evolution

General information
State: Published
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
Source-ID: 268823
Publication: Research › Poster – Annual report year: 2010

Effective population size and temporal genetic stability in Atlantic cod (Gadus morhua) in the southern Gulf of St. Lawrence

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), Swain, D. P. (Ekstern), Pedersen, J. S. (Ekstern)
Publication date: 2009
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 268825
Publication: Research › Poster – Annual report year: 2009

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.

**General information**

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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources  
Authors: Eg Nielsen, E. (Intern), Hansen, J. H. (Intern), Poulsen, N. A. (Intern), Loeschke, V. (Ekstern), Moen, T. (Ekstern), Johansen, T. (Ekstern), MITTELHOLZER, C. (Ekstern), TARANGER, G. (Ekstern), ogden, R. (Ekstern), carvalho, G. R. (Ekstern)  
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Volume: 9  
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Scopus rating (2016): SJR 1.806 SNIP 1.266 CiteScore 3.12  
BFI (2015): BFI-level 1  
Scopus rating (2015): SJR 2.057 SNIP 1.174 CiteScore 3.37  
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Scopus rating (2014): SJR 2.2 SNIP 1.268 CiteScore 3.42  
Web of Science (2014): Indexed yes  
BFI (2013): BFI-level 1  
Scopus rating (2013): SJR 1.94 SNIP 1.197 CiteScore 3.52  
ISI indexed (2013): ISI indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): SJR 1.94 SNIP 1.137 CiteScore 3.43  
ISI indexed (2012): ISI indexed yes  
BFI (2011): BFI-level 1  
Scopus rating (2011): SJR 2.203 SNIP 1.223 CiteScore 3.73  
ISI indexed (2011): ISI indexed yes  
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 2.737 SNIP 1.385  
Web of Science (2010): Indexed yes  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 2.759 SNIP 1.286  
Web of Science (2009): Indexed yes  
BFI (2008): BFI-level 2  
Scopus rating (2008): SJR 2.426 SNIP 1.239  
Web of Science (2008): Indexed yes  
Scopus rating (2007): SJR 2.568 SNIP 1.238  
Web of Science (2007): Indexed yes  
Scopus rating (2006): SJR 2.554 SNIP 1.12  
Web of Science (2006): Indexed yes  
Scopus rating (2005): SJR 2.257 SNIP 0.969  
Web of Science (2005): Indexed yes  
Scopus rating (2004): SJR 1.51 SNIP 0.637  
Scopus rating (2003): SJR 1.252 SNIP 0.531
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.

General information

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

Publication information

Journal: Marine Ecology Progress Series
Volume: 376
ISSN (Print): 0171-8630
Ratings:
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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 2.4
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.75
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.79
ISI indexed (2013): ISI indexed yes
Population genomics of marine fishes: identifying adaptive variation in space and time

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Hansen, J. H. (Intern), Larsen, P. F. (Intern), Bekkevold, D. (Intern)
Pages: 3128-3150
Publication date: 2009
Main Research Area: Technical/natural sciences

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Journal: Molecular Ecology
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Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.9 SJR 3.508 SNIP 1.651
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.862 SNIP 1.606 CiteScore 5.73
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
Støtteopdræt - en succeshistorie for den vestjyske laks?

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern)
Pages: 16-23
Publication date: 2009
Main Research Area: Technical/natural sciences
ToR d) Assess the possibility for the development of an integrated global management model for Atlantic cod based on genetic information

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Publication date: 2009

Importance of fish biodiversity for the management of fisheries and ecosystems
A group of fisheries scientists participating in a European Union Network of Excellence (MARBEF) summarizes risks to the biodiversity of fish in European seas and recommends ways how existing fish diversity can be conserved, restored and managed. (C) 2008 Elsevier B.V. All rights reserved.

General information
State: Published
Organisations: Section for Population- and Ecosystem Dynamics, National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Hiddink, J. (Ekstern), MacKenzie, B. (Intern), Rijnsdorp, A. (Ekstern), Dulvy, N. (Ekstern), Eg Nielsen, E. (Intern), Bekkevold, D. (Intern), Heino, A. (Ekstern), Lorance, P. (Ekstern), Ojaveer, H. (Ekstern)
Pages: 6-8
Publication date: 2008
Interpopulation differences in expression of candidate genes for salinity tolerance in winter migrating anadromous brown trout (Salmo trutta L.)
Background: Winter migration of immature brown trout (Salmo trutta) into freshwater rivers has been hypothesized to result from physiologically stressful combinations of high salinity and low temperature in the sea. Results: We sampled brown trout from two Danish populations entering different saline conditions and quantified expression of the hsp70 and Na/K-ATPases alpha 1b genes following acclimation to freshwater and full-strength seawater at 2 degrees C and 10 degrees C. An interaction effect of low temperature and high salinity on expression of both hsp70 and Na/K-ATPase alpha 1b was found in trout from the river entering high saline conditions, while a temperature independent up-regulation of both genes in full-strength seawater was found for trout entering marine conditions with lower salinities. Conclusion: Overall our results support the hypothesis that physiologically stressful conditions in the sea drive sea-run brown trout into freshwater rivers in winter. However, our results also demonstrate intra-specific differences in expression of important stress and osmoregulative genes most likely reflecting adaptive differences between trout populations on a regional scale, thus strongly suggesting local adaptations driven by the local marine environment.
Intraspecific variation in expression of candidate genes for osmoregulation, heme biosynthesis and stress resistance suggests local adaptation in European flounder (Platichthys flesus)

Despite the recent discovery of significant genetic structuring in a large number of marine organisms, the evolutionary significance of these often minute genetic differences are still poorly understood. To elucidate the adaptive relevance of low genetic differentiation among marine fish populations, we studied expression differences of osmoregulatory and stress genes in genetically weakly differentiated populations of the European flounder (Platichthys flesus), distributed across a natural salinity gradient. Flounders were maintained in a long-term reciprocal transplantation experiment mimicking natural salinities in the North Sea and the Baltic Sea. Applying real-time quantitative PCR and microarray analysis we studied expression of four candidate genes (hsp70, angiotensinogen, Na/K-ATPase-alpha and 5-aminolevulinic acid synthase (ALAS)) in gill, kidney and liver tissues. Genes involved in osmoregulative processes (Na/K-ATPases-alpha and angiotensinogen) showed highly plastic but similar expression in the two populations dependent on environmental salinity. However, we observed a unique sixfold up-regulation of hsp70 in kidney tissue of flounder from the North Sea following long-term acclimation to Baltic salinities. Similarly, significant differences between North Sea and Baltic flounders in expression of ALAS in response to different salinities were found in gill and liver tissue. These findings strongly suggest that gene expression in flounders is shaped by adaptation to local environmental conditions. This identification of adaptive differences in high gene flow marine organisms adds a new dimension to our current understanding of evolutionary processes in the sea and is of paramount importance for identification, protection and sustainable management of marine biodiversity.
Nedsat salttolerance kan forklare hvorfor havørreder trækker op i ferskvand om vinteren

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Larsen, P. (Ekstern), Eg Nielsen, E. (Intern)
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: www.fiskepleje.dk
Original language: Danish
Links:
http://www.dfu.min.dk/fiskepleje/salttolerance.htm
Source: orbit
Source-ID: 226419
Publication: Research › Journal article – Annual report year: 2008

Sequencing the fish genome for quality – the new success story of cod

General information
State: Published
Waking the dead: the value of population genetic analyses of historical samples

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)
Pages: 450-461
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Fish and Fisheries
Volume: 9
Issue number: 4, special issue
ISSN (Print): 1467-2960
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 7.7 SJR 3.606 SNIP 3.245
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.668 SNIP 3.034 CiteScore 7.05
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.462 SNIP 3.327 CiteScore 7.13
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.488 SNIP 3.12 CiteScore 6.19
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.565 SNIP 2.852 CiteScore 6.14
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 4.025 SNIP 2.854 CiteScore 6.2
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.456 SNIP 2.434
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.617 SNIP 2.61
Adaptive differences in gene expression in European flounder (Platichthys flesus)

General information
State: Published
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), Kruhøffer, M. (Ekstern), Grønkjær, P. (Ekstern), George, S. (Ekstern), Dyrskjøt, L. (Ekstern), Loeschcke, V. (Ekstern)
Pages: 4674-4683
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology
Volume: 16
Issue number: 22
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
Adaptive divergence in a high gene flow environment: Hsc70 variation in the European flounder (Platichthys flesus L.)

**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), Frydenberg, J. (Ekstern), Loeschcke, V. (Ekstern)
Pages: 592-600
Publication date: 2007
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Heredity
Volume: 99
Issue number: 6
ISSN (Print): 0018-067X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.56 SJR 2.03 SNIP 1.243
**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
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**
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
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
Scopus rating (2000): SJR 1.964 SNIP 1.677
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 2.417 SNIP 1.816
Original language: English
DOIs:
10.1111/j.1365-294X.2007.03367.x
Source: orbit
Source-ID: 225726
Publication: Research - peer-review › Journal article – Annual report year: 2007

Genetic identification of individuals and populations

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Koljonen, M. (Ekstern), King, T. (Ekstern), Eg Nielsen, E. (Intern)
Pages: 270-298
Publication date: 2007

Host publication information
Title of host publication: The Atlantic salmon: Genetics, conservation and management
Volume: 9
Place of publication: Oxford
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

Publication information
Journal: Canadian Journal of Fisheries and Aquatic Sciences
Volume: 64
Issue number: 10
ISSN (Print): 0706-652X
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 2.56 SJR 1.322 SNIP 1.163
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.256 SNIP 1.051 CiteScore 2.22
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.443 SNIP 1.379 CiteScore 2.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.421 SNIP 1.081 CiteScore 2.25
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.324 SNIP 1.196 CiteScore 2.29
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.423 SNIP 1.09 CiteScore 2.13
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.425 SNIP 1.118
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.451 SNIP 1.196
Web of Science (2009): Indexed yes
Investigating the genetics of populations

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Villanueva, B. (Ekstern), Eg Nielsen, E. (Intern), Bekkevold, D. (Intern)
Pages: 86-113
Publication date: 2007

Host publication information
Title of host publication: The Atlantic salmon: Genetics, conservation and management
Volume: 4
Place of publication: Oxford
Publisher: Blackwell Publishing Ltd
Editors: Verspoor, E., Stradmeyer, L., Nielsen, J.
ISBN (Print): 978-1-4051-1582-7
Main Research Area: Technical/natural sciences
Source-ID: 225670
Publication: Research - peer-review › Book chapter – Annual report year: 2007

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: Eg Nielsen, E. (Intern), MacKenzie, B. (Intern), Magnussen, E. (Ekstern), Meldrup, D. (Intern)
Pages: 1-3
Publication date: 2007
Main Research Area: Technical/natural sciences
Population size reductions

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Consuegra, S. (Ekstern), Eg Nielsen, E. (Intern)
Pages: 239-269
Publication date: 2007

Host publication information
Title of host publication: The Atlantic salmon: Genetics, conservation and management
Volume: 8
Place of publication: Oxford
Publisher: Blackwell Publishing Ltd
Editors: Verspoor, E., Stradmeyer, L., Nielsen, J.
ISBN (Print): 978-1-4051-1582-7
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 225151
Publication: Research - peer-review › Book chapter – Annual report year: 2007

Straying of Atlantic salmon, Salmo salar, from delayed and coastal releases in the Baltic Sea, with special focus on the Swedish west coast

General information
State: Published
Organisations: Section for Freshwater Fisheries Ecology, National Institute of Aquatic Resources, Institute Management, Section for Population Ecology and Genetics
Authors: Pedersen, S. (Intern), Rasmussen, G. (Intern), Eg Nielsen, E. (Intern), Karlsson, L. (Ekstern), Nyberg, P. (Ekstern)
Pages: 21-32
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Fisheries Management and Ecology
Volume: 14
Issue number: 1
ISSN (Print): 0969-997X
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 1.85 SJR 0.843 SNIP 0.88
The Danish fish fauna during the warm Atlantic period (ca. 7000-3900 bc): Forerunner of future changes?

Vast amounts of fish bone lie preserved in Denmark's soil as remains of prehistoric fishing. Fishing was particularly important during the Atlantic period (ca. 7000-3900 bc, i.e. part of the Mesolithic Stone Age). At this time, sea temperature and salinity were higher in waters around Denmark than today. Analyses of more than 100,000 fish bones from various settlements from this period document which fish species were common in coastal Danish waters at this time. This study provides a basis for comparing the fish fauna in the warm Stone Age sea with the tendencies seen and predicted today as a result of rising sea temperatures. One example concerns the anchovy (Engraulis encrasicolus), which lived in the Stone Age sea, and has become more numerous in Danish waters since the mid-1990s. Other warm water fishes represented among the Stone Age bone samples include smoothhound (Mustelus sp.), common stingray (Dasyatis pastinaca), European sea bass (Dicentrarchus labrax), black sea bream (Spondyliosoma cantharus) and swordfish (Xiphias gladius). Surprisingly, Atlantic cod (Gadus morhua), whose biomass in the Kattegat and eastern Baltic Sea is presently at record...
low levels, was one of the most frequently caught species in the Danish Stone Age sea. These results demonstrate that major changes to the fish fauna near Denmark will occur as climate changes. However, exploitable cod populations can potentially be maintained in waters near Denmark, including the North Sea, but the vulnerability to climate change and the risk of stock collapse will increase at present high fishing mortalities.

**General information**
State: Published
Organisations: Section for Population- and Ecosystem Dynamics, National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Enghoff, I. (Ekstern), MacKenzie, B. (Intern), Eg Nielsen, E. (Intern)
Pages: 167-180
Publication date: 2007
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Fisheries Research
Volume: 87
Issue number: 2-3
ISSN (Print): 0165-7836
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 2.21 SJR 1.12 SNIP 1.136
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 1.067 SNIP 1.133 CiteScore 2.01
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 1.105 SNIP 1.312 CiteScore 2.17
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 1.037 SNIP 1.173 CiteScore 1.85
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.93 SNIP 1.177 CiteScore 1.78
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 1.154 SNIP 1.135 CiteScore 1.7
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 1.041 SNIP 1.1
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 0.985 SNIP 1.065
- Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 2
- Scopus rating (2008): SJR 0.938 SNIP 1.142
- Web of Science (2008): Indexed yes
- Scopus rating (2007): SJR 1.022 SNIP 1.075
- Web of Science (2007): Indexed yes
- Scopus rating (2006): SJR 1.025 SNIP 1.274
The Danish fish fauna during the warm Atlantic period (ca. 7,000-3,900 BC): forerunner of future changes?

General information
State: Published
Organisations: Section for Population- and Ecosystem Dynamics, National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Enghoff, I. B. (Ekstern), MacKenzie, B. (Intern), Eg Nielsen, E. (Intern)
Pages: 1-36
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES Council Meeting
Volume: E:03
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

Bibliographical note
This paper has been published in: Fisheries research 87: 167-180 (2007)
Source: orbit
Source-ID: 225386
Publication: Research - peer-review › Journal article – Annual report year: 2007

What DNA can do for you: Genetic methods in fishery management and biodiversity conservation

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern)
Pages: 20-26
Publication date: 2007
Main Research Area: Technical/natural sciences
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
Genetic impact of gadoid culture on wild fish populations: predictions, lessons from salmonids and how adverse effects can be minimised

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Bekkevold, D. (Intern), Hansen, M. M. (Intern), Eg Nielsen, E. (Intern)
Pages: 198-208
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES Journal of Marine Science
Volume: 63
Issue number: 2
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
Genetic restoration of a stocked brown trout Salmo trutta population using microsatellite DNA analysis of historical and contemporary samples

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

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

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

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

5. Synthesis and applications. This study demonstrates the feasibility of restoring populations that have been admixed with exogenous individuals, by identifying non-admixed individuals using genetic markers. However, the results also highlight the problem that numbers of identified non-admixed individuals may be small, necessitating identification of nearby, closely related populations that can be incorporated into breeding programmes.
HYBRIDLAB (version 1.0): a program for generating simulated hybrids from population samples

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Bach, L. (Ekstern), Kotlicki, P. (Ekstern)
Pages: 971-973
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology Resources
Volume: 6
Issue number: 4
ISSN (Print): 1755-098X
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
Web of Science (2016): Indexed yes
Scopus rating (2016): CiteScore 6.06 SJR 2.864 SNIP 2.176
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.305 SNIP 1.564 CiteScore 4.47
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.842 SNIP 2.217 CiteScore 5.04
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 3.472 SNIP 2.986 CiteScore 7.31
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.172 SNIP 1.87 CiteScore 4.26
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.395 SNIP 1.173 CiteScore 2.75
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.94 SNIP 0.814
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.277 SNIP 1.291
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.926 SNIP 0.938
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.042 SNIP 0.928
Scopus rating (2006): SJR 0.927 SNIP 0.958
Web of Science (2006): Indexed yes
DNA from archived otoliths was used to explore the temporal stability of the genetic composition of two cod populations, the Moray Firth (North Sea) sampled in 1965 and 2002, and the Bornholm Basin (Baltic Sea) sampled in 1928 and 1997. We found no significant changes in the allele frequencies for the Moray Firth population, while subtle but significant genetic changes over time were detected for the Bornholm Basin population. Estimates of the effective population size (N-e) generally exceeded 500 for both populations when employing a number of varieties of the temporal genetic method. However, confidence intervals were very wide and N-e's most likely range in the thousands. There was no apparent loss of genetic variability and no evidence of a genetic bottleneck for either of the populations. Calculations of the expected levels of genetic variability under different scenarios of N-e showed that the number of alleles commonly reported at microsatellite loci in Atlantic cod is best explained by N-e's exceeding thousand. Recent fishery-induced bottlenecks can, however, not be ruled out as an explanation for the apparent discrepancy between high levels of variability and recently reported estimates of N-e.
Underwater but not out of sight: genetic monitoring of effective population size in the endangered North Sea houting (Coregonus oxyrhynchus)

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

Publication information
Journal: Canadian Journal of Fisheries and Aquatic Sciences
Volume: 63
ISSN (Print): 0706-652X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes

BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.469 SNIP 1.823 CiteScore 5.56
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.513 SNIP 1.915
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.455 SNIP 2.024
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.326 SNIP 2.086
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.937 SNIP 1.918
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.932 SNIP 2.111
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.756 SNIP 2.099
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.544 SNIP 1.731
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.148 SNIP 1.564
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.964 SNIP 1.677
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 2.417 SNIP 1.816
Original language: English
DOIs:
10.1111/j.1365-294X.2005.02777.x
Source: orbit
Source-ID: 227153
Publication: Research - peer-review › Journal article – Annual report year: 2006
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
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.324 SNIP 1.196 CiteScore 2.29
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.423 SNIP 1.09 CiteScore 2.13
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.425 SNIP 1.118
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.451 SNIP 1.196
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.589 SNIP 1.379
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.621 SNIP 1.236
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.354 SNIP 1.267
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.558 SNIP 1.553
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.744 SNIP 1.542
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.097 SNIP 1.622
Scopus rating (2002): SJR 1.909 SNIP 1.457
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.769 SNIP 1.46
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.5 SNIP 1.464
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.928 SNIP 1.436
Original language: English
DOIs:
10.1139/F05-260
Source: orbit
Source-ID: 225690
Publication: Research - peer-review › Journal article – Annual report year: 2006
Linking individual migratory behaviour of Atlantic salmon to their genetic origin
Many stocks of fish consist of mixtures of individuals originating from different populations. This is particularly true for many salmon and trout stocks, where fish of different genetic background are being found in the same rivers and/or lakes due to stocking activities or straying caused by increased aquaculture activities. The interpretation of results from studies of survival and behaviour of fish from such “mixed stocks” require information of the genetic background of individual fish. We used genetic analysis combined with radiotelemetry to study upstream migration of Atlantic salmon (Salmo salar) in a Danish lowland river. The river has a small population of native salmon, but salmon juveniles from Irish, Scottish and Swedish populations have been stocked and return as adults. A total of 39 salmon were caught by electrofishing and tagged by surgical implantation. A tissue sample (fin clip) from each tagged salmon was analysed using microsatellite DNA analysis of 6 loci. Assignment tests were used to infer the population of origin. The results showed that the salmon run was composed of approximately 1/3 “native fish”, 1/3 foreign stocked fish and 1/3 escaped farmed salmon. The results indicate that stocked, foreign salmon had a slightly higher mortality and moved more up and down in the river than the native salmon did, but all salmon had problems passing the physical obstructions in the river. The DNA analyses enabled us to compare the behaviour of fish of different genetic origin, but the interpretation of the results was hampered by a high mortality of tagged fish. This study demonstrates that the combination of recent genetic methods and telemetry provides a potent tool for better management of mixed stock fisheries.
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: Eg 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
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 2.56 SJR 1.322 SNIP 1.163
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.256 SNIP 1.051 CiteScore 2.22
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.443 SNIP 1.379 CiteScore 2.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.421 SNIP 1.081 CiteScore 2.25
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.324 SNIP 1.196 CiteScore 2.29
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.423 SNIP 1.09 CiteScore 2.13
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.425 SNIP 1.118
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.451 SNIP 1.196
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.589 SNIP 1.379
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.621 SNIP 1.236
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.354 SNIP 1.267
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.558 SNIP 1.553
Stocking impact and temporal stability of genetic composition in a brackish northern pike population (Esox lucius L.), assessed using microsatellite DNA analysis of historical and contemporary samples

During the last decade, brackish northern pike populations in Denmark have been subject to stocking programmes, using nonindigenous pike from freshwater lakes, in order to compensate for drastic population declines. The present study was designed to investigate the genetic impact of stocking freshwater pike into a brackish pike population in Stege Nor, Denmark. We analysed polymorphism at eight microsatellite loci in samples representing the indigenous Stege Nor population prior to stocking (ie from 1956 to 1957), along with a sample of the contemporary Stege Nor population and samples from the three populations used for stocking. Despite large numbers of stocked fry, the results from both individual and population level admixture analyses demonstrated extremely poor performance and 250), but there were indications of bottlenecks in all samples and populations. We ascribe this finding to historical rather than recent bottlenecks, possibly dating back to founder events associated with postglacial recolonisation.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Larsen, P. F. (Intern), Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Jensen, L. (Ekstern), Loeschcke, V. (Ekstern)
Pages: 136-143
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Heredity
Volume: 95
Issue number: 2
ISSN (Print): 0018-067X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.56 SJR 2.03 SNIP 1.243
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.094 SNIP 1.298 CiteScore 3.47
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.162 SNIP 1.304 CiteScore 3.42
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.029 SNIP 1.149 CiteScore 3.44
ISI indexed (2013): ISI indexed yes
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.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Nielsen, P. (Ekstern), Meldrup, D. (Intern), Hansen, M. M. (Intern)
Pages: 585-595
Publication date: 2004
National forvaltningsplan for laks

General information
State: Published
Organisations: Section for Freshwater Fisheries Ecology, National Institute of Aquatic Resources, Section for Population Ecology and Genetics, Skov- og Naturstyrelsen
Authors: Simonsen, P. (Ekstern), Kjellerup, L. (Ekstern), Koed, A. (Intern), Eg Nielsen, E. (Intern)
Number of pages: 63
Publication date: 2004

Publication information
Publisher: Miljøministeriet, Skov- og Naturstyrelsen
ISBN (Print): 87-72-79589-1
Original language: Danish
Main Research Area: Technical/natural sciences
Links:

Bibliographical note
Denne forvaltningsplan er blevet udarbejdet med fiskerifagligt bidrag fra Danmarks Fiskeriundersøgelser ved Anders Koed og Einar Eg Nielsen
Source: orbit
Source-ID: 227422
Publication: Research - peer-review › Book – Annual report year: 2004

Vildfisk er bare bedst

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern)
Pages: 8-10
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Sportsfiskeren
Volume: 79
Issue number: 2
ISSN (Print): 0038-8211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 225692
Publication: Research › Journal article – Annual report year: 2004

Dambrugslaks duer ikke!

General information
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
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Hansen, M. M. (Intern), Ruzzante, D. (Ekstern), Meldrup, D. (Intern), Grønkjær, P. (Ekstern)
Pages: 1497-1508
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology
Volume: 12
Issue number: 6
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
Fragmentation by weirs in a riverine system: A study of genetic variation in time and space among populations of European grayling (Thymallus thymallus) in a Danish river system

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Meldgaard, T. (Ekstern), Eg Nielsen, E. (Intern), Loeschcke, V. (Ekstern)
Pages: 735-747
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Conservation Genetics
Volume: 4
Issue number: 6
ISSN (Print): 1566-0621
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 0.746 SNIP 0.803 CiteScore 1.62
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.837 SNIP 0.786 CiteScore 1.72
BFI (2014): BFI-level 1
Genetiske fingeraftryk identificerer torsk

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)
Pages: 28-32
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Fisk og Hav
Issue number: 55
ISSN (Print): 0105-9211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Links:
Source: orbit
Source-ID: 226835
Publication: Research › Journal article – Annual report year: 2003
Genudsæt laksene i Ribe Å

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern)
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: http://www.fiskepleje.dk
Original language: Danish
Links:
http://130.226.135.19/fiskepleje/genudsetlaksribeaa.htm
Source: orbit
Source-ID: 226836
Publication: Research › Journal article – Annual report year: 2003

Long-term temporal changes of genetic composition in brown trout (Salmo trutta L.) populations inhabiting an unstable environment

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Østergaard, S. (Ekstern), Hansen, M. M. (Intern), Loeschcke, V. (Ekstern), Eg Nielsen, E. (Intern)
Pages: 3123-3135
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology
Volume: 12
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
Managing marine genetic diversity: time for action?

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Kenchington, E. (Ekstern), Heino, M. (Ekstern), Eg Nielsen, E. (Intern)
Pages: 1172-1176
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES Journal of Marine Science
Volume: 60
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
Monitering af laks (Salmo salar) i vestsvenske elve - Fase 2

General information
State: Published
Organisations: Section for Freshwater Fisheries Ecology, National Institute of Aquatic Resources, Institute Management, Section for Population Ecology and Genetics
Authors: Pedersen, S. (Intern), Rasmussen, G. (Intern), Eg Nielsen, E. (Intern)
Publication date: 2003

Publication information
Publisher: [s.n.]
Original language: Danish
Main Research Area: Technical/natural sciences

Bibliographical note
Rapport til DFFE
Source: orbit
Source-ID: 226181
Publication: Research › Journal article – Annual report year: 2003
Developments in the use of DNA from archived samples (scales, otoliths, bones) for analyzing fish populations (TOR C)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern)
Pages: 5-13
Publication date: 2002
Conference: ICES Council Meeting 2002, Copenhagen, Denmark, 01/10/2002 - 01/10/2002
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES C.M. 2002/
Volume: F:03
Original language: English

Bibliographical note
Report on the Working Group on the Application of Genetics in Fisheries and Mariculture
Source: orbit
Source-ID: 226822
Publication: Research › Conference article – Annual report year: 2002

Genetik og fiskepleje

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)
Number of pages: 199
Pages: 173-181
Publication date: 2002

Host publication information
Title of host publication: At leve med de ferske vande - dengang, nu og i fremtiden
Place of publication: Silkeborg
Publisher: Ferskvandsfiskeriforeningen for Danmark
Editors: Goldschmidt, H., Braagaard, S.
ISBN (Print): 87-98-92230-0
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 226833
Publication: Research › Book chapter – Annual report year: 2002

Genetisk bestandsstruktur hos fisk

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Bekkevold, D. (Intern)
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: http://www.fiskepleje.dk
Original language: Danish
Links:
http://www.dfu.min.dk/fiskepleje/popgen1a.htm
Source: orbit
Source-ID: 225661
Publication: Research › Journal article – Annual report year: 2002
Long-term effective population sizes, temporal stability of genetic composition and potential for local adaptation in anadromous brown trout (Salmo trutta) populations

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

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern)
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: www.fiskepleje.dk
Original language: Danish
Links:
http://www.dfu.min.dk/fiskepleje/nyheder.htm
Source: orbit
Source-ID: 226841
Publication: Research › Journal article – Annual report year: 2002

Populationsgenetik og fiskepleje

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern)
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: http://www.fiskepleje.dk
Original language: Danish
Links:
http://www.dfu.min.dk/fiskepleje/popgen1.htm
Source: orbit
Source-ID: 225680
Publication: Research › Journal article – Annual report year: 2002

Torskens fingeraftryk

General information
State: Published
Admixture analysis and stocking impact assessment in brown trout (Salmo trutta), estimated with incomplete baseline data

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

General information

State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Bekkevold, D. (Intern), Mensberg, K. D. (Intern)
Pages: 1853-1860
Publication date: 2001
Main Research Area: Technical/natural sciences
A new approach to prioritizing marine fish and shellfish populations for conservation

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Kenchington, E. (Ekstern)
Pages: 328-343
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Fish and Fisheries
Volume: 2
Issue number: 4
ISSN (Print): 1467-2960
Ratings:
Assigning individual fish to populations using microsatellite DNA markers

**General information**

**State:** Published

**Organisations:** Section for Population Ecology and Genetics, National Institute of Aquatic Resources

**Authors:** Hansen, M. M. (Intern), Kenchington, E. (Ekstern), Eg Nielsen, E. (Intern)

**Pages:** 93-112

**Publication date:** 2001

**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** Fish and Fisheries

**Volume:** 2
Brown trout (Salmo trutta) stocking impact assessment using microsatellite DNA markers

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

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Ruzzante, D. (Ekstern), Eg Nielsen, E. (Intern), Mensberg, K. D. (Intern)
Pages: 148-160
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Ecological Applications
Volume: 11
Issue number: 1
ISSN (Print): 1051-0761
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 4.4 SJR 2.265 SNIP 1.576
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.76 SNIP 1.759 CiteScore 4.63
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.593 SNIP 1.842 CiteScore 4.59
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.676 SNIP 1.863 CiteScore 4.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.965 SNIP 1.937 CiteScore 4.55
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.286 SNIP 1.975 CiteScore 4.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.784 SNIP 1.675
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.664 SNIP 1.759
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.869 SNIP 1.749
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.805 SNIP 1.876
Scopus rating (2006): SJR 3.065 SNIP 2.06
Scopus rating (2005): SJR 2.819 SNIP 1.966
Dårlige sædvaner i opdrætsforeninger

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Sivebæk, F. (Intern)
Pages: 3-4
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Miljø og vandpleje
Volume: 27
Original language: Danish
Source: orbit
Source-ID: 225647
Publication: Research › Journal article – Annual report year: 2001

Dårlige sædvaner i opdrætsforeninger?

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Sivebæk, F. (Intern)
Pages: 86-89
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Ferskvandsfiskeribladet
Volume: 99
ISSN (Print): 0015-0223
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 225648
Publication: Research › Journal article – Annual report year: 2001

Fred laksen i Varde Å

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology
Looking for a needle in a haystack: Discovery of indigenous Atlantic salmon (Salmo salar L.) in stocked populations

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), Bach, L. (Ekstern)
Pages: 219-232
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Conservation Genetics
Volume: 2
Issue number: 3
ISSN (Print): 1566-0621
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 0.746 SNIP 0.803 CiteScore 1.62
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.837 SNIP 0.786 CiteScore 1.72
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.942 SNIP 0.993 CiteScore 1.98
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.871 SNIP 0.968 CiteScore 2.1
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.875 SNIP 0.962 CiteScore 1.7
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.824 SNIP 0.892 CiteScore 1.61
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.729 SNIP 0.808
BFI (2009): BFI-level 1
Matrilinear phylogeography of Atlantic salmon (Salmo salar L.) in Europe and postglacial colonization of the Baltic Sea area

Sixty-four samples from 46 salmon populations totalling 2369 specimens were used for polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) analysis of the mitochondrial ND1 region. The final analyses included 3095 specimens from 60 populations in Northern Europe. A subsample was analysed by RFLP of ND3/4/5/6. Representative RFLP haplotypes from different parts of the distribution area were sequenced and the phylogeny of European haplotypes and their relations to the North American lineage was described. The four common European haplotypes derive from the ancestral ND1-BBBA (rooting the European clade to the North American) by one-step substitutions: AAAA < AABA < BBBA > BBBB. The Swedish west-coast populations differ from the geographically close southern Baltic, indicating absence of inward and limited outward gene flow through the Danish straits during the last 8000 years. Within the Baltic Sea, only three ND1 haplotypes were detected and there was no variation for ND3/4/5/6. In the whole southern Baltic and in lakes Vanern, Ladoga and Onega the haplotype AABA dominated. Proposed postglacial colonization routes to the Baltic Sea are discussed in relation to the haplotype distribution pattern.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Pages: 89-102
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology
Volume: 10
Issue number: 1
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
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

Publication information
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
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Original language: English
DOIs:
10.1038/35095112

Bibliographical note
Brief communications - Fisheries
Source: orbit
Source-ID: 226843
Publication: Research - peer-review » Journal article – Annual report year: 2001
Populationsgenetiske undersøgelser af Sjællandske ørredbestande

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern)
Pages: 7-9
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Årsberetning / Tuse Å's Ørredsammenslutning
Volume: 2000
Original language: Danish
Source: orbit
Source-ID: 225681
Publication: Research › Journal article – Annual report year: 2001

Review and report on new developments in the identification of genes of relevance to aquaculture and studies of wild populations

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern), Bossier, P. (Ekstern), Boudry, P. (Ekstern), Hansen, M. M. (ed.) (Intern)
Pages: 5-15
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES C.M. 2001/
Volume: F:03
Original language: English

Bibliographical note
Source: orbit
Source-ID: 226847
Publication: Research › Conference article – Annual report year: 2001

En nål i en høstak - genetiske undersøgelser af danske laksebestande

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology
Authors: Eg Nielsen, E. (Intern), Koed, A. (Intern)
Pages: 9-13
Publication date: 2000
Main Research Area: Technical/natural sciences

Publication information
Journal: Miljø- og vandpleje
Volume: 25
ISSN (Print): 1397-5951
Original language: Danish
Source: orbit
Source-ID: 226823
Publication: Research › Journal article – Annual report year: 2000
Genetic monitoring of supportive breeding in brown trout (Salmo trutta L.), using microsatellite DNA markers

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

In a brown trout Salmo trutta population, there was a much higher frequency of injuries among mature male parr than among immature or female parr. The quantitative data are discussed in relation to spawning success and overall fitness.

(C) 2000 The Fisheries Society of the British Isles.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Broberg, M. (Ekstern), Eg Nielsen, E. (Intern), Dieperink, C. (Ekstern)
Pages: 1610-1612
Publication date: 2000
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Biology
Volume: 57
Issue number: 6
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
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.895 SNIP 0.946 CiteScore 1.66
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.774 SNIP 0.834
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.773 SNIP 0.891
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.883 SNIP 0.968
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.996 SNIP 1.06
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.897 SNIP 1.051
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.827 SNIP 0.898
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.945 SNIP 1.148
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.937 SNIP 1.096
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.949 SNIP 1.056
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.874 SNIP 1.1
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.751 SNIP 0.993
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.025 SNIP 1.176

Original language: English
Source: orbit
Source-ID: 225001
Publication: Research - peer-review › Journal article – Annual report year: 2000

**Microsatellite and mitochondrial DNA polymorphism reveals life history dependent interbreeding between hatchery and wild brown trout (Salmo trutta L.)**

The effects of stocking hatchery trout into wild populations were studied in a Danish river, using microsatellite and mitochondrial DNA (mtDNA) markers. Baseline samples were taken from hatchery trout and wild trout assumed to be unaffected by previous stocking. Also, samples were taken from resident and sea trout from a stocked section of the river. Genetic differentiation between the hatchery strain and the local wild population was modest (microsatellite F-ST = 0.06). Using assignment tests, more than 90% of individuals from the baseline samples were classified correctly. Assignment tests involving samples from the stocked river section suggested that the contribution by hatchery trout was low among sea trout (<7%), but high (46%) among resident trout. Hybrid index analysis and a high percentage of mtDNA haplotypes specific to indigenous trout observed among resident trout that were assigned to the hatchery strain suggested that interbreeding took place between hatchery and wild trout. The latter result also indicated that male hatchery trout contributed more to interbreeding than females. We suggest that stronger selection acts against stocked hatchery trout that become anadromous compared to hatchery trout that become resident. As most resident trout are males this could also explain why gene flow from hatchery to wild trout appeared to be male biased. The results show that even despite
modest differentiation at neutral loci domesticated trout may still perform worse than local populations and it is important to be aware of differential survival and reproductive success both between life-history types and between sexes.

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

Publication information
Journal: Molecular Ecology
Volume: 9
Issue number: 5
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
Scopus rating (2008): SJR 3.326 SNIP 2.086
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.937 SNIP 1.918
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.932 SNIP 2.111
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.756 SNIP 2.099
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.544 SNIP 1.731
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.148 SNIP 1.564
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.964 SNIP 1.677
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 2.417 SNIP 1.816
Original language: English
Source: orbit
Source-ID: 225677
Publication: Research - peer-review › Journal article – Annual report year: 2000

**Populationsgenetik i fiskeplejen: Erfaringer fra Karup Å**

**General information**
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern)
Pages: 64-71
Publication date: 2000
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Fisk og Hav
Issue number: 51
ISSN (Print): 0105-9211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Links:
Source: orbit
Source-ID: 225679
Publication: Research › Journal article – Annual report year: 2000

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**Principles for prioritisation of marine finfish and shellfish populations for conservation**

**General information**
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Eg Nielsen, E. (Intern)
Pages: 8-16
Publication date: 2000
Main Research Area: Technical/natural sciences

**Publication information**
Journal: ICES C.M. 2000/
Volume: F:03
Original language: English

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**Bibliographical note**
Report from the Working Group on the Application of Genetics in Fisheries and Mariculture
Source: orbit
Source-ID: 226844
Red laksen i Varde Å

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology
Authors: Eg Nielsen, E. (Intern), Koed, A. (Intern)
Pages: 267-270
Publication date: 2000
Main Research Area: Technical/natural sciences

Publication information
Journal: Ferskvandsfiskeribladet
Volume: 98
ISSN (Print): 0015-0223
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 226845
Publication: Research › Journal article – Annual report year: 2000

Analysis af DNA from old scale samples: Technical aspects, applications and perspectives for conservation

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), Loeschcke, V. (Ekstern)
Pages: 265-276
Publication date: 1999
Main Research Area: Technical/natural sciences

Publication information
Journal: Hereditas
Volume: 130
ISSN (Print): 0018-0661
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 0.328 SNIP 0.422 CiteScore 0.9
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.437 SNIP 0.743 CiteScore 0.93
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.352 SNIP 0.887 CiteScore 0.87
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.5 SNIP 0.724 CiteScore 1.01
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.417 SNIP 0.709 CiteScore 1
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.466 SNIP 0.742 CiteScore 1.06
Danmarks Fiskerilundersøgelser ønsker bedre dialog

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology
Authors: Eg Nielsen, E. (Intern), Koed, A. (Intern)
Pages: 42
Publication date: 1999
Main Research Area: Technical/natural sciences

Publication information
Journal: Sportsfiskeren
Volume: 74
Issue number: 6
ISSN (Print): 0038-8211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 226819
Publication: Research › Journal article – Annual report year: 1999

Det ved vi om laksen netop nu

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology
Authors: Eg Nielsen, E. (Intern), Koed, A. (Intern)
Pages: 34
Publication date: 1999
Main Research Area: Technical/natural sciences

Publication information
Journal: Sportsfiskeren
Volume: 74
Fem år med laksehandlingsplanen

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology
Authors: Eg Nielsen, E. (Intern), Koed, A. (Intern)
Pages: 35
Publication date: 1999
Main Research Area: Technical/natural sciences

Publication information
Journal: Sportsfiskeren
Volume: 74
Issue number: 3
ISSN (Print): 0038-8211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 226821
Publication: Research › Journal article – Annual report year: 1999

Gamle skæl - et nyt værktøj til populationsgenetiske undersøgelser af laksefisk

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)
Pages: 2-11
Publication date: 1999
Main Research Area: Technical/natural sciences

Publication information
Journal: Fisk og Hav
Volume: 49
ISSN (Print): 0105-9211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 226828
Publication: Research › Journal article – Annual report year: 1999

Genetic variation in time and space : Microsatellite analysis of extinct and extant populations of Atlantic salmon

Information on genetic composition of past and present populations may be obtained by analyzing DNA from archival samples. A study is presented on the genetic population structure of extant and extinct local populations of Atlantic salmon from 1913 to 1989 using dried scales as a source of DNA. Variation at six microsatellite loci was studied. Tests for
differentiation among populations and among time series within populations showed that population structure was stable over time. This was also confirmed by a neighbor-joining dendrogram which showed a clear clustering of samples from individual rivers that covered a time span of up to 76 years. These results suggest that salmon populations evolve as semi-independent units connected by modest amounts of gene flow. Additionally, a clear association between geographic and genetic distance was found. This relationship has otherwise been difficult to establish in several recent studies. The discrepancy may be due to impact of human activities on the genetic structure of present populations, whereas old samples represent populations in a more unaffected state. However, other explanations related to differences in the sampling of past and present populations may be equally valid.
Improved primer sequences for the mitochondrial ND1, ND3/4 and ND5/6 segments in salmonid fishes: application to RFLP analysis of Atlantic salmon

New specific primers for the mtDNA segments ND1, ND3/4 and ND5/6 designed from the rainbow trout sequence, improved PCR amplification for salmonid fishes. RFLP analysis revealed restriction site variation for all three segments in Atlantic salmon. Eleven haplotypes were detected in a screening of 30 individuals from four European populations. (C) 1998 The Fisheries society of the British Isles.
Analysis of microsatellite DNA from old scale samples of Atlantic salmon Salmo salar: A comparison of genetic composition over 60 years

Microsatellite analysis was applied to scale samples of Atlantic salmon collected up to 60 years ago. Samples from the 1930s, from a now endangered Danish population, were compared with recent samples (1989), to test if the present population consists of descendants from the original one. Allele frequencies had changed over time, but individuals from the two samples caught about 60 years apart clustered together when compared with the closest neighbouring population and another reference population. However, fewer alleles were detected in the recent sample from the endangered population, most likely due to a population bottleneck or sampling artefacts.

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), Loeschcke, V. (Ekstern)
Pages: 487-492
Publication date: 1997
Main Research Area: Technical/natural sciences

Publication information
Journal: Molecular Ecology
Volume: 6
Issue number: 5
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
**Den genetiske struktur hos atlantisk laks**

**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)
Pages: 18-19
Publication date: 1997
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Sportsfiskeren
Volume: 72
ISSN (Print): 0038-8211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 226820
Publication: Research - peer-review › Journal article – Annual report year: 1997
The problem of sampling families rather than populations: Relatedness among individuals in samples of juvenile brown trout Salmo trutta L.

In species exhibiting a nonrandom distribution of closely related individuals, sampling of a few families may lead to biased estimates of allele frequencies in populations. This problem was studied in two brown trout populations, based on analysis of mtDNA and microsatellites. In both samples mtDNA haplotype frequencies differed significantly between age classes, and in one sample 17 out of 18 individuals less than 1 year of age shared one particular mtDNA haplotype. Estimates of relatedness showed that these individuals most likely represented only three full-sib families. Older trout exhibiting the same haplotypes generally were not closely related.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern), Mensberg, K. D. (Intern)
Pages: 469-474
Publication date: 1997
Main Research Area: Technical/natural sciences

Publication Information
Journal: Molecular Ecology
Volume: 6
Issue number: 5
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
Scopus rating (2008): SJR 3.326 SNIP 2.086
Genetic structure of European populations of *Salmo salar* L. (Atlantic salmon) inferred from mitochondrial DNA

The genetic relationships between the only natural population of Atlantic salmon (*Salmo salar* L.) in Denmark and seven other European salmon populations were studied using RFLP analysis of PCR amplified mitochondrial DNA segments. Six different haplotypes were detected by restriction enzyme analyses of the NADH dehydrogenase 1 segment, employing four endonucleases. Significant genetic differentiation was observed among populations. A hierarchical analysis of the distribution of the mtDNA variability revealed that only a small part was distributed among geographical groups within the study area. No correlation was found between genetic and geographic distance among populations. The effective migration of females (*Nm*) among rivers was estimated to be approximately one per generation.
Laksefisk og genetik (1. del)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern)
Pages: 20-21
Publication date: 1996
Main Research Area: Technical/natural sciences

Publication information
Journal: Sportsfiskeren
Volume: 4
ISSN (Print): 0038-8211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 226830
Publication: Research - peer-review › Journal article – Annual report year: 1996
Laksefisk og genetik (2. del)

**General information**
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern)
Pages: 20-21
Publication date: 1996
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Sportsfiskeren
Volume: 5
ISSN (Print): 0038-8211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 225673
Publication: Research › Journal article – Annual report year: 1996

Ørredracer og hav- og bækørred

**General information**
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Eg Nielsen, E. (Intern)
Pages: 18-19
Publication date: 1996
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Sportsfiskeren
Volume: 9
ISSN (Print): 0038-8211
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 225694
Publication: Research › Journal article – Annual report year: 1996

**Projects:**

*Population Genomics of Archived Shark Samples*
National Institute of Aquatic Resources
Period: 01/01/2018 → 31/12/2020
Number of participants: 3
Phd Student:
Christensen, Camilla (Intern)
Supervisor:
Bekkevold, Dorte (Intern)
Main Supervisor:
Eg Nielsen, Einar (Intern)
Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)
Project: PhD

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

Reproductive Physiology of Female European Eel
National Institute of Aquatic Resources
Period: 15/12/2016 → 14/12/2019
Number of participants: 4
PhD Student:
Jørgensen, Michelle Grace Pinto (Intern)
Supervisor:
Kjørsvik, Elin (Ekstern)
Eg Nielsen, Einar (Intern)
Main Supervisor:
Tomkiewicz, Jonna (Intern)

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

Ballast water - Tool for supporting the delimitation of a "same risk area" (39348)
A project financed by the Danish Maritime Fund via the Danish Nature Agency, to develop a decision support tool for authorities and consultants involved with the ballast water convention and measures preventing the spread of marine invasive species. The tool will support decision makers in member nations of the International Maritime Organisation (IMO) to identify and delimit marine areas with high connectivity considering hydrography and species biology. Identification of marine areas with high connectivity can provide a basis for granting exemptions in relation to the ballast water convention and the requirement for ships to treat ballast water before being discharged into the sea. The tool development is based on existing freeware including "IBM Lib" (DTU Aqua's own individual-based modeling system for linking individual-based models to hydrographical model data), Netlogo (a widely used IBM simulation system) and R (a statistical programming and data handling package).

This project is coordinated by DTU Aqua.
The project is funded by the Danish Maritime Fund via the Danish Nature Agency.
National Institute of Aquatic Resources
Section for Marine Living Resources
Danish Meteorological Institute
Anchor-Lab
Period: 01/03/2016 → 01/12/2016
Number of participants: 9
Research areas: Marine Living Resources & Observation Technology
Project participant:
Mosegaard, Henrik (Intern)
Stage, Bjarne (Intern)
Eg Nielsen, Einar (Intern)
Worsøe Clausen, Lotte (Intern)
van Deurs, Mikael (Intern)
Andersen, Niels Gerner (Intern)
Project Manager, organisational:
Pedersen, Eva Maria (Intern)
Project Manager, academic:
Hansen, Flemming Thorbjørn (Intern)
Project Coordinator:
Christensen, Asbjørn (Intern)

**Strengthening the Danish populations of Atlantic salmon – Increasing populations, genetic resources and recreational fishing (39340)**

In the beginning of the 1980’ies indigenous Danish salmon populations were close to extinction due to habitat degradation and stocking with non-native strains. Conservation efforts, led to a resurge of the populations in western Jutland. However, following the initial increases, Danish salmon populations have stagnated in recent years. Whether this is a response to limiting local factors or a correlated response across population (e.g. to climate change), is unknown. A profitable recreational fishery has developed on the Danish salmon. If the productivity of Danish salmon populations can be improved, this fishery and the related economical gain have the potential to increase correspondingly.

Atlantic salmon has a highly complex and specialized life cycle where the weakest link(s) determines the productivity of the salmon population. Accordingly, there is a need for a multifaceted research project The main objectives of this project will be reached through six work packages aiming to: 1. Identify key local and global bottlenecks production of salmon across four life-stages, 2. Determine genetic characteristics (‘quality’) of local populations and identify how measures of ‘quality’ should be implemented into stocking programmes and 3. Communicate and implement insights on optimal management and exploitation to stakeholders.

The overarching aim of the project is to provide research based knowledge that can be directly implemented into a self-sustainable management framework that maximizes salmon population sizes, and hereby vastly increases local income from a recreational fishery with a high economic potential.

This project is coordinated by Danish Center for Wild Salmon.

The project is funded by Innovation Fund Denmark.

Section for Freshwater Fisheries Ecology
National Institute of Aquatic Resources

Danish Center for Wild Salmon
Period: 01/01/2016 → 31/12/2019
Number of participants: 5
Research areas: Freshwater Fisheries and Ecology & Population Genetics
Project participant:
Mena, Belén Jiménez (Intern)
Project Manager, academic:
Koed, Anders (Intern)
Eg Nielsen, Einar (Intern)
Bekkevold, Dorte (Intern)
Aarestrup, Kim (Intern)

**An icean of : Assessing environmental DNA to monitor aquatic organisms in marine environments**

National Institute of Aquatic Resources
The vision of AtlantOS is to improve and innovate Atlantic observing by using the Framework of Ocean Observing to obtain an international, more sustainable, more efficient, more integrated, and fit-for-purpose system. Hence, the AtlantOS initiative will have a long-lasting and sustainable contribution to the societal, economic and scientific benefit arising from this integrated approach. This will be achieved by improving the value for money, extent, completeness, quality and ease of access to Atlantic Ocean data required by industries, product supplying agencies, scientist and citizens. The overarching target of the AtlantOS initiative is to deliver an advanced framework for the development of an integrated Atlantic Ocean Observing System that goes beyond the state-of –the-art, and leaves a legacy of sustainability after the life of the project.

The specific task of DTU Aqua is to conduct analysis of environmental DNA (e-DNA) using an Environmental Sample Processor (ESP). All living organisms secrete DNA to the surrounding environment. Recently it has been shown that such “e-DNA” can be extracted from seawater and used to identify the organisms present within a designated sea area. The “ESP” is a moored automated DNA laboratory, which can be deployed for up to three months for in-situ analysis and at the same time send back real-time analytical results. Hitherto it has been used for identification of marine bacteria, phyto- and zooplankton with very good results. We will modify the ESP to allow its use for e-DNA analysis. The aim is to conduct unprecedented “proof of concept” of e-DNA sensors for monitoring of important species in a number of sea areas and time periods.

The project is funded by EU, Horizon 2020.

This project is coordinated by DTU Aqua and has 54 additional partners across Europe

National Institute of Aquatic Resources
Section for Marine Living Resources
GEOMAR - Helmholtz Centre for Ocean Research Kiel
Natural Environment Research Council
Marine Institute
National Center for Scientific Research
International Council for the Exploration of the Sea
Institute of Marine Research
Scottish Association for Marine Science

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)
Project Manager, academic:
Eg Nielsen, Einar (Intern)

Strategies for the gradual elimination of discards in European fisheries (DiscardLess) (39238)

DiscardLess will help provide the knowledge, tools and technologies as well as the involvement of the stakeholders to achieve the gradual elimination of discarding. These will be integrated into Discard Mitigation Strategies (DMS) proposing cost-effective solutions at all stages of the seafood supply chain.

This project is coordinated by DTU Aqua.

The project is funded by EU, Horizon2020.

National Institute of Aquatic Resources
Section for Ecosystem based Marine Management
IFREMER
Instituto Español de Oceanografía
University of Bergen
Strathclyde University
University of Copenhagen
Université de Bretagne Occidentale
Sea Fish Industry Authority
Marine Scotland Science
FAO
Simrad Spain SLU
Dynamic user-driven marine e-maps for the advancement of Danish industrial fisheries (GUPD-VIND) (39246)
This project aims at strengthening Danish industrial fisheries development in order to (i) reduce the search time and fuel consumption per. ton of fish caught (revenues: 16 million DKK/year), (ii) make better use of the sprat quota (revenues: 15 million DKK/year, by a full quota uptake), (iii) pave the way for sustainable self-management of resources in the industrial fisheries sector and (iv) contribute to creating and maintaining jobs in the local fishing community.

The specific objectives of the project: Development of an IT tool that will contain (i) a platform to improve sharing of knowledge and registration of observable and derived variables (data), and (ii) user-defined and user-controlled digital Marine Maps with those specific data that fishermen consider important as background information in the planning and
implementation of fishing trips. These marine data include (but are not limited to) a portfolio of Marine Maps spanning from
the North Sea hydrography and bottom conditions over distribution of plankton and fish to water-DNA.

The needs for a technological development of this fishery comes from increasing average vessel size, while the number of
large vessels is reduced to about 1/8 of what it was in the past. The immediate consequence is a reduction in the
collective search performance and knowledge sharing. In addition, the area based management of the sandeel fishery
introduced in 2011 has contributed to a reduction of fishermen's opportunities to diversify fishing and explore a wider
variety of fishing grounds. Finally, the sprat fishery is uncertain because of by-catch limits and a very variable CPUE
driven by wind and weather. This has led to an underutilization of the sprat quota by around 100,000 tons per year.
Fisherman knowledge of good fishing opportunities is based on the correspondence between historical catches and
observable variables at the time of capture, such as the seasons, wind, waves and tides, and it is precisely this kind of
knowledge that the project wants to combine with a technological solution, so that all relevant data is made widely
available to the fishermen by developing user-controlled dynamic digital Marine Maps. The project includes a business
plan for the IT company Anchor Lab, which develops the user-controlled Marine Maps, and plans for derived effects in
terms of better utilization of the sprat quota and fuel savings through the use of the Marine Maps. Besides the economic
effects, the project contributes to CO2 reduction, and supports the technological development of a modern industrial
fishery sector, based on a natural resource to be managed by the EU in accordance with ICES' advice.

This project is coordinated by DTU Aqua.

The project is funded by the Ministry of Environment and Food of Denmark through the Green Development and
Demonstration Program (GUDP).

National Institute of Aquatic Resources
Section for Marine Living Resources
Danish Meteorological Institute
Anchor-Lab
Period: 01/01/2015 → 30/06/2018
Number of participants: 8
Research areas: Marine Living Resources & Marine Populations and Ecosystem Dynamics & Population Genetics &
Observation Technology
Project participant:
Christensen, Asbjørn (Intern)
Stage, Bjarne (Intern)
Eg Nielsen, Einar (Intern)
Worsøe Clausen, Lotte (Intern)
van Deurs, Mikael (Intern)
Andersen, Niels Gerner (Intern)
Pedersen, Eva Maria (Intern)
Project Coordinator:
Mosegaard, Henrik (Intern)

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

National Institute of Aquatic Resources
Period: 01/11/2013 → 22/01/2018
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
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)

Project

The early life of the European eel in the ichthyoplankton community of the Sargasso Sea

National Institute of Aquatic Resources
Period: 01/06/2013 → 01/12/2016
Number of participants: 6

Phd Student:
Ayala, Daniel Jiro (Intern)

Supervisor:
Riemann, Lasse (Ekstern)

Main Supervisor:
Munk, Peter (Intern)

Examiner:
Eg Nielsen, Einar (Intern)
Grønkjær, Peter (Ekstern)
Miller, Michael J. (Ekstern)

Financing sources
Source: Internal funding (public)
The development of tools for tracing and evaluating the genetic impact of fish from aquaculture (AquaTrace) (38948)

The genetic changes associated with domestication in aquaculture pose an increasing threat to the integrity of native fish gene pools. Consequently, there is a burgeoning need for the development of molecular tools to assess and monitor the genetic impact of escaped or released farmed fish. In addition, exploration of basic links between genetic differences among farmed and wild fish and differences in important life-history traits with fitness consequences are crucial prerequisites for designing biologically informed management strategies.

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

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

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

The project is funded by EU, Framework Programme 7.

National Institute of Aquatic Resources
Section for Marine Living Resources
Havforskningssinstituttet
Università degli Studi di Padova
Universidad de Santiago de Compostela
Katholieke Universiteit
TRACE Wildlife Forensics Network Limited
European Commission - Joint Research Center
INRA Institut National de La Recherche Agronomique
Bangor University
Period: 01/11/2012 → 31/10/2016
Number of participants: 5
Research area: Population Genetics
Project participant:
Bekkevold, Dorte (Intern)
Mensberg, Karen-Lise Dons (Intern)
Project Manager, organisational:
Thomsen, Kirsten (Intern)
Phd Student:
Frank-Gopolos, Thomas (Intern)
Project Coordinator:
Eg Nielsen, Einar (Intern)
Project

Salmon Management Plan revision (38944)

The Atlantic salmon is one of a number of species afforded special protection, along with their habitats, under the EU Habitats and Species Directive (Council Directive 92/43/EEC). This Directive provides for the creation of a network of protected sites across the EU known as ‘Natura 2000’, and includes Special Areas of Conservation (SACs) designated for salmon. In Denmark salmon is under the responsibility of the Ministry of the Environment (ME). ME has engaged DTU Aqua to update and revise the latest Danish Management Plan of Salmon (2004).
The project is coordinated by the Ministry of Environment.

National Institute of Aquatic Resources
Section for Freshwater Fisheries Ecology

Danish Ministry of the Environment
Period: 01/10/2012 → 31/01/2013
Number of participants: 3
Research area: Freshwater Fisheries and Ecology
Project participant:
Sivebæk, Finn (Intern)
Eg Nielsen, Einar (Intern)

Project Manager, academic:
Koed, Anders (Intern)

Development of genetic tools to distinguish Greenland’s cod stocks (38956)
The goal of this project is to develop genetic tools that can improve the management of Atlantic cod (Gadus morhua) in Greenland by enabling identification of separate population components. Building on results from a previous study that demonstrated pronounced population structure among cod inhabiting Greenlandic waters, we will 1) develop cost-effective DNA tests to reveal the population of origin for unknown individuals, 2) apply these tests in concrete case studies relevant for stock assessment and management advise, and 3) develop a user manual for implementing these tests in the management of cod in Greenland.

National Institute of Aquatic Resources
Section for Marine Living Resources

Greenland Institute of Natural Resources
Period: 01/09/2012 → 30/11/2012
Number of participants: 2
Research area: Population Genetics
Project participant:
Eg Nielsen, Einar (Intern)

Project Manager, academic:
Therkildsen, Nina Overgaard (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)

Project

How Danish fisheries can exploit the CFP discard ban – An elucidation (39075)

European fisheries should ultimately operate without discards. This is clearly expressed by both the European Union and the most important fishery nations outside the Union in Europe. This is in accordance with the overall intention to reduce the ecological impact through changing production and consumption patterns. The most important tool introduced by the Union is the Landing Obligation (LO). The new Common Fisheries Policy (CFP) will move towards a gradual elimination of discards on a case-by-case basis (EC, 2013). This policy is fully implemented in 2019. To be in due time, before the implementation of the LO, a project trying to describe the consequence of this new policy, was done in the years 2012 to 2014. The state of the art of knowledge of discard and the future use of this fraction that will be landed have been evaluated.

The final report suggests that the practical implementation of the LO-principle may take place as a scheme where large scale trials on results based management demonstrate the possible needs of prescriptive regulation in addition to full catch accountability.

The report thoroughly investigates the issues related to a management that can give the fishermen the incentive and tools to comply with full catch accountability It assesses the amounts of discard and offal in Danish fisheries and it points to solutions regarding handling and marketing of the “discard fraction” in the form of fresh raw material or silage solutions.

The report recommended to:
- Evaluate the economy of a silage solution on vessels and in relevant harbours. The evaluation should be made as a commercial venture projects including storage, handling distribution, marketing and economic performance.
- Analyse the values fish under reference sizes if sold for human consumption.
- Establish reliable and cheap methods to quantify species composition in silage.

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
AquaMind
Period: 01/01/2012 → 31/12/2014
Number of participants: 2
Research areas: Fisheries Management & Population Genetics
Project participant:
Eg Nielsen, Einar (Intern)
Project Coordinator:
Larsen, Erling (Intern)
Project

Historical changes in population distribution and micro-evolution in response to climate variability: Retrospective genomic analysis of archived fish tissue collections
National Institute of Aquatic Resources
Period: 01/09/2011 → 05/11/2014
Number of participants: 5
Phd Student:
Bonanomi, Sara (Intern)
Main Supervisor:
Eg Nielsen, Einar (Intern)
Examiner:
Bekkevold, Dorte (Intern)
Ogden, Rob (Ekstern)
Olafsdottir, Gudbjorg Asta (Ekstern)

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

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

Climate change on marine ecosystems and resource economics (NorMER) (38898)
Marine ecosystems are under pressure from both anthropogenic climate change and high exploitation rates. A major challenge to managers and scientists is to identify ways that oceans can provide food and other services in a sustainable way under changing climatic and socioeconomic conditions. As physical, biological and socioeconomic factors interact at several levels, cross-disciplinary approaches are needed to meet this challenge.

This Nordic project has
(1) evaluated climate effects on Nordic marine ecosystems,
(2) Build new tools for predicting biological consequences of climate change,
(3) quantified impacts on profit, employment, and harvesting of cod.
This has been achieved through the work of 16 PhDs, 4 postdocs, 1 climate scientist, and the combined expertise of 45 senior scientists located at 10 institutions in 8 Nordic countries.

The project was coordinated by University of Oslo, Norway.

The project was funded by Nordforsk, Nordic Council of Ministers.

National Institute of Aquatic Resources
Centre for Ocean Life
University of Oslo
Stockholm University
Åbo Academy University
University of Helsinki
Swedish Meteorological and Hydrological Institute
University of Iceland
University of the Faroe Islands
Greenland Institute of National Resources
University of Bergen

Period: 01/01/2011 → 31/12/2015
Number of participants: 6
Research areas: Oceanography & Marine Population and Ecosystem Dynamics & Population Genetics
Project participant:
Andersen, Ken Haste (Intern)
Visser, Andre (Intern)
Thygesen, Uffe Høgsbro (Intern)
Eg Nielsen, Einar (Intern)
MacKenzie, Brian (Intern)
Project Manager, academic:
Kiørboe, Thomas (Intern)

The population of whitefish (Coregonus lavaretus) in Ringkøbing Fjord: Effects of fishery, stocking and natural reproduction (38827)

Objectives of the project are to improve our knowledge on the whitefish population in the Ringkøbing Fjord Lagoon and effects associated with the commercial exploitation of the population, i.e., to what extent the traditional gill-net (46 mm monofilnet) fishery for whitefish affect both the whitefish population and other species of fish in the lagoon. Another goal is to establish how much natural reproduction and stocking of hatchery reared fry contributes to the adult population. These results will provide a much better basis for the management of whitefish populations in Denmark in general and in Western Jutland in particular.

The natural population of whitefish in the Ringkøbing Fjord Lagoon has been the subject of an extensive fishery for more than 100 years. The fishery is primarily performed by commercial fishermen, but estimated from the number of recreational fishers in the area, a substantial amount is caught by this group as well. The lagoon holds the largest population of whitefish in Denmark. The official landing statistics (only covering the commercial catches) show that the catch through the 20th century typically has varied between 10 and 60 tons per year (e.g., mean 1980-2000 25.1 tons per year). Since 2001 the landings have increased to a mean of 55 tons per year (range 14-94 t), with a mean value of 1.2 m DKK. This constitutes 75-95% of the total Danish whitefish fishery.

Since 1986, ca. 4 million hatchery-reared fry have been stocked in the lagoon each year. 3.6 million are stocked as newly hatched larvae in April. 0.4 million are raised to a size of 3-4 cm before stocking in late May.

The population of sea trout (Salmo trutta) in the main tributary of the lagoon, the River Skjern, is much smaller than expected, considering the environmental conditions of both the river and the lagoon and the size of the river. One possible reason is by-catch in the whitefish fishery. The landing of sea trout and the endangered salmon (Salmo salar) from the lagoon is prohibited and the discard mortality for sea trout is considered to be very high. Investigations on the subject of by-catch in gill-nets set for whitefish in the Baltic Sea supports this hypothesis.

In the project we estimate the catch of whitefish and the by-catch of other fish species in the whitefish gill-net fishery, with special emphasis on salmonids, by a combination of experimental fishery, monitoring selected commercial fishing trips and a questionnaire the fishermen on their effort. A number of different approaches re time and place of fishing and net construction is tested to describe how much by-catch can be minimized.
The result of natural spawning in River Skjern is investigated by a combination of catching newly hatched larvae with drift-nets and e-DNA analysis of water samples from the river. The latter method is a very novel approach.

Through the experimental fishing, supplemental data on the whitefish, salmonids as well as other species (less detailed) are collected to describe population dynamic parameters (size and age distribution, growth, condition etc.), primarily of whitefish and salmonids.

The results show that by-catch of sea-trout in the whitefish gill-net fishery is unavoidable, but also that the by-catch can be reduced substantially by employing specific gears and methods. The by-catch of salmon is insignificant while the by-catch of other species, especially flounder, is substantial. These results will be reported in autumn 2016. The investigation on natural reproduction in the River Skjern is still ongoing and will be reported in 2017.

This project is coordinated by DTU Aqua.

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

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**National Institute of Aquatic Resources**

**Section for Freshwater Fisheries Ecology**

**Period:** 01/01/2011 → 31/12/2016

**Number of participants:** 4

**Research area:** Freshwater Fisheries and Ecology & Population Genetics

**Project participant:**

- Eg Nielsen, Einar (Intern)
- Hansen, Brian Klitgaard (Intern)
- Berg, Søren (Intern)
- Støttrup, Josianne Gatt (Intern)

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**The Atlantic cod (Gadus morhua) in Greenlandic waters – past and future under climate change (38873)**

This project aimed at understanding and predicting the population dynamics of Atlantic cod (Gadus morhua) in Greenlandic waters in response to climate change. This was achieved through biological, chemical, and genetic analysis of unique cod otolith collections, generating historical time series on growth, food composition, and genetic population structure. Relationships between environmental changes and the historical distribution, size and growth of individual cod populations were elucidated and used to predict their dynamics under different climate scenarios. The project generated fundamental insights, but also contributed significantly to proactive management of cod in Greenland.

The project was coordinated by DTU Aqua.

The project was funded by the Greenland Climate Research Centre.

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**National Institute of Aquatic Resources**

**Section for Marine Living Resources**

**Aarhus University**

**Greenland Institute of Natural Resources**

**Period:** 01/01/2010 → 31/12/2013

**Number of participants:** 2

**Research area:** Population Genetics

**Project participant:**

- Therkildsen, Nina Overgaard (Intern)

**Project Manager, academic:**

- Eg Nielsen, Einar (Intern)

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**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:**
The molecular basis of local adaptation in brown trout

National Institute of Aquatic Resources
Period: 01/02/2009 → 25/04/2012
Number of participants: 8
Phd Student:
Meier, Kristian (Intern)
Supervisor:
Als, Thomas Damm (Intern)
Hansen, Michael Møller (Intern)
Skov, Christian (Intern)
Main Supervisor:
Bekkevold, Dorte (Intern)
Examiner:
Eg Nielsen, Einar (Intern)
Allendorf, Fred W. (Ekstern)
Knutsen, Halvor (Ekstern)

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

Developing fisheries management indicators and targets (DEFINEIT) (38763)
DEFINEIT constructed operational models of fish stock dynamics explicitly taking into account exploitation and climatic conditions and combine these models with basic economic models. To ensure an outstanding scientific level in each of these areas, the project brought together key competences in operational multispecies modelling, stock recruitment relationships, population dynamics of non-target fish species and economic modelling of fisheries from a wide geographic area ranging from the Barents Sea to the North Sea. The project used multispecies models to investigate changes in predation induced by differences in the distribution and the amount of alternative food. Effects of technical interactions in the fishing process were considered to avoid delivering management advice for different stocks which is mutually inconsistent. Integrating the knowledge gained, the project suggested methods for estimating reference points. The project identified the main causes of variation in recruitment patterns between stocks as well as the key processes from spawning to recruitment of selected stocks. The consequences of using proxies to describe stock reproductive potential were determined and survival during early life stages was investigated in order to identify the role of the physical and biological environment. The improved understanding of recruitment variability was used in individual stock assessment and included in multispecies models to provide reliable predictions. The maximum level of fishing effort consistent with sustainment of susceptible species was estimated along with the effect of discard of by-catch on economic yield. The project developed resource indicators that combine economic, social and biological indicators and relate directly to the benefit for the society. Future stock dynamics limits to sustainable ecosystem exploitation and the fishing levels delivering maximum sustainable economic yield under selected climatic scenarios were analyzed in unison to ensure the delivery of mutually consistent management advice. General properties of the ecosystems were used to suggest rules of thumb for management in areas where the amount of data available is insufficient to construct similar models.

The project was coordinated by DTU Aqua.

The project was funded by EU, MariFish, ERA-NET.
National Institute of Aquatic Resources
Section for Ecosystem based Marine Management
Cefas
Institute of Marine Research
Hellenic Centre for Marine Research
Marine Research Institute
University of Copenhagen
University of St Andrews
University of Southern Denmark
Wageningen IMARES
Imperial College of Science, Technology and Medicine
Period: 01/01/2009 → 30/06/2012
Number of participants: 9
Research areas: Ecosystem based Marine Management & Marine Living Resources & Marine Populations and Ecosystem Dynamics & Population Genetics
Project participant:
Gislason, Henrik (Intern)
Payne, Mark (Intern)
Worsøe Clausen, Lotte (Intern)
Mosegaard, Henrik (Intern)
Bekkevold, Dorte (Intern)
Eg Nielsen, Einar (Intern)
Vinther, Morten (Intern)
Lewy, Peter (Intern)
Project Manager, academic:
Rindorf, Anna (Intern)

Local adaption in Baltic Sea small pelagic fishes
National Institute of Aquatic Resources
Period: 01/09/2008 → 28/03/2012
Number of participants: 8
Phd Student:
Limborg, Morten (Intern)
Supervisor:
Hansen, Michael Møller (Intern)
MacKenzie, Brian (Intern)
Eg Nielsen, Einar (Intern)
Main Supervisor:
Bekkevold, Dorte (Intern)
Examiner:
Mosegaard, Henrik (Intern)
Hauser, Lorenz (Ekstern)
Vasemägi, Anti (Ekstern)

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

Advancing understanding of Atlantic Salmon at sea: Merging genetics and ecology to resolve stock-specific migration and distribution patterns (SALSEA-Merge) (38282)
Over the past two decades, an increasing proportion of North Atlantic salmon are dying at sea during their oceanic feeding migration. The specific reasons for the decline in this important species are as yet unknown, however, climate change is likely to be an important factor. In some rivers in the southern part of the species range, wild salmon now face extinction. This is in spite of unprecedented management measures to halt this decline. Arguably the greatest challenge in salmon conservation is to gain insight into the spatial and ecological use of the marine environment by different regional and river stocks, which are known to show variation in marine growth, condition, and survival. Salmon populations may migrate to different marine zones, whose environmental conditions may vary. To date it has been impossible to sample and identify the origin of sufficient numbers of wild salmon at sea to enable this vital question to be addressed.

The aim of SALSEA-Merge was to provide the basis for advancing our understanding of oceanic-scale, ecological and ecosystem processes. Such knowledge is fundamental to the future sustainable management of this key marine species. Through a partnership of nine European nations the program delivered innovation in the areas of: genetic stock identification techniques, new genetic marker development, fine scale estimates of growth on a weekly and monthly basis, the use of novel high seas pelagic trawling technology and individual stock linked estimates of food and feeding patterns. In addition, the use of the three-dimensional Regional Ocean Modeling System, merging hydrography, oceanographic, genetic and ecological data, provided novel stock specific migration and distribution models.

This widely supported project provided the basis for a comprehensive investigation into the problems facing salmon at sea. It also acted as an important model for understanding the factors affecting survival of many other important marine species.

The project was coordinated by Institute of Marine Research, Norway.

The project was funded by EU, Framework Programme 7.

National Institute of Aquatic Resources
Section for Marine Living Resources
Institute of Marine Research
Marine Institute
Marine Scotland
Norwegian Institute for Nature Research
University of Exeter
National University of Ireland
Queen's University Belfast
Swansea University
Institute of Freshwater Fisheries
University of Turku
Universidad de Oviedo
Genindex
Finnish Game and Fisheries Research Institute
The Faroese Fisheries Laboratory
Atlantic Salmon Trust
North Atlantic Salmon Conservation Organisation
TOTAL Fondation d'entreprise pour la Biodiversité et la Mer
Conservatoire National du Saumon Sauvage
Loughs Agency
Period: 01/01/2008 → 31/12/2011
Number of participants: 1
Research areas: Population Genetics & Freshwater Fisheries and Ecology
Project Manager, academic:
Eg Nielsen, Einar (Intern)
Project
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.
The project was funded by EU, Framework Programme 7.

National Institute of Aquatic Resources
Section for Marine Living Resources
Bangor University
University of Padua
Universidad Complutense
Katholieke Universiteit
University of Bologna
University of Bergen
European Commission - Joint Research Center
University of Bremen
Wildlife DNA Services
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)

Understanding the mechanisms of stock recovery (UNCOVER) (38104)
The UNCOVER project has produced a rational scientific basis for developing Long-Term Management Plans (LTMP) and recovery strategies for 11 of the ecologically and socioeconomically most important fish stocks/fisheries in the Norwegian and Barents Seas, the North Sea, the Baltic Sea and the Bay of Biscay and Iberian Peninsula.

UNCOVER’s objectives were to:
(i) identify changes experienced during stock depletion/collapses,
(ii) to understand prospects for recovery,
(iii) to enhance the scientific understanding of the mechanisms of fish stock/fishery recovery, and
(iv) to formulate recommendations how best to implement LTMPs/recovery plans.

The project recommends that such plans ideally should include:
(i) Consideration of stock-regulating environmental processes,
(ii) Incorporation of fisheries effects on stock structure and reproductive potential,
(iii) Consideration of changes in habitat dynamics due to global change,
(iv) Incorporation of biological and technological multispecies interactions,
(v) Integration of economically optimized harvesting,
(vi) Exploration of the socio-economic implications and political constraints from existing and alternative recovery plans,
(vii) Investigations on the acceptance of plans by stakeholders and specifically incentives for compliance by the fishery,
(viii) Agreements with and among stakeholders.

UNCOVER has provided imperative policy support underpinning the following fundamental areas:
(i) Evolution of the Common Fisheries Policy with respect to several aims of the ‘Green Paper’;
(ii) Contributing to the Marine Strategy Framework Directive with respect to fish stocks/communities;
(iii) achieving Maximum Sustainable Yield (MSY) for depleted fish stocks. This has been done by contributing to
LTMPs/recovery plans for fish stocks/fisheries, demonstrating how to shift from scientific advice based on limit reference
points towards setting and attaining targets such as MSY, and furthering ecosystem-based management through
incorporating multispecies, environmental and habitat, climate variability/change, and human dimensions into these plans.

The project was coordinated by Institut für Ostseefischerei, Bundesforschungsanstalt für Fischerei, Germany.

National Institute of Aquatic Resources
Section for Marine Living Resources
Bundesforschungsanstalt für Fischerei
Marine Research Unit, Marine and Food Technological Centre
Cefas
University of Portsmouth
Marine Laboratory
Instituto Español de Oceanografía
Aalborg University
Leibniz Institut für Meereswissenschaften, Universität Kiel
IFREMER
Institute of Marine Research
Sea Fisheries Institute
Knipovich Polar Research Institute of Marine Fisheries and Oceanography
Nederlands Instituut voor Visserij Onderzoek b.v.
University of Aberdeen
University of Bergen
University of Hamburg

Period: 01/01/2006 → 31/12/2010
Number of participants: 14
Research areas: Marine Living Resources & Fish Biology
Contact person:
Köster, Fritz (Intern)
Project participant:
Tomkiewicz, Jonna (Intern)
Vinther, Morten (Intern)
Payne, Mark (Intern)
Munk, Peter (Intern)
Støttrup, Josianne Gatt (Intern)
Storr-Paulsen, Marie (Intern)
Eg Nielsen, Einar (Intern)
Brander, Keith (Intern)
Andersen, Ken Haste (Intern)
Huwer, Bastian (Intern)
Bastardie, Francois (Intern)
Project Manager, academic:
Neuenfeldt, Stefan (Intern)
MacKenzie, Brian (Intern)

Scaling from individuals to populations (SLIP) (38726)
The research school SLIP (Scaling from Individuals to Populations) focuses on how individual behavior and mutual
interactions generate the dynamics observed at the population level. This topic forms the link between the basic and
applied marine ecological research environments in Denmark and requires input from biology, mathematics and statistics.
SLIP is one of the five research networks and research schools under the Danish Network for Aquaculture and Fisheries Research (Fishnet). SLIP has arranged a number of national and international PhD courses and workshops and has served to focus the interest on size and trait-based modeling, as well as on improved understanding of the physiology, genetics and behavior of marine organisms, in particular fish.

The project is coordinated by DTU Aqua.

DTU Data Analysis
National Institute of Aquatic Resources
Section for Marine Living Resources
Roskilde University
Royal Veterinary and Agricultural University
Aarhus University
University of Copenhagen

Period: 01/01/2000 → 31/12/2008
Number of participants: 9
Research area: Marine Populations and Ecosystem Dynamics

Project participant:
Höffle, Hannes (Intern)
Gürkan, Zeren (Intern)
Therkildsen, Nina Overgaard (Intern)
Sichlau, Mie Hylstofte (Intern)
Mosgaard, Thomas (Intern)
Frisk, Christina (Intern)

Project Manager, academic:
Gislason, Henrik (Intern)
Kiørboe, Thomas (Intern)
Eg Nielsen, Einar (Intern)

Activities:

ICES - Science Committee meeting - SCICOM (External organisation)
Period: 2012 → …
Einar Eg Nielsen (Participant)
National Institute of Aquatic Resources
Section for Population Ecology and Genetics
Degree of recognition: International

Related external organisation

ICES - Working Group on the Application of Genetics in Fisheries and Mariculture - WGAGFM (External organisation)
Period: 2012 → …
Einar Eg Nielsen (Participant)
National Institute of Aquatic Resources
Section for Population Ecology and Genetics
Degree of recognition: International

Related external organisation

ICES - Working Group on the Application of Genetics In Fisheries and Mariculture - WGAGFM
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar