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Publications:

Population genetics of pike

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Wennerström, L. (Ekstern), Bekkevold, D. (Intern), Laikre, L. (Ekstern)
Number of pages: 402
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Den skeptiske optimist: Udfordringer og perspektiver i anvendelse af eDNA til marin monitering og fiskeriforvaltning

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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)
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Event: Abstract from Dansk Havforskermøde, Helsingør, Denmark.
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Dynamiske brugerstyrede havkort til værdiløft af dansk industrifiskeri (GUDP-VIND)

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Oceans and Arctic, Section for Marine Ecology and Oceanography, AnchorLab, Danish Meteorological Institute, Danish Fishermen's Producers' Organization
Authors: Mosegaard, H. (Intern), Pedersen, E. M. (Intern), Sparrevoehn, C. R. (Ekstern), Lund, H. S. (Ekstern), Skov, O. (Ekstern), Dueholm, M. (Ekstern), She, J. (Ekstern), Christensen, A. (Intern), Stage, B. (Intern), Worsøe Clausen, L. (Intern), Deurs, M. V. (Intern), Bekkevold, D. (Intern), Andersen, N. G. (Intern)
Publication date: 2017
Event: Abstract from Dansk Havforskermøde, Helsingør, Denmark.
Main Research Area: Technical/natural sciences
Low genetic and phenotypic divergence in a contact zone between freshwater and marine sticklebacks: gene flow constrains adaptation

Background: Distinct hybrid zones and phenotypic and genomic divergence is often observed between marine and freshwater three-spine sticklebacks (Gasterosteus aculeatus). Nevertheless, cases also exist where marine-freshwater divergence is diffuse despite seemingly similar environmental settings. In order to assess what characterizes these highly different outcomes, we focused on the latter kind of system in the Odder River, Denmark. Here, a previous study based on RAD (Restriction site Associated DNA) resequencing found non-significant genomewide differentiation between marine and freshwater sticklebacks. In the present study, we analyzed samples on a finer geographical scale. We assessed if the system should be regarded as panmictic, or if fine-scale genetic structure and local selection was present but dominated by strong migration. We also asked if specific population components, that is the two sexes and different lateral plate morphs, contributed disproportionally more to dispersal.

Results: We assessed variation at 96 SNPs and the Eda gene that affects lateral plate number, conducted molecular sex identification, and analyzed morphological traits. Genetic differentiation estimated by FST was non-significant throughout the system. Nevertheless, spatial autocorrelation analysis suggested fine scale genetic structure with a genetic patch size of 770 m. There was no evidence for sex-biased dispersal, but full-plated individuals showed higher dispersal than low- and partial-plated individuals. The system was dominated by full-plated morphs characteristic of marine sticklebacks, but in the upstream part of the river body shape and frequency of low-plated morphs changed in the direction expected for freshwater sticklebacks. Five markers including Eda were under possible diversifying selection. However, only subtle clinal patterns were observed for traits and markers. Conclusions: We suggest that gene flow from marine sticklebacks overwhelms adaptation to freshwater conditions, but the short genetic patch size means that the effect of gene flow on the most upstream region must be indirect and occurs over generations. The occurrence of both weak unimodal and strong bimodal hybrid zones within the same species is striking. We suggest environmental and demographic factors that could determine these outcomes, but also highlight the possibility that long-term population history and the presence or absence of genomic incompatibilities could be a contributing factor.
Non-parallel divergence across Danish freshwater and marine three-spined stickleback *Gasterosteus aculeatus* populations

This work investigated whether multiple freshwater populations of three-spined stickleback *Gasterosteus aculeatus* in different freshwater catchments in the Jutland Peninsula, Denmark, derived from the same marine populations show repeated adaptive responses. A total of 327 *G. aculeatus* collected at 13 sampling locations were screened for genetic variation using a combination of 70 genes putatively under selection and 26 neutral genes along with a marker linked to the ectodysplasin gene (*eda*), which is strongly correlated with plate armour morphs in the species. A highly significant genetic differentiation was found that was higher among different freshwater samples than between marine–freshwater samples. Tests for selection between marine and freshwater populations showed a very low degree of parallelism and no single nucleotide polymorphism was detected as outlier in all freshwater–marine pairwise comparisons, including the *eda*. This suggests that *G. aculeatus* is not necessarily the prime example of parallel local adaptation suggested in much of the literature and that important exceptions exist (i.e. the Jutland Peninsula). While marine populations in the results described here showed a high phenotype–genotype correlation at *eda*, a low association was found for most of the freshwater populations. The most extreme case was found in the freshwater Lake Hald where all low-plated phenotypes were either homozygotes for the allele supposed to be associated with completely plated morphs or heterozygotes, but none were homozygotes for the putative low-plated allele. Re-examination of data from seven *G. aculeatus* studies agrees in showing a high but partial association between phenotype–genotype at *eda* in *G. aculeatus* freshwater populations and that mismatches occur everywhere in the European regions studied (higher in some areas, i.e. Denmark). This is independent of the *eda* marker used.

General information

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University, Universite Laval
Authors: Pujolar, J. M. (Ekstern), Ferchaud, A. (Ekstern), Bekkevold, D. (Intern), Hansen, M. M. (Ekstern)
Pages: 175-194
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information

Journal: Journal of Fish Biology
Pike (Esox lucius L.) on the edge: consistent individual movement patterns in transitional waters of the western Baltic

Pike in the western Baltic Sea live on the edge of their salinity tolerance. Under physiologically challenging conditions, organism may respond by moving to environmentally more benign areas during critical periods, such as during spawning. We hypothesised that pike in a brackish lagoon (8–10 ppt salinity) would perform spawning- and feeding-related movements between areas with different salinity regimes. Twenty-two pike were caught prior to spawning, tagged with acoustic transmitters, and their movements were tracked for 18 months. Pike showed two main patterns of movements that were consistent within individuals across two years. Whereas some individuals stayed in the lagoon year-round, most pike left the lagoon for longer periods after spawning and returned to the lagoon prior to following year’s spawning season. We found no evidence that probability of moving out of the lagoon co-varied with either length or condition factor. Despite the fact that the lagoon’s salinity is close to the reported upper limit for pike egg development, results indicated that all pike spawned in the lagoon. Correspondingly, genetic data showed that all fish belonged to the same reproductive population unit. Movement patterns thus appear to reflect individual variation in home-range and/or resource optimisation following ideal free principles.
Responsible genetic approach to stock restoration, sea ranching and stock enhancement of marine fishes and invertebrates

The origins of agriculture date to about 9000 years, but commercial culture and supplementation of marine populations reach back only a few centuries. Hence, wild populations still play a major role in seafood production. Closed culture, stock restorations, sea ranching and stock enhancements of marine fishes and invertebrates have been implemented with various outcomes. A review of the literature indicates that considerable effort has been directed toward culture technologies to maximize production, but scant attention has been given to genetic risks to wild populations. Genetic risks from stock enhancements can be substantial, because of inattention to brood-stock sizes, and because hybridization between hatchery-reared and wild individuals can lower the fitness or lead to the extinction of a natural population. In many cases, small brood-stock sizes have led to the loss of genetic diversity. In some cases, hatchery-reared individuals appear to have replaced, rather than supplemented, wild populations. Here, we outline a responsible approach to managing genetic resources that includes six steps: (1) assess the costs and benefits of a stock restoration or enhancement, (2) set goals and genetic benchmarks, (3) use appropriate brood stock and limit domestication, (4) design release strategies that maximize the effectiveness of supplementation efforts, (5) track individuals after release and (6) minimize genetic impacts on wild populations. Stock supplementation is often viewed as an immediate solution to a stock decline, but should be undertaken as a last resort because of the high cost of implementation and the substantial ecological and genetic risks to wild populations.
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)
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Genetic structure of West Greenland populations of lumpfish Cyclopterus lumpus

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.

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State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Greenland Institute of Natural Resources, Greenland Institute of Natural Resources
Authors: Mayoral, E. G. (Intern), Olsen, M. (Ekstern), Hedeholm, R. (Ekstern), Post, S. L. (Intern), Eg Nielsen, E. (Intern), Bekkevold, D. (Intern)
Pages: 2625-2642
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BFI (2014): BFI-level 1
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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Scopus rating (2012): SJR 0.93 SNIP 1.035 CiteScore 1.88
ISI indexed (2012): ISI indexed yes
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BFI (2011): BFI-level 1
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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
Outlier loci detect intraspecific biodiversity amongst spring and autumn spawning herring across local scales

Herring, Clupea harengus, is one of the ecologically and commercially most important species in European northern seas, where two distinct ecotypes have been described based on spawning time; spring and autumn. To date, it is unknown if these spring and autumn spawning herring constitute genetically distinct units. We assessed levels of genetic divergence between spring and autumn spawning herring in the Baltic Sea using two types of DNA markers, microsatellites and Single Nucleotide Polymorphisms, and compared the results with data for autumn spawning North Sea herring. Temporally replicated analyses reveal clear genetic differences between ecotypes and hence support reproductive isolation. Loci showing non-neutral behaviour, so-called outlier loci, show convergence between autumn spawning herring from demographically disjoint populations, potentially reflecting selective processes associated with autumn spawning ecotypes. The abundance and exploitation of the two ecotypes have varied strongly over space and time in the Baltic Sea, where autumn spawners have faced strong depression for decades. The results therefore have practical implications by highlighting the need for specific management of these co-occurring ecotypes to meet requirements for sustainable exploitation and ensure optimal livelihood for coastal communities.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Estonian University of Life Sciences, University of Tartu, Queen's University Belfast
Authors: Bekkevold, D. (Intern), Gross, R. (Ekstern), Arula, T. (Ekstern), Helyar, S. J. (Ekstern), Ojaveer, H. (Ekstern)
Publication date: 2016
Main Research Area: Technical/natural sciences

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Volume: 11
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Steps toward nation-wide monitoring of non-indigenous species in Danish marine waters under the Marine Strategy Framework Directive

This report is the outcome of MONIS 2 – or in full, “Monitoring of Non-Indigenous Species in Danish Marine Water, phase 2” – and includes three deliverable: (1) a national Target Species List including 50 species, (2) a draft Technical Guidance Report, and (3) in silico designed and tested primers and probes for 48 of the 50 species on the Target Species List. The list is based on discussions at a workshop and subsequent scoring and ranking of relevant species. The draft Technical Guidance report is anchored in existing Standard Operating Procedures (i.e. protocols for sampling, storage and analysis) and adapted to the requirements of the Danish NOVANA programme. In addition, the report includes suggestions for next steps to take to implement and improve monitoring and assessment activities in regard to non-indigenous species in Danish marine water

General information
A holistic ecosystem approach for marine management and conservation: Opportunities through the application of genetic and genomic approaches

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Andersen, J. H. (Ekstern), Møller, P. R. (Ekstern), Kallenbach, E. (Ekstern), Hesselsøe, M. (Ekstern), Knudsen, S. W. (Ekstern), Bekkevold, D. (Intern), Hansen, B. K. (Intern), Thaulow, J. (Ekstern)
Number of pages: 122
Publication date: 2016

Connectivity, growth and survival in a spatially structured fish population, which is currently managed as seven separate stock units

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Section for Marine Ecology and Oceanography
Authors: Martinsohn, J. T. (Ekstern), Volckaert, F. (Ekstern), Bekkevold, D. (Intern)
Number of pages: 2
Publication date: 2015
Event: Paper presented at ICES Annual Science Conference 2015, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
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Bibliographical note
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From regionally predictable to locally complex population structure in a freshwater top predator: River systems are not always the unit of connectivity in Northern Pike Esox lucius

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

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

Species showing complex life cycles provide excellent opportunities to study the genetic associations between life cycle stages, as selective pressures may differ before and after metamorphosis. The European eel presents a complex life cycle with two metamorphoses, a first metamorphosis from larvae into glass eels (juvenile stage) and a second metamorphosis into silver eels (adult stage). We tested the hypothesis that different genes and gene pathways will be under selection at different life stages when comparing the genetic associations between glass eels and silver eels. Results: We used two sets of markers to test for selection: first, we genotyped individuals using a panel of 80 coding-gene single nucleotide
polymorphisms (SNPs) developed in American eel; second, we investigated selection at the genome level using a total of 153,423 RAD-sequencing generated SNPs widely distributed across the genome. Using the RAD approach, outlier tests identified a total of 2413 (1.57 %) potentially selected SNPs. Functional annotation analysis identified signal transduction pathways as the most over-represented group of genes, including MAPK/Erk signalling, calcium signalling and GnRH (gonadotropin-releasing hormone) signalling. Many of the over-represented pathways were related to growth, while others could result from the different conditions that eels inhabit during their life cycle. Conclusions: The observation of different genes and gene pathways under selection when comparing glass eels vs. silver eels supports the adaptive decoupling hypothesis for the benefits of metamorphosis. Partitioning the life cycle into discrete morphological phases may be overall beneficial since it allows the different life stages to respond independently to their unique selection pressures. This might translate into a more effective use of food and niche resources and/or performance of phase-specific tasks (e.g. feeding in the case of glass eels, migrating and reproducing in the case of silver eels

**General information**

State: Published  
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, National Museum of Natural Sciences, Marine Biology and Biotechnology Center, Aarhus University, Universite Laval  
Authors: Pujolar, J. (Ekstern), Jacobsen, M. (Ekstern), Bekkevold, D. (Intern), Lobón-Cerviá, J. (Ekstern), Jónsson, B. (Ekstern), Bernatchez, L. (Ekstern), Hansen, M. M. (Ekstern)  
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BFI (2011): BFI-level 1  
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Spring and autumn spawning herring in the Gulf of Riga: intraspecific biodiversity across small local scales

**General information**
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Bekkevold, D. (Intern), Gross, R. (Ekstern), Arula, T. (Ekstern), Ojaveer, H. (Ekstern)
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Thermal and maternal environments shape the value of early hatching in a natural population of a strongly cannibalistic freshwater fish

Hatching early in the season is often assumed to elevate fitness, particularly in cannibalistic fish in which size-dependent predation mortality is a major selective force. While the importance of the thermal environment for the growth of fish is undisputed, the relevance of maternal effects for offspring growth in the wild is largely unknown. Otoliths of 366 age-0 pike (Esox lucius L.) were sampled in a natural lake over three seasons. All offspring were assigned to more than 330 potential mothers using 16 informative microsatellites. We found temperature and past maternal environment (as represented by juvenile growth rate), but not female total length, to jointly contribute to explain within- and among-season size variation in juvenile pike. While there was no statistical evidence for maternal effects on offspring growth rate, fast female juvenile growth positively correlated with the offspring length in early summer. One mechanism could be related to fast-growing females spawning somewhat earlier in the season. However, the more likely mechanism emerging in our study was that fast-growing females could have been in better condition prior to spawning, in turn possibly producing higher numbers of high-quality eggs. Our study is among the few to reveal carry-over effects related to past maternal environments on offspring performance in a naturally reproducing fish stock. At the same time, our study underscores recent arguments that size-dependent maternal effects may not be expressed in the wild and that early hatching does not generally produce size advantages in light of stochastically varying temperature conditions

**General information**
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Berlin
Authors: Pagel, T. (Ekstern), Bekkevold, D. (Intern), Pohlmeier, S. (Ekstern), Wolter, C. (Ekstern), Arlinghaus, R. (Ekstern)
Pages: 951-965
Publication date: 2015
A low-density SNP array for analyzing differential selection in freshwater and marine populations of three-spine stickleback (Gasterosteus aculeatus)

Background: The three-spine stickleback (Gasterosteus aculeatus) has become an important model species for studying both contemporary and parallel evolution. In particular, differential adaptation to freshwater and marine environments has led to high differentiation between freshwater and marine stickleback populations at the phenotypic trait of lateral plate morphology and the underlying candidate gene Ectodysplasin (EDA). Many studies have focused on this trait and candidate gene, although other genes involved in marine-freshwater adaptation may be equally important. In order to develop a resource for rapid and cost efficient analysis of genetic divergence between freshwater and marine sticklebacks, we generated a low-density SNP (Single Nucleotide Polymorphism) array encompassing markers of chromosome regions under putative directional selection, along with neutral markers for background.

Results: RAD (Restriction site Associated DNA) sequencing of sixty individuals representing two freshwater and one marine population led to the identification of 33,993 SNP markers. Ninety-six of these were chosen for the low-density SNP array, among which 70 represented SNPs under putatively directional selection in freshwater vs. marine environments, whereas 26 SNPs were assumed to be neutral. Annotation of these regions revealed several genes that are candidates for affecting stickleback phenotypic variation, some of which have been observed in previous studies whereas others are new.

Conclusions: We have developed a cost-efficient low-density SNP array that allows for rapid screening of polymorphisms in three-spine stickleback. The array provides a valuable tool for analyzing adaptive divergence between freshwater and marine stickleback populations beyond the well-established candidate gene Ectodysplasin (EDA).

General information
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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University, BGI-Shenzhen
Authors: Ferchaud, A. (Ekstern), Pedersen, S. H. (Ekstern), Bekkevold, D. (Intern), Jian, J. (Ekstern), Niu, Y. (Ekstern), Hansen, M. M. (Ekstern)
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Scopus rating (2011): SJR 2.271 SNIP 1.197 CiteScore 4.38
Assessing patterns of hybridization between North Atlantic eels using diagnostic single-nucleotide polymorphisms

The two North Atlantic eel species, the European eel (Anguilla anguilla) and the American eel (Anguilla rostrata), spawn in partial sympatry in the Sargasso Sea, providing ample opportunity to interbreed. In this study, we used a RAD (Restriction site Associated DNA) sequencing approach to identify species-specific diagnostic single-nucleotide polymorphisms (SNPs) and design a low-density array that combined with screening of a diagnostic mitochondrial DNA marker. Eels from Iceland (N=159) and from the neighboring Faroe Islands (N=29) were genotyped, along with 94 larvae (49 European and 45 American eel) collected in the Sargasso Sea. Our SNP survey showed that the majority of Icelandic eels are pure European eels but there is also an important contribution of individuals of admixed ancestry (10.7%). Although most of the hybrids were identified as F1 hybrids from European eel female × American eel male crosses, backcrosses were also detected, including a first-generation backcross (F1 hybrid × pure European eel) and three individuals identified as second-generation backcrosses originating from American eel × F1 hybrid backcrosses interbreeding with pure European eels. In comparison, no hybrids were observed in the Faroe Islands, the closest bodies of land to Iceland. It is possible that hybrids show an intermediate migratory behaviour between the two parental species that ultimately brings hybrid larvae to the shores of Iceland, situated roughly halfway between the Sargasso Sea and Europe. Only two hybrids were observed among Sargasso Sea larvae, both backcrosses, but no F1 hybrids, that points to temporal variation in the occurrence of hybridization.

General information

State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University, University of the Faroe Islands, Marine Biology and Biotechnology Center, BGI-Shenzhen, BGI-Europe, University of Leuven, Universite Laval
Pages: 627-637
Publication date: 2014
Main Research Area: Technical/natural sciences
Local adaptation at the transcriptome level in brown trout: Evidence from early life history temperature genomic reaction norms

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

**General information**

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources, Aarhus University, Universite Laval
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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.
Prey or predator – expanding the food web role of sandeel (Ammodytes marinus)

We report an unexpected observation of lesser sandeel Ammodytes marinus foraging on juveniles and late larval stages of the same species. This recording sheds new light on the cannibalistic and piscivorous capacity of forage fish and raises a number of questions about the role of forage fish in marine food webs. In 2012 and 2013 the stomachs of 748 sandeels from 36 different commercial sandeel hauls in the central North Sea were opened. 9% of these stomachs contained late stage sandeel larvae. In order to better understand the cannibalistic nature of sandeels, we made a detailed analysis of another 450 sandeels from a single haul with a high frequency of apparent cannibals. One-third of the stomachs contained a minimum of one young sandeel (mean length 2.7 cm; max. length 4.9 cm), 10 percent contained 5 or more, and one stomach contained 18. Analyses of sample DNA confirmed that predator and prey were conspecifics. Larger specimens were more likely to be cannibals. However, among cannibals the specific sandeel larva consumption was independent of cannibal size. We argue that this piscivorous cannibalistic behaviour may not only be a key factor in explaining recruitment fluctuations in North Sea sandeel stocks, but it may also add a new element to the complexity of energy flow in marine food chains.

General information

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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: Eigaard, O. R. (Intern), Deurs, M. V. (Intern), Behrens, J. (Intern), Bekkevold, D. (Intern), Brander, K. (Intern), Plambech, M. (Intern), Schreiber Plet-Hansen, K. (Intern), Mosegaard, H. (Intern)
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, University of Salford
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"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).

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.

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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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Scopus rating (2009): SJR 3.455 SNIP 2.024
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Scopus rating (2008): SJR 3.326 SNIP 2.086
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
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Web of Science (2006): Indexed yes
FishPopTrace: a new genetic technique for fisheries monitoring and the identification of IUU

The importance of marine organisms for both economic and ecological reasons is enormous; and knowledge of population structure and connectivity is crucial for the sustainable utilization and conservation of exploited fish stocks. However, in most cases our understanding of these spatial patterns of natural variation at a genetic level is limited. For marine fish, the maintenance of local stocks containing adaptive diversity is associated with the sustainability and resilience of marine fisheries in the face of climatic and anthropogenic threats. However, many previous genetic studies have observed weak genetic structure in marine fish and, combined with a pelagic larval stage, this has supported the hypothesis that gene flow is extensive and that there is little opportunity for differentiation and local adaptation any scale other than macrogeographic. However, the application of single nucleotide polymorphisms (SNPs) has the potential to demonstrate previously undetected spatial and temporal population structuring and signatures of adaptive variation. In addition, SNPs are uniquely applicable for the identification and monitoring of wild fish populations and the traceability/authenticity of products throughout the food supply chain, allowing effective enforcement of fisheries regulations, and the identification of IUU. Here we demonstrate the utility of SNP panels developed in a European Commission-funded consortium, FishPopTrace, to scenarios that are relevant for the identification of potential illegal fishing and/or mislabelling for a commercially important Atlantic species herring (Clupea harengus).

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Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Population Ecology and Genetics
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Gene-associated markers provide tools for tackling illegal fishing and false eco-certification

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

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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Universidad Complutense, Aarhus University
High-resolution stock discrimination of Atlantic herring (Clupea harengus) based on otolith shape, microstructure, and genetic markers

One of the most rapidly developing applications of otolith research is shape analysis, often used for population discrimination as well as for species identification. Otolith shape is influenced by the environment through physiology, but also shows consistent and temporally stable differences between populations, which suggest genetic control as well. Thus otolith shape serves as a population marker, suitable for individual assignment. Here we use otolith morphological characteristics (otolith shape and larval otolith microstructure) combined with genetic markers to discriminate between different populations of Atlantic...
herring (Clupea harengus) in the western Baltic and adjacent waters. We analyse a baseline (spawning individuals from several populations validated by genetic markers) for separation of adult herring (2+) based on otolith shape and juveniles using genetically validated otolith shape characteristics as separation parameters. Otolith shape was found to clearly discriminate between individuals at all ages from different spawning populations. The identified distances between populations based on otolith shape matched previously obtained genetic distances and were, when combined with the otolith microstructure, able to discriminate between populations that are spatially different but spawning in the same season.

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Organisations: National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Mosegaard, H. (Intern), Worsøe Clausen, L. (Intern), Bekkevold, D. (Intern)
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Imprints from genetic drift and mutation imply relative divergence times across marine transition zones in a Pan European small pelagic fish (Sprattus sprattus)
Geographic distributions of most temperate marine fishes are affected by postglacial recolonisation events, which have left complex genetic imprints on populations of marine species. This study investigated population structure and demographic history of European sprat (Sprattus sprattus L.) by combining inference from both mtDNA and microsatellite genetic markers throughout the species’ distribution. We compared effects from genetic drift and mutation for both genetic markers in shaping genetic differentiation across four transition zones. Microsatellite markers revealed significant isolation by distance and a complex population structure across the species’ distribution (overall yST¼0.038, P<0.01). Across transition zones markers indicated larger effects of genetic drift over mutations in the northern distribution of sprat contrasting a stronger relative impact of mutation in the species’ southern distribution in the Mediterranean region. These results were interpreted to reflect more recent divergence times between northern populations in accordance with previous findings. This study demonstrates the usefulness of comparing inference from different markers and estimators of divergence for phylogeographic and population genetic studies in species with weak genetic structure, as is the case in many marine species.

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Authors: Limborg, M. (Intern), Hanel, R. (Ekstern), Debes, P. (Ekstern), Ring, A. (Ekstern), Andre, C. (Ekstern), Tsigenopoulos, C. (Ekstern), Bekkevold, D. (Intern)
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Mitogenome sequencing reveals shallow evolutionary histories and recent divergence time between morphologically and ecologically distinct European whitefish (Coregonus spp.)

The advent of second-generation sequencing has made it possible to quickly and economically generate whole mitochondrial genome (mitogenome) sequences. To date, mitogenome studies of nonmodel organisms have demonstrated increased power for resolving interspecies relationships. We explored an alternate use of such data to recover relationships and population history of closely related lineages with a shallow evolutionary history. Using a GS-FLX platform, we sequenced 106 mitogenomes from the Coregonus lavaretus (Europe) and Coregonus clupeaformis (North America) species complexes to investigate the evolutionary history of the endangered Danish North Sea houting (NSH) and other closely related Danish and Baltic European lake whitefish (ELW). Two well-supported clades were found within both ELW and NSH, probably reflecting historical introgression via Baltic migrants. Although ELW and NSH are not reciprocally monophyletic, they share no haplotypes, suggesting recent, but strong, reproductive isolation. The divergence time between NSH and the geographically closest ELW population was estimated using IMa, assuming isolation with migration and a new mutation rate estimate chosen to avoid time-dependency effects. The estimate of c. 2700 bp was remarkably similar to results obtained using microsatellite markers. Within North American C. clupeaformis, the divergence time between the two lineages (Atlantic and Acadian) was estimated as between 20 000 and 60 000 bp. Under the assumption that NSH and ELW colonized Denmark following the last glacial maximum, Bayesian Serial SimCoal analysis showed consistency with a scenario of long-term stability, resulting from a rapid initial sixfold population expansion. The findings illustrate the utility of mitogenome data for resolving recent intraspecific divergence events and provide evidence for recent reproductive isolation of the phenotypically divergent NSH

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Authors: Jacobsen, M. W. (Ekstern), Hansen, M. M. (Ekstern), Orlando, L. (Ekstern), Bekkevold, D. (Intern), Bernatchez, L. (Ekstern), Willerslev, E. (Ekstern), Gilbert, M. P. (Ekstern)
Population structure and adaptation in fishes: Insights from clupeid and salmonid species

Marine fishes represent a valuable resource for the global economy and food consumption. Accordingly, many species experience high levels of exploitation necessitating effective management plans. However, long term sustainability may be jeopardized from insufficient knowledge about intra-specific population structure and adaptive divergence. The large population sizes and high migration rates common to most marine fishes impede the differentiating effect of genetic drift, having led to expectations of no population structure and that the occurrence of local adaptation should be rare in these species. Comprehensive genetic analyses on the small pelagic fish European sprat (Sprattus sprattus) revealed significant population structure throughout its distribution with an overall pattern of reduced connectivity across environmental transition zones. Population structure reflected both historical separations over glacial time scales and more recent colonisation of new habitats. Further, strong genetic divergence at several regional scales demonstrated limited connectivity among sea-going and local fjord populations along the Norwegian coast as well as indications for the potential of locally adapted populations in the brackish Baltic Sea.

If forces of natural selection are able to override the homogenizing effects of high gene flow, the detection of adaptive signatures has often been constrained by a general lack of genomic resources. However, advances in sequencing technologies now enable cost-effective developments of gene-associated markers facilitating detection of adaptive divergence. To further address the potential existence of locally adapted populations in small pelagic fishes, we developed hundreds of transcriptome derived markers to identify genes affected by natural selection in Atlantic herring (Clupea harengus). Comprehensive sampling throughout the northeastern Atlantic revealed clear genetic structure among regions, and coupled with environmental inference strong signatures of divergent selection at a range of candidate genes suggested adaptation to local temperature and salinity conditions. A similar genome-scan based investigation of local adaptation was conducted in the salmonid Oncorhynchus mykiss. Despite profound socio-economic importance many populations have experienced strong declines and future conservation can be improved from identification of key drivers of neutral parameters and genes expected to maintain genetic diversity among populations. In contrast to marine fishes, salmonids are characterised by low gene flow, and together with the highly diverse habitats and phenotypes found among populations this suggest ample potential for local adaptation to evolve. However, the genetic architecture and spatial scale of local adaptation is poorly known, and evidence has often been restricted to one or few genes at local scales. We found divergent selection for several genes often relating to local habitat conditions. Inference from known gene functions provided further evidence for adaptively important roles played by immune response genes. Overall, results from this PhD revealed complex patterns of population structure and evidence for locally adapted populations in small pelagic fishes as well as interesting patterns of adaptively important candidate genes in a salmonid. These results contribute to our understanding of the evolutionary processes shaping biodiversity in the wild and findings may be extended from the actual species studied to assist managing fish resources under an evolutionarily sustainable framework in the future.

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SNP discovery using next generation transcriptomic sequencing in Atlantic herring (Clupea harengus)

The introduction of Next Generation Sequencing (NGS) has revolutionised population genetics, providing studies of non-model species with unprecedented genomic coverage, allowing evolutionary biologists to address questions previously far beyond the reach of available resources. Furthermore, the simple mutation model of Single Nucleotide Polymorphisms (SNPs) permits cost-effective high-throughput genotyping in thousands of individuals simultaneously. Genomic resources are scarce for the Atlantic herring (Clupea harengus), a small pelagic species that sustains high revenue fisheries. This paper details the development of 578 SNPs using a combined NGS and high-throughput genotyping approach. Eight individuals covering the species distribution in the eastern Atlantic were bar-coded and multiplexed into a single cDNA library and sequenced using the 454 GS FLX platform. SNP discovery was performed by de novo sequence clustering and contig assembly, followed by the mapping of reads against consensus contig sequences. Selection of candidate SNPs for genotyping was conducted using an in silico approach. SNP validation and genotyping were performed simultaneously using an Illumina 1,536 GoldenGate assay. Although the conversion rate of candidate SNPs in the genotyping assay cannot be predicted in advance, this approach has the potential to maximise cost and time efficiencies by avoiding expensive and time-consuming laboratory stages of SNP validation. Additionally, the in silico approach leads to lower ascertainment bias in the resulting SNP panel as marker selection is based only on the ability to design primers and the predicted presence of intron-exon boundaries. Consequently SNPs with a wider spectrum of minor allele frequencies (MAFs) will be genotyped in the final panel. The genomic resources presented here represent a valuable multi-purpose resource for developing informative marker panels for population discrimination, microarray development and for population genomic studies in the wild.
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.

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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.2012.05498.x
Source: dtu
Source-ID: n:oai:DTIC-ART:blackwell/363155944::15311
Publication: Research - peer-review › Journal article – Annual report year: 2012
The molecular basis of local adaptation: A case study focusing on brown trout (Salmo trutta L.)

General information
State: Published
Organisations: National Institute of Aquatic Resources
Authors: Meier, K. (Intern), Skov, C. (Intern), Als, T. D. (Intern), Bekkevold, D. (Intern), Hansen, M. M. (Intern)
Number of pages: 236
Publication date: 2012

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
State: Published
Organisations: National Institute of Aquatic Resources, Section for Population Ecology and Genetics, Section for Freshwater Fisheries Ecology, 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

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

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Meier, K. (Intern), Hansen, M. M. (Ekstern), Bekkevold, D. (Intern), Skaala, Ø. (Ekstern), Mensberg, K. D. (Intern)
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

State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Marine Living Resources, Royal Zoological Society of Scotland, University of Bologna, Katholieke Universiteit, Bangor University
Authors: Helyar, S. (Ekstern), Hansen, J. H. (Intern), Bekkevold, D. (Intern), Taylor, M. I. (Ekstern), Ogden, R. (Ekstern), Limborg, M. (Intern), Cariani, A. (Ekstern), Maes, G. E. (Ekstern), Diopere, E. (Ekstern), Carvalho, G. R. (Ekstern), Eg Nielsen, E. (Intern)
Pages: 123-136
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information

Journal: Molecular Ecology Resources
Volume: 11
Issue number: Suppl.1
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
Genetic mixed-stock analysis of Atlantic herring populations in a mixed feeding area

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Bekkevold, D. (Intern), Worsøe Clausen, L. (Intern), Mariani, S. (Ekstern), André, C. (Ekstern), Hatfield, E. (Ekstern), Torstensen, E. (Ekstern), Ryman, N. (Ekstern), Carvalho, G. (Ekstern), Ruzzante, D. (Ekstern)
Pages: 187-199
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information
Journal: Marine Ecology - Progress Series
Volume: 442
ISSN (Print): 0171-8630
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 2.4
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
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
Source-ID: 281688
Publication: Research - peer-review › Journal article – Annual report year: 2011

Detecting population structure in a high gene-flow species, Atlantic herring (Clupea harengus): direct, simultaneous evaluation of neutral vs putatively selected loci

In many marine fish species, genetic population structure is typically weak because populations are large, evolutionarily young and have a high potential for gene flow. We tested whether genetic markers influenced by natural selection are...
more efficient than the presumed neutral genetic markers to detect population structure in Atlantic herring (Clupea harengus), a migratory pelagic species with large effective population sizes. We compared the spatial and temporal patterns of divergence and statistical power of three traditional genetic marker types, microsatellites, allozymes and mitochondrial DNA, with one microsatellite locus, Cpa112, previously shown to be influenced by divergent selection associated with salinity, and one locus located in the major histocompatibility complex class IIA (MHC-IIA) gene, using the same individuals across analyses. Samples were collected in 2002 and 2003 at two locations in the North Sea, one location in the Skagerrak and one location in the low-saline Baltic Sea. Levels of divergence for putatively neutral markers were generally low, with the exception of single outlier locus/sample combinations; microsatellites were the most statistically powerful markers under neutral expectations. We found no evidence of selection acting on the MHC locus. Cpa112, however, was highly divergent in the Baltic samples. Simulations addressing the statistical power for detecting population divergence showed that when using Cpa112 alone, compared with using eight presumed neutral microsatellite loci, sample sizes could be reduced by up to a tenth while still retaining high statistical power. Our results show that the loci influenced by selection can serve as powerful markers for detecting population structure in high gene-flow marine fish species.

**General information**

State: Published

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

Authors: André, C. (Ekstern), Larsson, L. C. (Ekstern), Laikre, L. (Ekstern), Bekkevold, D. (Intern), Brigham, J. (Ekstern), Carvalho, G. R. (Ekstern), Dahlgren, T. G. (Ekstern), Hutchinson, W. F. (Ekstern), Mariani, S. (Ekstern), Mudde, K. (Ekstern), Ruzzante, D. E. (Ekstern), Ryman, N. (Ekstern)

Pages: 270-280

Publication date: 2010

Main Research Area: Technical/natural sciences

**Publication information**

Journal: Heredity

Volume: 106

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

BFI (2012): BFI-level 2

Scopus rating (2012): SJR 2.088 SNIP 1.356 CiteScore 3.5

ISI indexed (2012): ISI indexed yes

Web of Science (2012): Indexed yes

BFI (2011): BFI-level 2

Scopus rating (2011): SJR 2.279 SNIP 1.289 CiteScore 3.58

ISI indexed (2011): ISI indexed yes

Web of Science (2011): Indexed yes

BFI (2010): BFI-level 2

Scopus rating (2010): SJR 2.376 SNIP 1.253

Web of Science (2010): Indexed yes

BFI (2009): BFI-level 2

Scopus rating (2009): SJR 2.244 SNIP 1.268

BFI (2008): BFI-level 1
High salinity tolerance in eggs and fry of a brackish Esox lucius population

General information
State: Published
Organisations: Section for Freshwater Fisheries Ecology, National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Jørgensen, A. (Ekstern), Hansen, B. (Ekstern), Vismann, B. (Ekstern), Jacobsen, L. (Intern), Skov, C. (Intern), Berg, S. (Intern), Bekkevold, D. (Intern)
Pages: 554-560
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Fisheries Management and Ecology
Volume: 17
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
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.988 SNIP 1.159 CiteScore 1.91
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.913 SNIP 0.995 CiteScore 1.85
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.737 SNIP 0.807 CiteScore 1.36
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.636 SNIP 0.868 CiteScore 1.32
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Disentangling the effects of evolutionary, demographic, and environmental factors influencing genetic structure of natural populations: Atlantic herring as a case study

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Gaggiotti, O. E. (Ekstern), Bekkevold, D. (Intern), Jørgensen, H. B. (Ekstern), Foll, M. (Ekstern), Carvalho, G. R. (Ekstern), Andre, C. (Ekstern), Ruzzante, D. E. (Ekstern)
Pages: 2939-2951
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Evolution
Volume: 63
Issue number: 11
ISSN (Print): 0014-3820
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
Factors such as oceanographic retention, isolation by distance and secondary contact zones have, among others, been suggested to explain the low, but statistically significant, neutral population structure observed in many marine fishes. European sprat Sprattus sprattus is not known to display philopatric spawning behaviour or to exhibit local retention of eggs and larvae. It thus constitutes a good model for studying population structure in a characteristic small pelagic fish with high dispersal potential and an opportunistic life history. We analysed 931 specimens of sprat from nine spawning locations in and around the North- and Baltic Sea area and from a geographically distant population from the Adriatic Sea. Analyses of nine microsatellite loci revealed a sharp genetic division separating samples from the Northeastern Atlantic and the Baltic Sea (pairwise \( \theta = 0.019–0.035 \)), concurring with a steep salinity gradient. We found, at most, weak structure among samples within the Northeastern Atlantic region and within the Baltic Sea (pairwise \( \theta = 0.001–0.009 \)). The Adriatic Sea population was highly differentiated from all northern samples (pairwise \( \theta = 0.071–0.092 \)). Overall, the observed population structure resembles that of most other marine fishes studied in the North/Baltic Sea areas. Nevertheless, spatially explicit differences are observed among species, likely reflecting specific life-histories. Such fine-scale population structure should be taken into account, e.g. in ecosystem-based stock management.

**Genetic population structure of European sprat (Sprattus sprattus L.): differentiation across a steep environmental gradient in a small pelagic fish**

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

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Carvalho, G. (Ekstern), Helyar, S. (Ekstern), Bekkevold, D. (Intern), Volkert, F. (Ekstern), Hanel, R. (Ekstern), McPhee, D. (Ekstern), Ford, M. (Ekstern), Carlsson, J. (Ekstern), Trautner, J. (Ekstern), Ogden, R. (Ekstern), Martinsohn, J. (Ekstern)
Publication date: 2009

Host publication information
Title of host publication: ICES C.M.
Volume: MCC:03
Place of publication: Copenhagen
Publisher: International Council for the Exploration of the Sea
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 254171
Publication: Research › Article in proceedings – Annual report year: 2009

Characterization of nine polymorphic microsatellite markers in sprat (Sprattus sprattus L.)
Nine polymorphic microsatellites were isolated from sprat (Sprattus sprattus) using a microsatellite enrichment protocol and selective hybridization with a biotinylated (AC)(12) probe. The loci showed different variation patterns in a Baltic Sea population (44 individuals) with mean number of alleles at 12.7 and mean observed heterozygosity at 0.78. These microsatellite loci are expected to be used for taxonomic considerations in sprat, stock differentiation and population genetic analysis.
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.
Application and validation of otolith microstructure as a stock identification method in mixed Atlantic herring (Clupea harengus L) stocks in the North Sea and western Baltic

General information
State: Published
Organisations: Section for Population- and Ecosystem Dynamics, National Institute of Aquatic Resources, Section for Population Ecology and Genetics, Marine Scotland
Authors: Worsøe Clausen, L. (Intern), Bekkevold, D. (Intern), Hatfield, E. (Ekstern), Mosegaard, H. (Intern)
Pages: 377-385
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES Journal of Marine Science
Volume: 64
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
Divergent origins of sympatric herring population components determined using genetic mixture analysis

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Population- and Ecosystem Dynamics
Authors: Bekkevold, D. (Intern), Worsøe Clausen, L. (Intern), Mariani, S. (Ekstern), André, C. (Ekstern), Christensen, T. (Ekstern), Mosegaard, H. (Intern)
Pages: 187-196
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Marine Ecology - Progress Series
Volume: 337
ISSN (Print): 0171-8630
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Gene flow, effective population size and selection at major histocompatibility complex genes: brown trout in the Hardanger Fjord, Norway

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

Publication information
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: orbit
Source-ID: 225670
Publication: Research - peer-review › Book chapter – Annual report year: 2007

Restaurering af søer: Udsætning af gedder

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), Berg, S. (Intern), Jacobsen, L. (Intern), Bekkevold, D. (Intern), Olsen, J. (Ekstern)
Pages: 129-134
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Vand og jord
Volume: 4
ISSN (Print): 0908-7761
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: 227449
Publication: Research › Journal article – Annual report year: 2007

Weak population differentiation in northern European populations of the endangered anadromous clupeid Alosa fallax

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Volk, J. (Ekstern), Bekkevold, D. (Intern), Loeschcke, V. (Ekstern)
Pages: 461-469
Publication date: 2007
Main Research Area: Technical/natural sciences
Biocomplexity in a highly migratory pelagic marine fish, Atlantic herring

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Population- and Ecosystem Dynamics
Authors: Ruzzante, D. (Ekstern), Mariani, S. (Ekstern), Bekkevold, D. (Intern), André, C. (Ekstern), Mosegaard, H. (Intern), Worsøe Clausen, L. (Intern), Dahlgren, T. (Ekstern), Hutchinson, W. (Ekstern), Hatfield, E. (Ekstern), Torstensen, E. (Ekstern), Brigham, J. (Ekstern), Simmonds, E. (Ekstern), Laikre, L. (Ekstern), Larsson, L. (Ekstern), Stet, R. (Ekstern), Ryman, N. (Ekstern), Carvalho, G. (Ekstern)
Pages: 1459-1464
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Royal Society of London. Proceedings B. Biological Sciences
Volume: 273
Issue number: 1593
ISSN (Print): 0962-8452
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 3.89 SJR 2.541 SNIP 1.474
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.948 SNIP 1.535 CiteScore 4.08
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.916 SNIP 1.673 CiteScore 4.18
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.091 SNIP 1.762 CiteScore 5.08
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.947 SNIP 1.881 CiteScore 4.99
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.234 SNIP 1.789 CiteScore 5.02
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.894 SNIP 1.61
Web of Science (2010): Indexed yes
Considerations of population structuring in Atlantic herring, Clupea harengus L. assessment and management in the North Sea, Skagerrak, Kattegat and western Baltic

General information
State: Published
Organisations: Section for Population- and Ecosystem Dynamics, National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Hatfield, E. (Ekstern), Worsøe Clausen, L. (Intern), Mosegaard, H. (Intern), Bekkevold, D. (Intern), Mariani, S. (Ekstern), Hutchinson, W. (Ekstern), Carvalho, G. (Ekstern), Ruzzante, D. (Ekstern), Ryman, N. (Ekstern), André, C. (Ekstern), Dahlgren, T. (Ekstern), Torstensen, E. (Ekstern), Simmonds, E. (Ekstern)
Pages: 245
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Biology
Volume: 69
Issue number: Suppl. C
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
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
Genetic restoration of a stocked brown trout Salmo trutta population using microsatellite DNA analysis of historical and contemporary samples

1. Gene flow from domesticated to wild populations is a major threat to wild salmonid fish. However, few studies have addressed how populations could be restored after admixture has occurred. We analysed the prospects for restoring the previously intensively stocked brown trout population of the Skjern River, Denmark, by identifying remaining non-admixed individuals to be used for supportive breeding. 2. We analysed microsatellite DNA markers in historical (1940-50s) and contemporary (1992-2004) samples from the Skjern River system, from the strain of domesticated trout previously used for stocking, and from the neighbouring Stora River. We analysed admixture proportions to estimate the genetic contribution by domesticated trout. We identified non-admixed trout using assignment tests, and further analysed the possible sources of indigenous trout by estimating contemporary migration among populations. 3. Genetic differentiation between the historical Stora and Skjern river populations was low (theta(ST) = 0.004), suggesting considerable gene flow in the past. The contemporary Skjern and Stora river populations and a supportive breeding brood stock were strongly admixed, but some non-admixed individuals nevertheless remained in the wild-caught samples. In addition, two resident populations in isolated tributaries were found to be indigenous. The indigenous anadromous individuals from the Skjern River were unlikely to have been recruited from either the isolated tributary populations or the neighbouring Stora River and were presumably derived from unidentified spawning sites in the river system. 4. All but one non-admixed anadromous Skjern River trout were females, which we ascribed to sampling bias. Moreover, all non-admixed fish were late-spawning (January-February) whereas the majority of all trout caught for the study were ripe by November-December. The difference in spawning time could be an important factor delaying complete admixture of domesticated and indigenous trout. 5. Synthesis and applications. This study demonstrates the feasibility of restoring populations that have been admixed with exogenous individuals, by identifying non-admixed individuals using genetic markers. However, the results also highlight the problem that numbers of identified non-admixed individuals may be small, necessitating identification of nearby, closely related populations that can be incorporated into breeding programmes.

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Bekkevold, D. (Intern), Jensen, L. (Ekstern), Mensberg, K. D. (Intern), Eg Nielsen, E. (Intern)
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.5 SJR 2.869 SNIP 2.008
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.242 SNIP 1.96 CiteScore 5.38
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.998 SNIP 2.171 CiteScore 5.25
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.031 SNIP 2.225 CiteScore 5.45
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.122 SNIP 2.089 CiteScore 5.18
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.685 SNIP 2.294 CiteScore 5.23
ISI indexed (2011): ISI indexed yes
Male size composition affects male reproductive variance in Atlantic cod Gadus morhua L. spawning aggregations

Estimates of Atlantic cod Gadus morhua reproductive success, determined using experimental spawning groups and genetic paternity assignment of offspring, showed that within-group variance in male size correlated positively with the degree of male mating skew, predicting a decrease in male reproductive skew with decreasing size variation among males under natural conditions. (c) 2006 The Author Journal compilation (c) 2006 The Fisheries Society of the British Isles
Udsætning af geddeyngel i danske søer: Effektvurdering og perspektivering

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), Jacobsen, L. (Intern), Berg, S. (Intern), Olsen, J. (Ekstern), Bekkevold, D. (Intern)
Number of pages: 96
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Place of publication: Silkeborg
Application and validation of otolith microstructure as stock identifier in mixed Atlantic herring (Clupea harengus) stocks in the North Sea and Western Baltic

General information
State: Published
Organisations: Section for Population- and Ecosystem Dynamics, National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Worsøe Clausen, L. (Intern), Bekkevold, D. (Intern), Hatfield, E. M. C. (Ekstern), Mosegaard, H. (Intern)
Pages: 1-16
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES Council Meeting
ISSN (Print): 1015-4744
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Web of Science (2003): Indexed yes
Original language: English
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Environmental correlates of population differentiation in Atlantic herring

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources, Section for Population- and Ecosystem Dynamics
Authors: Bekkevold, D. (Intern), André, C. (Ekstern), Dahlgren, T. G. (Ekstern), Worsøe Clausen, L. (Intern), Torstensen, E. (Ekstern), Mosegaard, H. (Intern), Carvalho, G. (Ekstern), Christensen, T. B. (Ekstern), Ruzzante, D. E. (Ekstern)
Pages: 2656-2668
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Evolution
Volume: 59
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ISSN (Print): 0014-3820
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
Marine landscapes and population genetic structure of herring (Clupea harengus L.) in the Baltic Sea
Numerically small but statistically significant genetic differentiation has been found in many marine fish species despite very large census population sizes and absence of obvious barriers to migrating individuals. Analyses of morphological traits have previously identified local spawning groups of herring (Clupea harengus L.) in the environmentally heterogeneous Baltic Sea, whereas allozyme markers have not revealed differentiation. We analysed variation at nine microsatellite loci in 24 samples of spring-spawning herring collected at 11 spawning locations throughout the Baltic Sea. Significant temporal differentiation was observed at two locations, which we ascribe to sympatrically spawning but genetically divergent 'spawning waves'. Significant differentiation was also present on a geographical scale, though pairwise F-ST values were generally low, not exceeding 0.027. Partial Mantel tests showed no isolation by geographical distance, but significant associations were observed between genetic differentiation and environmental parameters (salinity and surface temperature) (0.001 < P)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Admixture analysis of herring feeding aggregations in the northern North Sea

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Mariani, S. (Ekstern), André, C. (Ekstern), Bekkevold, D. (Intern), Brigham, J. (Ekstern), Carvalho, G. (Ekstern), Dahlgren, T. (Ekstern), Hatfield, E. (Ekstern), Hutchinson, W. (Ekstern), Simmonds, E. (Ekstern), Torstensen, E. (Ekstern), Ruzzante, D. (Ekstern)
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: ICES C.M. 2004/
Volume: EE:32
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Publication: Research › Conference article – Annual report year: 2004

Depensation, probability of fertilization, and the mating system of Atlantic cod (Gadus morhua L.)

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Rowe, S. (Ekstern), Hutchings, J. (Ekstern), Bekkevold, D. (Intern), Rakitin, A. (Ekstern)
Pages: 1144-1150
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Main Research Area: Technical/natural sciences

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Journal: ICES Journal of Marine Science
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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
Genetic detection of sex-specific dispersal in historical and contemporary populations of anadromous brown trout Salmo trutta

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

General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Bekkevold, D. (Intern), Hansen, M. M. (Intern), Mensberg, K. D. (Intern)
Pages: 1707-1712
Publication date: 2004
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Journal: Molecular Ecology
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
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.2004.02156.x
Phenotypic characteristics in genetically different populations in the Skagerrak

General information
State: Published
Organisations: Section for Population- and Ecosystem Dynamics, National Institute of Aquatic Resources, Section for Population Ecology and Genetics
Authors: Worsøe Clausen, L. (Intern), Mosegaard, H. (Intern), Bekkevold, D. (Intern), Ruzzante, D. (Ekstern)
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Journal: ICES C.M. 2004/
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Store torsk har succes hos hunnerne

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State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Bekkevold, D. (Intern)
Pages: 33-42
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Journal: Fisk og Hav
Issue number: 55
ISSN (Print): 0105-9211
Ratings:
ISI indexed (2013): ISI indexed no
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Original language: Danish
Links:
http://www.aqua.dtu.dk/Publikationer/Fisk-og-hav.aspx
Source: orbit
Source-ID: 224887
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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:
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.

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Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Hansen, M. M. (Intern), Ruzzante, D. (Ekstern), Eg Nielsen, E. (Intern), Bekkevold, D. (Intern), Mensberg, K. D. (Intern)
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BFI (2018): BFI-level 2
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Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 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
Male reproductive competition in spawning aggregations of cod (Gadus morhua, L.)

Reproductive competition may lead to a large skew in reproductive success among individuals. Very few studies have analysed the paternity contribution of individual males in spawning aggregations of fish species with huge census population sizes. We quantified the variance in male reproductive success in spawning aggregations of cod under experimental conditions over an entire spawning season. Male reproductive success was estimated by microsatellite-based parentage analysis of offspring produced in six separate groups of spawning cod. In total, 1340 offspring and 102 spawnings distributed across a spawning season were analysed. Our results show that multiple males contributed sperm to most spawnings but that paternity frequencies were highly skewed among males, with larger males on average siring higher proportions of offspring. It was further indicated that male reproductive success was dependent on the magnitude of the size difference between a female and a male. We discuss our results in relation to the cod mating system. Finally, we suggest that the highly skewed distribution of paternity success observed in cod may be a factor contributing to the low effective population size/census population size ratios observed in many marine organisms.
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: 224884
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.
Evolutionary transition to a semelparous life history in the socially parasitic ant Acromyrmex insinuator
The recently discovered social parasite Acromyrmex insinuator (Schultz, Bekkevold and Boomsma 1998) exploits colonies of the leafcutter ant A. echinatior. We document that A. insinuator represents a rare early stage in the evolution of social parasitism, because a worker caste is still partially present and mating phenology has remained at least partially similar to that of the host. A. insinuator is tolerant of host queens, and sexual offspring produced in parasitized colonies can be either exclusively A. insinuator or a mix of A. insinuator and A. echinatior. The remarkably high abundance of A. insinuator in nests of the investigated Panamanian host population and the fact that A. insinuator colonies readily reproduce under laboratory conditions allowed us to test evolutionary predictions on reproductive life history evolution that are not possible in most other socially parasitic ants. We show that (1) A. insinuator has a semelparous 'big bang' reproductive life history which exploits host colonies without leaving reserves for survival; (2) social parasite sexuals are significantly smaller than A. echinatior host sexuals, but still large compared to host workers, confirming an evolutionary scenario of gradual size reduction and loss of the worker caste after transition towards a socially parasitic life history; (3) major changes in the life history of ants can evolve relatively quickly compared to adaptations in morphology, caste differentiation and mating phenology.

General information
Multiple mating and facultative polygyny in the Panamanian leafcutter ant Acromyrmex echinatior

Queen mating frequency of the facultatively polygynous ant Acromyrmex echinatior was investigated by analysing genetic variation at an (AG)n repeat microsatellite locus in workers and sexuals of 20 colonies from a single Panamanian population. Thirteen colonies were found to be monogynous, 5 colonies contained multiple queens, whereas the queen number of 2 colonies remained unresolved. Microsatellite genotypes indicated that 12 out of 13 queens were inseminated by multiple males (polyandry). The mean queen mating frequency was 2.53 and the mean genetically effective paternity frequency was 2.23. These values range among the highest found in ants, and the results are in keeping with the high mating frequencies reported for other species of leafcutter ants. Consistent skew in the proportional representation of different patrilines within colonies was found, and this remained constant in two consecutive samples of offspring. Dissections showed that all examined queens from multiple-queen colonies were mated egg-layers. The mean relatedness value among nestmate workers in polygynous colonies was lower than that for monogynous colonies. No diploid males were detected in a sample of 70 genotyped males. Worker production of males was detected in one queenless colony. We discuss our findings in relation to known patterns of multiple maternity and paternity in other eusocial Hymenoptera.

General information
State: Published
Organisations: Aarhus University
Authors: Bekkevold, D. (Intern), Frydenberg, J. (Forskerdatabase), Boomsma, J. J. (Forskerdatabase)
Pages: 103-109
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Main Research Area: Technical/natural sciences

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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.278 SNIP 0.996 CiteScore 2.36
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.39 SNIP 0.94 CiteScore 2.3
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.623 SNIP 1.226 CiteScore 2.85
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.67 SNIP 1.319 CiteScore 3.05
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.535 SNIP 1.236 CiteScore 2.89
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.698 SNIP 1.202 CiteScore 2.94
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.598 SNIP 1.082
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.917 SNIP 1.278
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.999 SNIP 1.317
Scopus rating (2007): SJR 2.087 SNIP 1.424
Scopus rating (2006): SJR 1.653 SNIP 1.228
Scopus rating (2005): SJR 1.542 SNIP 1.167
Scopus rating (2004): SJR 1.752 SNIP 1.315
Acromyrmex insinuator new species: an incipient social parasite of fungus-growing ants

The two known social parasites of fungus-growing ants (tribe Attini) occupy an advanced grade of social parasitism characterized by absence of a worker caste and highly derived morphology and behavior. In contrast, the Panamanian Acromyrmex insinuator new species, described here, appears to occupy an early grade of social parasitism in which males, females, and minor workers are nearly indistinguishable from those of the host species. Based on allozyme and morphological evidence, the host, A. octospinosus ssp. echinactor, is clearly different and reproductively isolated from the sympatric A. octospinosus ssp. octospinosus, and is therefore elevated to species status.

General information
State: Published
Organisations: National Museum of Natural History, Smithsonian Institution, Aarhus University
Authors: Schultz, T. (Ekstern), Bekkevold, D. (Intern), Boomsma, J. J. (Forskerdatabase)
Pages: 457-471
Publication date: 1998
Main Research Area: Technical/natural sciences

Publication information
Journal: Insectes Sociaux
Volume: 45
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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 0.725 SNIP 0.981 CiteScore 1.49
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.826 SNIP 0.896 CiteScore 1.27
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.724 SNIP 0.612 CiteScore 1.2
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.76 SNIP 0.759 CiteScore 1.4
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.833 SNIP 0.865 CiteScore 1.47
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.913 SNIP 1.075 CiteScore 1.53
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.798 SNIP 0.801
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.91 SNIP 0.852
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.838 SNIP 0.69
Scopus rating (2007): SJR 1.145 SNIP 0.99
Scopus rating (2006): SJR 0.958 SNIP 0.904
Scopus rating (2005): SJR 0.97 SNIP 1.024
Scopus rating (2004): SJR 1.057 SNIP 1.173
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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 patterns and processes of population divergence in marine fishes
National Institute of Aquatic Resources
Period: 01/03/2016 → 28/02/2019
Number of participants: 3
PhD Student:
Le Moan, Alan (Intern)
Supervisor:
Bekkevold, Dorte (Intern)
Main Supervisor:
Hansen, Jakob Hemmer (Intern)

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

Genetic adaptations underlying population structure in herring, Clupea harengus (GENSINC) (39355)
The objective is to document genetic differentiation and local adaptations in Atlantic herring populations spanning the majority of the species' distribution in the Northeast Atlantic, thereby strengthening the scientific basis for management of herring stocks. This will be done by using new genomic analyses and by taking advantage of unique multi-generational experimental populations under controlled environmental conditions. Whole genome resequencing of 19 populations of herring from East Atlantic (including the North Sea, Skagerrak, Kattegat, and the Baltic Sea revealed low genetic
differentiation at the great majority of examined genes. This supports earlier genetic studies suggesting that genetic drift at selectively neutral loci is extremely low in these populations. However, highly significant differentiation at a limited number of loci (<5%) was detected between Atlantic and Baltic herring, as well as between spring- and autumn-spawning herring irrespective of the geographic origin of the fish. The results showed that alleles underlying ecological adaptation in herring provide a wealth of information about population subdivisions. An aim of the project is to sequence DNA from a much broader spectrum of herring populations, to assess evolutionary processes acting on the distribution and dynamics of herring populations exhibiting different ecological and phenotypic traits (e.g. spawning time). Concurrently the activities will aim to identify population specific markers that could be used in genetic monitoring of herring stocks.

In order to further study the biological significance of the genetic variants underlying ecological adaptation in the Atlantic herring University of Bergen has established world-unique experimental populations by crossing Atlantic herring (adapted to a salinity of 35 psu) and Baltic herring (adapted to 6 psu). These fish will be used to generate a highly informative F2 intercross that will segregate at the loci responsible for ecological adaptation. Another experimental population consisting of hybrids between spring and autumn spawning herring is planned within this project, allowing novel studies on the genetic basis of reproduction timing in herring. Such multigenerational experiments are considered essential to understand evolutionary and population genetic responses to environmental change.

This project is coordinated by the University of Bergen, Norway. This project is funded by the Research Council of Norway.

National Institute of Aquatic Resources
Section for Marine Living Resources
University of Bergen
Uppsala University
Institute of Marine Research
Queen's University Belfast

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.
Marine migration behaviour of salmonids and gadoids assessed using biotelemetry and genetic stock identification

National Institute of Aquatic Resources
Period: 15/12/2015 → 29/03/2019
Number of participants: 3
Phd Student:
Kristensen, Martin Lykke (Intern)
Supervisor:
Bekkevold, Dorte (Intern)
Main Supervisor:
Aarestrup, Kim (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Anden EU-finansiering
Project: PhD

Forward management of sandeel in the North Sea (39316)
The project will define and align the management of sandeel considering the goals and desires of the fishing industry, administration and science while taking the biology and importance of the sandeel in the ecosystem into account.

The project is structured by several work-packages, each dealing with specific aspects of sandeel biology and/or fishery relevant for management. Among these will the sandeel population structure and its influence on stock assessment, CPUE and counselling be discussed. Analyses of fisheries development and sandeel availability over the fishing season will enable a more accurate calculation of fishing mortality. Furthermore, it is examined whether the increasing concentration of fishing effort on certain banks potentially causes an error in the stock assessment in relation to recruitment from unfished banks. The project will perform a statistical evaluation of fisheries-independent data for sandeel in the North Sea and evaluate existing and alternative methods of stock assessment for sandeel in the North Sea with current and alternative management areas, including implementing an analytical stock assessment of sandeel in sandeel area 4. Finally the project will evaluate existing biological and management reference points, and discuss these in relation to ecosystem reference points.

Throughout the project period, a series of workshops and meetings will be held in order to discuss possible management strategies for sandeel in the North Sea. These discussions will imply a number of fundamental prerequisites defined in collaboration between management, fisheries and science in order to form the basis for an optimal management of sandeel.

This project is coordinated by DTU Aqua.

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

National Institute of Aquatic Resources
Section for Marine Living Resources
Danish Pelagic Producers Organisation
Danish Fishermen's Association
Marine Ingredients Denmark
Period: 11/11/2015 → 16/11/2017
Number of participants: 8
Research areas: Marine Living Resources & Population Genetics & Fish Biology & Marine Populations and Ecosystem Dynamics & Fisheries Management & Ecosystem based Marine Management
Project participant:
Rindorf, Anna (Intern)
vан Deurs, Mikael (Intern)
Berg, Casper Willestofte (Intern)
Mosegaard, Henrik (Intern)
Bekkevold, Dorte (Intern)
Mortensen, Lars O. (Intern)
Christensen, Asbjørn (Intern)
Project Coordinator:
Worsøe Clausen, Lotte (Intern)
Project

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

National Institute of Aquatic Resources
Period: 01/10/2015 → 11/03/2019
Number of participants: 3
Phd Student:
Hansen, Brian Klitgaard (Intern)
Supervisor:
Bekkevold, Dorte (Intern)
Main Supervisor:
Eg Nielsen, Einar (Intern)

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

Expertise in marine and aquatic ecology and genomics for sustainable management of fish and shellfish in Skagerrak-Kattegat-Øresund (MarGen) (39301)
The marine and freshwater regions encompassing Skagerrak, Kattegat, Øresund and the North Sea are biologically highly productive and contain plentiful living aquatic resources that are important for the region. At the same time the coastal areas are densely populated and industrialized, fish and shellfish resources are heavily harvested, and waters are subject to pollution and eutrophication. The region is also markedly affected by the ongoing global warming, with sea temperature rising nearly 2 degrees C during the last 40 years. These environmental pressures call for investigations into the consequences for aquatic organisms, their potential for adapting to environmental changes, and for identifying management strategies that could mitigate deteriorating environmental conditions, using state-of-the-art methodology. Here, we will capitalize on the revolutionizing developments in genomics, electronic tagging and computer modelling to obtain insights on the ecology, evolution and management of aquatic biodiversity in the region.

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

This project is coordinated by DTU Aqua.

The project is funded by EU, InterReg (regional collaboration).
National Institute of Aquatic Resources
Section for Marine Living Resources
Institute of Marine Research
University of Gothenburg
Aarhus University
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
Hampiðjan hf
SafetyNet Technologies LTD
Marine Institute
NAYS Ltd
Pôle AQUIMER
University of the Azores
Cefas
Matís ltd.
Biodiversity changes - causes, consequences and management implications (BIO-C3) (39117)

BIO-C3 will investigate the dynamics of biodiversity in the Baltic Sea, their causes and the consequences for the function of food webs, including implications for biodiversity management policies.

Baltic biodiversity is historically dynamic responding to various drivers operating at different time and space scales. Species diversity is generally low and contains many recent immigrants and glacial relict species because of low salinity and relatively young age. Nevertheless, Baltic food webs sustain many goods and services valued by society.

We focus on functional consequences of ongoing and projected distributional and compositional changes of benthic and pelagic communities with a focus on invasive and resident key species. Using spatial and temporal projections of abiotic/biotic drivers including their interaction (climate change, eutrophication, species invasions, fisheries), we will assess how biodiversity (e.g., of species, traits, habitats) responds in time, space and along gradients of human impact and hydrography. We will investigate the potential and genetic basis for colonisation, acclimation and adaptation of species and populations to the Baltic Sea, and how compositional and adaptive changes of Baltic biodiversity affect ecosystem functions with an emphasis on trophic linkage and food web dynamics.

Results will feed into impact assessments that guide management policies including improved operationalization of status indicators, and guidelines for MPAs.

The project is coordinated by Helmholtz Centre for Ocean Research, Kiel (GEOMAR). DTU Aqua is co-coordinator.

The project is funded equally by EU, BONUS (Science for a Better Future of the Baltic Sea Region), ERA-NET.
Tracing the dynamics of mixed stocks in a transition area: Herring in Skagerrak-Kattegat and Western Baltic

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

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

**The early life of eel in the Sargasso Sea – Influence of oceanography and climate (SARGASSO-EEL) (39107)**

The recruitment of the European eel has been in dramatic decline during the last 30 years, and is at a severe low of only 3-5% of earlier magnitude. This change and its influence on the eel fishery have led to an intensified research in the oceanic phase of the European eel.

In order to contribute to further understanding of the life cycle of eel the Danish eel expedition set out in 2014 for the eel spawning grounds in the Sargasso Sea. Here a consortium of Danish scientists and international collaborators focused on the linkages between oceanography, biological production, eel spawning and the growth and drift of eel larvae.

During the expedition, a wide range of organisms was collected: From the smallest plankton of less than a millimeter to very large fish. A number of research groups are now working on samples and data from the expedition and assembling information on key processes in the early life of eels. Preliminary findings indicate that biological and physical changes have taken place in the spawning areas that may affect the eel larvae’s chances of survival and their journey to Europe.

The project was coordinated by DTU Aqua.

The project is funded by the Carlsberg Foundation and Danish Centre of Marine Research (cruise).

National Institute of Aquatic Resources  
Section for Marine Ecology and Oceanography  
University of Copenhagen  
Aarhus University  
Pierre and Marie Curie University - University of Paris VI  
Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), Berlin  
Université de la Méditerranée  
University of Alaska Fairbanks  
University of Rhode Island  
Sir Alister Hardy Foundation for Ocean Science (SAHFOS)

**International Council for the Exploration of the Sea**  
Period: 01/08/2013 → 01/08/2016  
Number of participants: 11  
**Research areas:** Marine Populations and Ecosystem Dynamics & Fish Biology & Oceanography  
**Project participant:**  
Thomsen, Helge Abildhauge (Intern)
Sørensen, Sune Riis (Intern)
Bekkevold, Dorte (Intern)
Malanski, Evandro (Intern)
Jaspers, Cornelia (Intern)
Koski, Marja (Intern)
Christoffersen, Mads (Intern)
Hansen, Susanne (Intern)
Phd Student:
Ayala, Daniel Jiro (Intern)
Project Manager, academic:
Nielsen, Torkel Gissel (Intern)
Project Coordinator:
Munk, Peter (Intern)

Short-term projections for short-lived species managed under MSY: Management of the sandeel stock in the North Sea (39148)
The industrial fishery for small short-lived species represents the economically most important fishery in Denmark, and traditionally the North Sea sandeel (Ammodytes marinus) has played a key role in this fishery. Currently, quota advice for sandeel is based on the so-called B-escapement strategy, the purposes of which is to ensure that the spawning stock biomass remains large enough to maintain the survival of the population even after fish-eating fish, birds, and mammals have taken their share; and whatever is left is made available to the fishery. This type of management strategy relies on accurate predictions about the size of the incoming year class (the recruitment), if the criteria of MSY are to be fulfilled.

The aim of the project was therefore to ensure that the short-term prognosis reflects current knowledge about the biology of sandeels in the North Sea and applies all relevant data time-series.

A new recruitment index was introduced. Seasonal and spatial patterns in log-book based catch rates of age-1 fish were analysed and compared to recruitment indices from the year before. Spatial differences in local larval retention strength were found.

A genetic tool that allowed us to distinguish between different sandeel species in a quick and accurate way was developed. Lastly, development of a state based assessment model that can handle seasonal data (something which is necessary for sandeel) and estimate shifting selection patterns was initiated.

All of this work is currently contributing significantly to the preparation of the coming North Sea sandeel benchmark assessment in ICES to be held in the fall of 2016.

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 Marine Living Resources
Sir Alister Hardy Foundation for Ocean Science
Centre for Environment Fisheries and Aquaculture Science
Period: 22/07/2013 → 01/05/2015
Number of participants: 6
Research areas: Marine Living Resources & Population Genetics
Project participant:
Mosegaard, Henrik (Intern)
Azour, Farivar (Intern)
Christensen, Asbjørn (Intern)
Bekkevold, Dorte (Intern)
Project Manager, academic:
Worsøe Clausen, Lotte (Intern)
Project Coordinator:
van Deurs, Mikael (Intern)

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

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

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

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

The project is funded by EU, Framework Programme 7.

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

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)
Genetic mapping of Danish trout populations (38828)
The objective of this project is to map the genetic structure of Danish trout populations and to develop genetic tools for use in management of Danish trout populations. This tool will be used for identifying indigenous populations of trout, and to identify causes for maintenance of genetic differentiation between populations. In the longer term we aim to map the geographical distribution of genetic diversity of most Danish trout populations. The genetic database will also be used to establish a molecular testing system allowing the determination of the river origin of individual sea trout, thereby describing migration patterns. This is done by developing genetic stock identification methods specifically targeting sea trout in Danish waters.

A genetic map with more detail (both geographically and genomic) compared to previous genetic studies will become an important tool for conservation and restoration of natural trout. It will be applied for identifying trout populations that are locally adapted or differs genetically from other populations and therefore are particularly important for maintaining genetic diversity. This tool will be used to define management units and assessment of evolutionary potential. A genetic map provides an overview of indigenous populations and conservation units, and will thus have important implications in counselling practical restoration efforts.

The identification of local adaptations of specific populations, and knowledge of whether individual stocks are adapted to life in their particular environment can be applied in identifying causes for maintenance of genetic differentiation between populations, e.g. whether certain populations are genetically adapted to spawn under certain environmental conditions or at certain times.

Individuals from approx. 50 rivers are selected in a manner that ensures a good coverage of Danish trout populations. These are genotyped for 6000 candidate SNPs (Single Nucleotide Polymorphisms) on an Illumina iSelect bead array. The SNP chip is developed in another DTU Aqua project (Living North Sea Project). Results from the 6000 SNPs will be used to identify a subset of SNPs that are particularly well suited to distinguish between Danish trout populations. These SNPs will be used as a genetic tool in the future and it is therefore extremely important to get proper coverage of Danish trout populations in the mapping of the genetic diversity.

The projects was coordinated by DTU Aqua.

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

National Institute of Aquatic Resources
Section for Marine Living Resources
Period: 01/01/2011 → ...
Number of participants: 3
Research areas: Population Genetics & Freshwater Fisheries and Ecology
Project participant:
Bekkevold, Dorte (Intern)
Als, Thomas Damm (Intern)
Aarestrup, Kim (Intern)

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

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

Scientific papers reporting results generated from this project include:

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

The project was coordinated by Department of Biological Sciences, Aarhus University.
The project was funded by the Danish Council for Independent Research.
Financing sources
Source: Internal funding (public)
Name of research programme: 1/3 DTU-stip, 2/3 FUR/andet
Project: PhD

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)

Fehmarn Belt science provision project: Fehmarn Belt fish and fisheries and related environmental investigations (38669)

Objectives and Background
The purpose of the project was to investigate main exploited fish stock and fisheries dynamics in relation to the marine environment with focus on the Fehmarn Belt area in the Western Baltic Sea, and to provide science and research based investigations and results, as well as reports and scientific peer reviewed journal papers on this. The work was associated to the scientific baseline investigations (2009-13) and impact assessment of the projection of the Fehmarn Belt Fixed Link between Denmark and Germany involving a science cooperation between DTU Aqua, Thünen-Institute and Femern Bælt A/S in order to generate knowledge on potential impacts of establishment of the fixed link. Focus was on the most important commercial fisheries and fish stocks in the area (cod, herring, and sprat, but also flatfish and eels).

Tasks and Deliverables
The work covered WP0: Prospective, planning and development of the investigations, producing outline and main contents of the science provision contract and coordination of tasks hereunder with DTU Aqua as inter-national project coordinator; WP1: Review of knowledge: Review, provision of data, and analyses of selected historical data on fish stock and fisheries dynamics; WP2: Extension of existing standard research surveys and linking to standard survey time series to detect potential effects on important fish stocks; WP3: Evaluation of potential integrated effects on important fish stocks and fisheries; WP4: Evaluation of potential effects of change and variability in hydrographical conditions on recruitment for important fish stocks (cod, herring, sprat); WP5: Evaluation of herring occurrences and migrations as well as separation of spring and autumn spawning herring stock components in the area.

WP1 included provision of state of the art knowledge from historical surveys and review of quality of survey indices, commercial fisheries data, and information on recruitment dynamics with emphasis on fluctuations in distribution and productivity with respect to environmental and anthropogenic drivers of change including species interactions and fisheries.

WP 2 included extension of existing standard surveys in the near field area and analysis of both the standard and extended time series with respect to tovariability in distribution, density and abundance patterns of relevant stocks, as well as developing advanced scientific survey evaluation models and methods for doing this.

WP 3 analyzed stock and fisheries dynamics by use and development of complex multi-fleet-multi-stock bio-economic management evaluation models performing analyses on a very high spatial and temporal resolution scale using integrated fisheries, stock and survey data. The models evaluated different management options and scenarios relevant for the establishment of the fixed link.
WP4 evaluated variability in recruitment and important spawning areas according to hydrographic features and in relation to impact of the fixed link among other by use and further development of complex hydro-dynamic models.
 WP 5 evaluated herring stock occurrence and migration patterns in the Baltic areas by use of genetic identity markers, otolith micro-structures and information from fisheries and research surveys in order to evaluate impact of the fixed link.
 The project has besides a long row of project reports produced around 30 scientific peer reviewed journal papers where DTU Aqua are first author on more than half and co-author on more than 20 of the papers.
 The project was coordinated by DTU Aqua.
 The project was funded by the 3 partners with external Funding from Femern Bælt A/S.

National Institute of Aquatic Resources
Section for Ecosystem based Marine Management
Johann Heinrich von Thünen-Institute

Femern A/S
Period: 01/01/2009 → 31/12/2013
Number of participants: 15
Research areas: Fisheries Management & Fish Biology & Marine Living Resources & Population Genetics
Project participant:
Worsøe Clausen, Lotte (Intern)
Bastardie, Francois (Intern)
Bekkevold, Dorte (Intern)
Huwer, Bastian (Intern)
Hüssy, Karin (Intern)
Storr-Paulsen, Marie (Intern)
Stæhr, Karl-Johan (Intern)
Sparrevoehn, Claus Reeds (Intern)
Jepsen, Niels (Intern)
Lewy, Peter (Intern)
Kristensen, Kasper (Intern)
Dutz, Jörg (Intern)
Christensen, Asbjørn (Intern)
Geitner, Kerstin (Intern)

Project Coordinator:
Nielsen, J. Rasmus (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
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. The new 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)

Monitoring effective population sizes of North Sea houting using genetic markers (38272)
This project was aimed at providing basic information on the genetic structure of lake whitefish and North Sea houting, species where population genetic data are needed in order to improve conservation and management efforts, including principles for stocking.

The project focused on North Sea houting within the framework of the EU LIFE project Urgent Actions for the endangered houting (Coregonus oxyrhinchus). It was investigated if there are other remaining indigenous populations than that in the Vidaa River, which is currently assumed to be the last remnant of this species/form. Moreover, effective population size
was estimated in order to assess if it was below the threshold where inbreeding and loss of genetic variation is an immediate concern. A paper was published on genetic monitoring of effective population size in North Sea houting, showing that the described methods are useful for monitoring purposes. All analyses were based on microsatellite DNA analysis of contemporary and historical samples. In addition, the results were used in the context of a US-based working group, aimed at defining and developing the emerging field of genetic monitoring, i.e. the use of genetic markers for monitoring populations.

The project was coordinated by the Nature Agency, Danish Ministry of the Environment, Denmark.

The project was funded by EU LIFE.

National Institute of Aquatic Resources
Section for Marine Living Resources

Danish Ministry of the Environment
Period: 01/01/2005 → 31/12/2011
Number of participants: 1
Research areas: Population Genetics & Freshwater Fisheries and Ecology
Project Manager, academic:
Bekkevold, Dorte (Intern)

Conservation of diversity in an exploited species: Spatio-temporal variation in the genetics of herring (Clupea harengus) in the North Sea and adjacent areas (HERGEN) (5512)

National Institute of Aquatic Resources
Section for Marine Living Resources
Wageningen IMARES
Stockholm University
University of Gothenburg
University of Hull
Institute of Marine Research
Marine Laboratory
Period: 01/01/2002 → 31/12/2005
Number of participants: 4
Research area: Population Genetics
Project participant:
Mosegaard, Henrik (Intern)
Worsøe Clausen, Lotte (Intern)
Project Manager, academic:
Bekkevold, Dorte (Intern)
Ruzzante, Daniel (Ekstern)

Gene flow from stocked salmonids to wild populations (38273)
The aim of the project was to develop and implement genetic marker based methods to assess population characteristics, such as genetically effective population sizes and exchange of dispersers among salmonid populations, focusing on brown trout, Salmo trutta. Strong focus was on an assessment of the genetic effects of stocking wild populations based on releases of juveniles of native wild brood-stock or from domesticated hatchery strains. Analyses of temporal samples, both archived and continuously sampled, have contributed to an understanding of effects of stocking on wild populations on short to long term.

National Institute of Aquatic Resources
Section for Marine Living Resources
Period: 01/01/2001 → 31/12/2015
Number of participants: 1
Research area: Population Genetics
Project Manager, academic:
Activities:

**ICES - Working Group on Application of Genetics in Fisheries and Mariculture - WGAGFM (External organisation)**

Period: 2014
Dorte Bekkevold (Chairman)
National Institute of Aquatic Resources
Section for Marine Living Resources
Degree of recognition: International

**Related external organisation**

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

**ICES - Working Group on Application of Genetics in Fisheries and Mariculture - WGAGFM (External organisation)**
Period: 2013 → …
Dorte Bekkevold (Chairman)
National Institute of Aquatic Resources
Section for Marine Living Resources
Degree of recognition: International

**Related external organisation**

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

**ICES - Working Group on the Application of Genetics in Fisheries and Mariculture - WGAGFM (External organisation)**
Period: 2012 → …
Dorte Bekkevold (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