Recombination patterns reveal information about centromere location on linkage maps

Linkage mapping is often used to identify genes associated with phenotypic traits and for aiding genome assemblies. Still, many emerging maps do not locate centromeres – an essential component of the genomic landscape. Here, we demonstrate that for genomes with strong chiasma interference, approximate centromere placement is possible by phasing the same data used to generate linkage maps. Assuming one obligate crossover per chromosome arm, information about centromere location can be revealed by tracking the accumulated recombination frequency along linkage groups, similar to half-tetrad analyses. We validate the method on a linkage map for sockeye salmon (Oncorhynchus nerka) with known centromeric regions. Further tests suggest that the method will work well in other salmonids and other eukaryotes. However, the method performed weakly when applied to a male linkage map (rainbow trout; O. mykiss) characterized by low and unevenly distributed recombination – a general feature of male meiosis in many species. Further, a high frequency of double crossovers along chromosome arms in barley reduced resolution for locating centromeric regions on most linkage groups. Despite these limitations, our method should work well for high-density maps in species with strong recombination interference and will enrich many existing and future mapping resources.
Sorting duplicated loci disentangles complexities of polyploid genomes masked by genotyping by sequencing

Many plants and animals of polyploid origin are currently enjoying a genomics explosion enabled by modern sequencing and genotyping technologies. However, routine filtering of duplicated loci in most studies using genotyping by sequencing introduces an unacceptable, but often overlooked, bias when detecting selection. Retained duplicates from ancient whole-genome duplications (WGDs) may be found throughout genomes, whereas retained duplicates from recent WGDs are concentrated at distal ends of some chromosome arms. Additionally, segmental duplicates can be found at distal ends or nearly anywhere in a genome. Evidence shows that these duplications facilitate adaptation through one of two pathways: neo-functionalization or increased gene expression. Filtering duplicates removes distal ends of some chromosomes, and distal ends are especially known to harbour adaptively important genes. Thus, filtering of duplicated loci impoverishes the interpretation of genomic data as signals from contiguous duplicated genes are ignored. We review existing strategies to genotype and map duplicated loci; we focus in detail on an overlooked strategy of using gynogenetic haploids (1N) as a part of new genotyping by sequencing studies. We provide guidelines on how to use this haploid strategy for studies on polyploid-origin vertebrates including how it can be used to screen duplicated loci in natural populations. We conclude by discussing areas of research that will benefit from better inclusion of polyploid loci; we particularly stress the sometimes overlooked fact that basing genomic studies on dense maps provides value added in the form of locating and annotating outlier loci or colocating outliers into islands of divergence.

General information
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Scopus rating (2004): SJR 2.756 SNIP 2.099
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Web of Science (2003): Indexed yes
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Gene-associated markers can assign origin in a weakly structured fish, Atlantic herring

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

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Authors: Limborg, M. (Intern)
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Klima og gener: perspektiver fra pukkelaks

Laksens genetik forudsiger vinder og tabere ved klimaforandringer

General information

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Linkage mapping reveals strong chiasma interference in Sockeye salmon: Implications for interpreting genomic data

Meiotic recombination is fundamental for generating new genetic variation and for securing proper disjunction. Further, recombination plays an essential role during the rediploidization process of polyploid-origin genomes because crossovers between pairs of homeologous chromosomes retain duplicated regions. A better understanding of how recombination affects genome evolution is crucial for interpreting genomic data; unfortunately, current knowledge mainly originates from a few model species. Salmonid fishes provide a valuable system for studying the effects of recombination in nonmodel species. Salmonid females generally produce thousands of embryos, providing large families for conducting inheritance studies. Further, salmonid genomes are currently rediploidizing after a whole genome duplication and can serve as models for studying the role of homeologous crossovers on genome evolution. Here, we present a detailed interrogation of recombination patterns in sockeye salmon (Oncorhynchus nerka). First, we use RAD sequencing of haploid and diploid gynogenetic families to construct a dense linkage map that includes paralogous loci and location of centromeres. We find a nonrandom distribution of paralogs that mainly cluster in extended regions distally located on 11 different chromosomes, consistent with ongoing homeologous recombination in these regions. We also estimate the strength of interference across each chromosome; results reveal strong interference and crossovers are mostly limited to one per arm. Interference was further shown to continue across centromeres, but metacentric chromosomes generally had at least one crossover on each arm. We discuss the relevance of these findings for both mapping and population genomic studies.
Characterizing neutral and adaptive variation in a duplicated salmonid genome

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Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Limborg, M. (Intern), Waples, R. K. (Ekstern), Seeb, L. W. (Ekstern), Seeb, J. E. (Ekstern)
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Genetic variation among major sockeye salmon populations in Kamchatka peninsula inferred from SNP and microsatellite DNA analyses
Sockeye salmon samples from six populations from Kamchatka Peninsula were tested for polymorphism at six microsatellite (STR) and forty-five single nucleotide polymorphism (SNP) loci. These populations included the five largest populations in the region. Statistically significant genetic differentiation among the local populations from this part of the species range examined was demonstrated. The STR variability points to pronounced genetic divergence of the populations from two geographical regions, Eastern and Western Kamchatka. The results of SNP analysis further revealed that the populations of the two northern Kamchatka rivers (Palana River and Pakhacha River) differed significantly from the other populations studied. We estimated the efficiency for both types of markers for individual assignment of fish taken in mixtures. Accuracy was generally higher for assignment with SNP data; however, pooling of the STR and SNP data sets provided higher accuracy than with either one alone.

Genomics and the future of conservation genetics revisited

Gynogenetic haploid and diploid mapping reveals chiasma interference and hidden islands of adaptive importance in a salmonid genome
Gynogenetic haploid and diploid mapping reveals chiasma interference and hidden islands of adaptive importance in a salmonid genome

Haploid-assisted mapping disentangles complexities of duplicated salmonid genomes

Parallel signatures of selection in temporally isolated lineages of pink salmon

Studying the effect of similar environments on diverse genetic backgrounds has long been a goal of evolutionary biologists with studies typically relying on experimental approaches. Pink salmon, a highly abundant and widely ranging salmonid, provide a naturally occurring opportunity to study the effects of similar environments on divergent genetic backgrounds due to a strict two-year semelparous life history. The species is composed of two reproductively isolated lineages with overlapping ranges that share the same spawning and rearing environments in alternate years. We used restriction site-associated DNA (RAD) sequencing to discover and genotype approximately 8000 SNP loci in three population pairs of even- and odd-year pink salmon along a latitudinal gradient in North America. We found greater differentiation within the odd-year than within the even-year lineage and greater differentiation in the southern pair from Puget Sound than in the northern Alaskan population pairs. We identified 15 SNPs reflecting signatures of parallel selection using both a differentiation-based method (BAYESCAN) and an environmental correlation method (BAYENV). These SNPs represent genomic regions that may be particularly informative in understanding adaptive evolution in pink salmon and exploring how differing genetic backgrounds within a species respond to selection from the same natural environment.
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Scopus rating (2014): SJR 3.446 SNIP 1.602 CiteScore 5.43
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Scopus rating (2006): SJR 2.937 SNIP 1.918
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Temporally isolated lineages of Pink salmon reveal unique signatures of selection on distinct pools of standing genetic variation

A species’ genetic diversity bears the marks of evolutionary processes that have occurred throughout its history. However, robust detection of selection in wild populations is difficult and often impeded by lack of replicate tests. Here, we investigate selection in pink salmon (Oncorhynchus gorbuscha) using genome scans coupled with inference from a haploid-assisted linkage map. Pink salmon have a strict 2-year semelparous life history which has resulted in temporally isolated (allochronic) lineages that remain sympatric through sharing of spawning habitats in alternate years. The lineages differ in a range of adaptive traits, suggesting different genetic backgrounds. We used genotyping by sequencing of haploids to generate a high-density linkage map with 7035 loci and screened an existing panel of 8036 loci for signatures of selection. The linkage map enabled identification of novel genomic regions displaying signatures of parallel selection shared between lineages. Furthermore, 24 loci demonstrated divergent selection and differences in genetic diversity between lineages, suggesting that adaptation in the 2 lineages has arisen from different pools of standing genetic variation. Findings have implications for understanding asynchronous population abundances as well as predicting future ecosystem impacts from lineage-specific responses to climate change.
The effects of medieval dams on genetic divergence and demographic history in brown trout populations

Background: Habitat fragmentation has accelerated within the last century, but may have been ongoing over longer time scales. We analyzed the timing and genetic consequences of fragmentation in two isolated lake-dwelling brown trout populations. They are from the same river system (the Gudenå River, Denmark) and have been isolated from downstream anadromous trout by dams established ca. 600-800 years ago. For reference, we included ten other anadromous populations and two hatchery strains. Based on analysis of 44 microsatellite loci we investigated if the lake populations have been naturally genetically differentiated from anadromous trout for thousands of years, or have diverged recently due to the establishment of dams. Results: Divergence time estimates were based on 1) Approximate Bayesian Computation and 2) a coalescent-based isolation-with-gene-flow model. Both methods suggested divergence times ca. 600-800 years bp, providing strong evidence for establishment of dams in the Medieval as the factor causing divergence. Bayesian cluster analysis showed influence of stocked trout in several reference populations, but not in the focal lake and anadromous populations. Estimates of effective population size using a linkage disequilibrium method ranged from 244 to > 1,000 in all but one anadromous population, but were lower (153 and 252) in the lake populations. Conclusions: We show that genetic divergence of lake-dwelling trout in two Danish lakes reflects establishment of water mills and impassable dams ca. 600-800 years ago rather than a natural genetic population structure. Although effective population sizes of the two lake populations are not critically low they may ultimately limit response to selection and thereby future adaptation. Our results demonstrate that populations may have been affected by anthropogenic disturbance over longer time scales than normally assumed

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Genomic signatures distinguish ancient from recent selection in pink salmon (Oncorhynchus gorbuscha)

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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.
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 at 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
Authors: Helyar, S. (Ekstern), Limborg, M. (Intern), Bekkevold, D. (Intern), Taylor, M. (Ekstern), Carvalho, G. (Ekstern)
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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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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, Po0.01). 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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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 environmental 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 related 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.

**Regnbueørredens DNA sladrer om klimatilpasninger**

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**Signatures of natural selection among lineages and habitats in Oncorhynchus mykiss**

Recent advances in molecular interrogation techniques now allow unprecedented genomic inference about the role of adaptive genetic divergence in wild populations. We used high-throughput genotyping to screen a genome-wide panel of 276 single nucleotide polymorphisms (SNPs) for the economically and culturally important salmonid Oncorhynchus mykiss. Samples included 805 individuals from 11 anadromous and resident populations from the northwestern United States and British Columbia, and represented two major lineages including paired populations of each life history within single drainages of each lineage. Overall patterns of variation affirmed clear distinctions between lineages and in most instances, isolation by distance within them. Evidence for divergent selection at eight candidate loci included significant landscape correlations, particularly with temperature. High diversity of two nonsynonymous mutations within the peptide-binding region of the major histocompatibility complex (MHC) class II (DAB) gene provided signatures of balancing selection. Weak signals for potential selection between sympatric resident and anadromous populations were revealed from genome scans and allele frequency comparisons. Our results suggest an important adaptive role for immune-related functions and present a large genomic resource for future studies.

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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 a 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.

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, Section for Population Ecology and Genetics, Aarhus University
Authors: Helyar, S. J. (Ekstern), Limborg, M. (Intern), Bekkevold, D. (Intern), Babbucci, M. (Ekstern), van Houdt, J. (Ekstern), Maes, G. E. (Ekstern), Bargelloni, L. (Ekstern), Nielsen, R. O. (Ekstern), Taylor, M. I. (Ekstern), Ogden, R. (Ekstern), Cariani, A. (Ekstern), Carvalho, G. R. (Ekstern), Consortium, F. (Ekstern), Panitz, F. (Forskerdatabase)
Pages: e42089
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.

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.
Genomic approaches of adaptation of marine organisms in changing environments: what can populations tell us about genes underlying phenotypic changes and what can genes tell us about adaptive evolution of populations?

**General information**

**State:** Published

**Organisations:** National Institute of Aquatic Resources, Section for Marine Living Resources, Institute for Agricultural and Fisheries Research, Radiological Protection Institute of Ireland
Microsatellite DNA reveals population genetic differentiation among sprat (Sprattus sprattus) sampled throughout the Northeast Atlantic, including Norwegian fjords

Glover, K. A., Skaala, Ø., Limborg, M., Kvamme, C., and Torstensen, E. Microsatellite DNA reveals population genetic differentiation among sprat (Sprattus sprattus) sampled throughout the Northeast Atlantic, including Norwegian fjords. – ICES Journal of Marine Science, 68: 2145–2151. Sprat (Sprattus sprattus), small pelagic shoaling fish, were sampled from the Celtic, North, and Baltic seas, and 10 Norwegian fjords. Significant overall genetic differentiation was observed among samples when analysed with eight microsatellite DNA loci (Global FST = 0.0065, p <0.0001). The greatest genetic differences were observed between the Baltic and all other samples (largest pairwise FST = 0.043, p <0.0001). No significant genetic differentiation was observed between a sample from the Celtic Sea (CEL) and the North Sea (NSEA; FST = 0.001, p = 0.16), but variable levels of genetic differentiation were observed among samples collected from Norwegian fjords (pairwise FST ranging from 0 to 0.0096, most non-significant). All fjord samples were significantly differentiated to NSEA and CEL samples. Further, all fjord samples displayed reduced allelic richness compared with NSEA and CEL samples. Clearly, sprat display population genetic differentiation throughout the Northeast Atlantic, and there may be limited connectivity between Norwegian fjord and sea-going populations.
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
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Publication: Research › Conference abstract for conference – Annual report year: 2011

Populationsstruktur hos små pelagiske fisk i et heterogent marint miljø viden fra – og anvendelse af genetiske metoder

General information
State: Published
Organisations: National Institute of Aquatic Resources, Section for Marine Living Resources
Authors: Limborg, M. (Intern), Bekkevold, D. (Intern)
Publication date: 2011
Main Research Area: Technical/natural sciences
Publication: Research › Conference abstract for conference – Annual report year: 2014

Signatures of natural selection among lineages and habitats in Oncorhynchus mykiss
Genetic population structure of European sprat (Sprattus sprattus L.): differentiation across a steep environmental gradient in a small pelagic fish

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

**General information**

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

Authors: Limborg, M. (Intern), Bekkevold, D. (Intern), Hanel, R. (Ekstern), Carl, A. (Ekstern), Ring, A. (Ekstern), Tsigenopoulos, C. (Ekstern)

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Managing fleets and fisheries

**General information**

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

Authors: Nielsen, J. R. (Intern), Limborg, M. (Intern)

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Managing fleets and fisheries rather than single stocks – conceptual change in European fisheries management advice

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ToR d) Assess the possibility for the development of an integrated global management model for Atlantic cod based on genetic information

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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.
General information
State: Published
Organisations: Section for Population Ecology and Genetics, National Institute of Aquatic Resources
Authors: Dailianis, T. (Ekstern), Limborg, M. (Intern), Hanel, R. (Ekstern), Bekkevold, D. (Intern), Lagnel, J. (Ekstern), Magoulias, A. (Ekstern), Tsigenopoulos, C. (Ekstern)
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Web of Science (2015): Indexed yes
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Scopus rating (2014): SJR 2.842 SNIP 2.217 CiteScore 5.04
Web of Science (2014): Indexed yes
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Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
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BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.395 SNIP 1.173 CiteScore 2.75
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.94 SNIP 0.814
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.277 SNIP 1.291
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.926 SNIP 0.938
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.042 SNIP 0.928
Scopus rating (2006): SJR 0.927 SNIP 0.958
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.057 SNIP 1.152
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Scopus rating (2002): SJR 0.465 SNIP 0.373
Projects:

Ecological speciation in salmonids: the genomic background for the evolution of eco-morphs (38957)
Speciation is a fundamental evolutionary process continuously creating the diversity of life. Salmonid fishes have fascinated scientists for centuries due to their iconic and diverse set of habitats and eco-morphs. In addition, the salmonid lineage underwent two whole-genome duplication events that provided an enormous DNA template to support adaptive radiation and speciation. These assets make salmonids excellent model species for studying fundamental issues relating to adaptation and speciation in the wild.

This project took advantage of a unique set of replicated samples representing different migratory eco-morphs in two species of salmonids, state-of-the-art genomic techniques and novel statistical methods to
- infer the genomic extent of adaptive divergence between different migratory eco-morphs in salmonid species.
- infer the genomic architecture during the early stages of ecological speciation by comparing different ecomorphs.
- identify footprints of selection at genomic regions of importance for adapting to local environmental conditions.

Knowledge about the mechanisms and conditions required for species to evolve by adapting to new surroundings is of paramount importance for predicting future responses to climatically (or anthropogenically) induced environmental change.

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National Institute of Aquatic Resources
Section for Marine Living Resources
University of Washington
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Number of participants: 1
Research area: Population Genetics
Project Coordinator:
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Local adaption in Baltic Sea small pelagic fishes
National Institute of Aquatic Resources
Period: 01/09/2008 → 28/03/2012
Number of participants: 8
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Eg Nielsen, Einar (Intern)
Main Supervisor:
Bekkevold, Dorte (Intern)
Examiner:
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Hauser, Lorenz (Ekstern)
Vasemàgi, Antí (Ekstern)

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