

Abstracts of Oral Papers not published in the Supplement

Spatial patterns in the structure of fish populations and communities – lessons from coral reefs

Numerous field studies have documented the sedentary habits of most species of fish on coral reefs. This habit of staying put, and a strong tendency to associate with specific types of habitat, result in reef fish species being distributed patchily across the available environment at a range of spatial scales. Local aggregations function as breeding groups that may be more or less isolated demographically from nearby groups of the same species, and the set of local groups is probably best represented as a metapopulation. Current studies of connectivity are attempts to quantify the extent of interconnection among local groups, a topic of considerable importance because of the growing prevalence of spatially based management approaches, such as the use of no-take marine reserves. Such management approaches should be based on sound knowledge of the spatial scales at which local groups are interconnected. In a similar way, communities of fish on coral reefs can best be thought of as metassemblages (or metacommunities), in which each of the individual species present at a local site represents one node in its own metapopulation, with the proviso that the metapopulations may well exist on different spatial scales. To date, the consequences of metassemblage structure for interspecific interactions have scarcely been explored. This paper reviews our knowledge of the spatial structure of reef fish populations and communities, discusses the approaches being used to define the spatial scales of connectivity that are involved, and discusses the likely lessons for spatial structuring of fish populations in other environments.

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Population structuring of Atlantic salmon within rivers: from meta-population linkage to phylogenetic divergence

Tagging and genetic studies indicate Atlantic salmon stocks in all but the smallest rivers across the species range can be expected to be structured into multiple genetic populations. The nature of structuring is highly variable. In parts of the species' range, it is associated with life-history divergence between anadromous and non-anadromous forms and, in some cases, involves in existence of distinct, highly differentiated sympatric populations of the two forms. In other cases, the two forms are parapatric and non-anadromous forms represented by multiple, highly phylogenetically diverged allopatric populations. Differentiation within anadromous stocks in most rivers is lower though still, in many cases, consistent with the existence of multiple distinct genetic populations. However, levels of divergence and behavioural evidence suggest that this structuring probably operates within a meta-population dynamic and, though gene flow among populations is clearly constrained, it is sufficient to preclude long-term phylogenetic divergence. The work on Atlantic salmon suggests that population structuring within other species may often be highly variable in nature. In many cases, the nature of the population structuring which occurs will have major implications for the management of a species, particularly as regards defining conservation priorities and the options for developing stock rebuilding programmes.

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Role of sub-stock structure in the maintenance of Icelandic cod metapopulations

Many commercially exploited fish species are presently managed as a single unit, despite the fact that they are composed of complex aggregations, or metapopulations, that may represent different spawning stocks or distinct sub-stocks. The number of sub-stocks comprising a stock has been referred to as "stock-richness". A common feature of over-exploitation is the collapse of both spatial and dynamic structure of the stocks resulting in loss of variability within and among stock units including stock-richness. In terms of the Icelandic cod stock, recent research have indicated that this stock may be composed of a multitude of sub-units, contributing disproportionately towards recruitment and the fishable stock. In METACOD (a 5th frame EU project), attempts are being made to establish the genetic, behavioural and oceanographic basis for the stock richness of the cod around Iceland, and the variations in productivity between sub-stocks. As such, spawning sites have been mapped and sub stocks have been identified based on genetic and tagging information as well as otolith shape and chemistry. Egg production by different stock units have been estimated and tracked with particle tracking based on high resolution hydrodynamic models providing results that were compared with observed distribution of 0-group cod. Finally, the use of these results in developing an advice on how catch and/or effort control measures might be structured in space and time to manage the population abundance and structure, will be discussed.

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Metapopulation structure and persistence of stream-dwelling Dolly Varden in the Shiisorapuchi River, Hokkaido, Japan

I summarise 7 years of research on the stream-dwelling Dolly Varden in the Shiisorapuchi River and show the effectiveness of a combination use of field survey both at local and regional scale with genetic analysis to elucidate a detailed population structure. The population expressed 'partial migration' between tributaries and the mainstream where most females migrated, but substantial proportion of the males were tributary residents. Number of mature adults was usually less than 100 per tributary. Because spawning occurred only in tributaries, each tributary represented a discrete breeding site. Microsatellite DNA analysis revealed a significant genetic structure within the river system (<35 km). Isolation-by-distance was apparent, indicating gene flow among nearby tributaries with low or no divergence observed among neighboring tributaries (<5–10 km). I tested whether a group of neighboring tributaries functioned as a single population (demographic unit) by assessing the level of synchrony in population dynamics (4 tributaries, 7 years, <6 km). Synchrony was significant only in 0+-fish between adjacent tributaries (0.5 km). Therefore, most tributaries could be considered to be a discrete demographic unit (or local populations). I also investigated whether extinction and colonization occurred at a tributary level. Pattern of occurrence in 78 tributaries suggested extinction and colonization dynamics, and an equilibrium-non-equilibrium cline in downstream direction. Extinction and colonization appeared to occur mainly in small tributaries. Therefore, Dolly Varden in the Shiisorapuchi River should exhibit a "mainland-island" or "source-sink" metapopulation structure. These

characters (female-biased migration, metapopulation structure) may be highly vulnerable to habitat alterations.

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Spatial structure of biological parameters in fish populations

Parameters like sex ratio, maturity, age distribution and condition in a fish population can be strongly structured on a relatively small spatial scale. The current paper explores the extent and scale of spatial variability in these biological parameters and the sensitivity of the stock assessment process to biases in these parameters. A number of fish stocks around Ireland are explored to illustrate these issues. Examples include the sex ratio of megrims, which varies considerably with depth. As there is a large difference in growth rate between the sexes, unrepresentative sampling can strongly influence the estimated weights at age. The second example concerns the proportion mature-at-age of Irish Sea cod. If sampling is targeted at the spawning aggregations, where the highest proportions mature are found, the spawning fraction of the population will be overestimated. With regards to the structure in age distributions, it is shown that the age-length-weights of haddock in inshore areas to the north of Ireland are significantly different from those of haddock in deeper waters, as inshore areas are dominated by one-year-old fish. This can lead to biased estimates of recruitment and numbers at age. Lastly, a large amount of spatial variability was found in the condition indices of whiting and haddock around Ireland. If inappropriate length-weight relationships are applied to a stock, weights-at-age estimates can be considerably biased. These examples will be used to quantify the potential effects of errors resulting from sampling designs that do not take spatial structure of biological parameters into account.

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Coho salmon colonization in recently deglaciated streams in Glacier Bay, Alaska: implications for Pacific salmon restoration

Processes associated with the evolution of ecological communities or metapopulation complexes are seldom documented from initial colonization events. Combining molecular genetic and geomorphological data we examine stream colonization events for coho salmon (*Oncorhynchus kisutch*) breeding in recently deglaciated streams (50–230 yrs BP) in Glacier Bay National Park, Alaska. Population estimates of genetic diversity, coancestry, and evidence of reproductive founder events were significantly related to stream age, reflecting the likely chronology of colonization by coho salmon into Glacier Bay. Several major and geographically proximal population associations were identified. Genetic relationships among populations correlated significantly with location (ocean basin, lower, middle, and upper bay regions) and to stream age suggesting a step-wise colonization process. Using knowledge gained of ecological processes of natural colonization within Glacier Bay, we discuss how genetic and demographic characteristics of newly founded populations change over time in response to successional changes in stream habitat. Data that identify progenitor populations and elucidate processes underlying successful natural colonization events can serve to guide restoration and conservation initiatives for declining or extirpated populations in degraded habitats across their native range.

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A general model of movement and life-history spatial dynamics for coastal teleosts

There are few marine teleosts in Australian coastal waters that undertake cohesive, predictable migrations and likewise few that are considered to constitute a single stock throughout their range. For many Australian marine teleosts there is insufficient knowledge to identify or demarcate stocks, with many species spread continuously, but with regionally variable abundance, throughout their range. Managing these species is challenging because the traditional concept of a unit stock often cannot be applied pragmatically to the spatial scales at which stock harvesting has developed and against which fisheries management strategies have aligned. Many coastal marine teleosts would be classified as a single genetic stock through their entire distribution but in such cases the geographic scale of the single stock approach is greater than can be effectively managed due to, for example, jurisdictional boundaries, spatially variable exploitation, and poor knowledge of the species' spatial dynamics. For many small-scale fisheries this issue must be managed in an economical yet scientifically defensible manner. Formal recognition of variability in habitat quality and spatial population dynamics throughout a species range provides an alternative platform for managing teleosts for which it has proven difficult to determine if separate stocks exist and, if applied conservatively, this approach can effectively replace the need for stock-structure studies in some cases. This approach is described for two species, the benthopelagic sparid *Pagrus auratus* and the small pelagic Clupeid *Sardinops sagax*, with the aim of developing a generalized conceptual model for spatially managing widely distributed coastal teleosts.

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Use of otolith geochemistry to determine population connectivity in a locally adapted marine species

Patterns of connectivity are important in understanding the geographic scale of local adaptation. High connectivity, or the exchange of individuals among subpopulations, is assumed in most marine species due to life histories that include widely dispersive stages. However, evidence of local adaptation in coastal species raises questions concerning the degree of connectivity. We examined geochemical signatures in the otoliths of juvenile *Menidia menidia* collected in 16 locations along the northeastern coast of the United States from New Jersey to Maine using laser ablation-inductively coupled plasma mass spectrometry (LA-ICPMS) and isotope ratio mass spectrometry. Juvenile fish showed significant site-specific differences and were assigned to natal sites with 85% classification accuracy using flexible discriminant analysis. Use of this algorithm allowed us to assign natal origin to spawning adults captured the following year in the same locations. Results show that *Menidia menidia* exhibit highly dispersive behavior with over 50% migrating greater than 200 km from natal sites. These findings suggest high connectivity and demonstrate marine species with largely open populations are capable of local adaptation despite apparently high gene flow.

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Can hatchling squids be re-classified to their site of origin, based on trace element fingerprints within statoliths?

Understanding the relative importance of different spawning areas in contributing recruits to fished populations is critical for ensuring resource sustainability, and an area currently poorly understood for cephalopods. Using LA-ICP-MS we assessed the potential of statolith trace elements as unique natural ‘fingerprints’ to identify the natal area of hatchling squid. Hatchling southern calamary were collected from six locations, each approximately 30 km apart, along the south-east Tasmanian coast. Significant differences in Fe, Sr, Mn, Ba, Mg, AS and Li were consistently found among locations, with discriminant analysis demonstrating that an average of 75% of hatchlings could be re-classified back to their correct site of origin based on their trace elements. Hatchlings from the main spawning area had a very distinctive elemental fingerprint, resulting in 95% re-classification success for individuals from this region. Two sites, both with adjacent exposed coastlines, had overlapping signatures bringing down the overall classification success. Elemental fingerprints in the hatch region of adult statoliths from the same six locations can now be used to retrospectively determine their natal origins. This work, together with the results from an extensive acoustic tracking and t-bar tagging program conducted during the spawning phase, will allow us to explore the dispersal scale of calamary, as well as the extent of self-seeding for each area, and the degree of connectivity among local populations.

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Use of stable isotopes to identify subpopulation structure in fishes

The use of stable isotope analysis (SIA) by ecologists is becoming increasingly common. SIA is generally used to describe the trophic ecology of target species, or to elucidate community interactions (e.g. food webs). However, it has excellent potential as a tool to identify and study structuring within fish populations. I will present examples where SIA was used to show resource segregation in polymorphic populations of European whitefish (*Coregonus lavaretus*), and the identification of distinct subpopulations in coastal populations of European eel (*Anguilla anguilla*).

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Egg retention promotes population structure in Atlantic cod

Previous studies have demonstrated that coastal Atlantic cod may constitute several genetically distinct populations along the Norwegian coast. Mechanisms preventing mixing of eggs and larvae will reinforce such population structure. These mechanisms include inshore spawning in sheltered areas. We studied possible egg retention within fjords through sampling of eggs in 20 Norwegian fjords along inshore-offshore transects. The general pattern across all fjords was a decrease of egg density when moving outwards, where fjords with shallow sills show an abrupt reduction in egg density over the sill. In a case study from 2001 we also demonstrate heterogeneous egg densities in an inshore coastal area throughout the spawning period, strongly indicating egg-retention. These studies thus support an ‘‘egg retention’’ hypothesis for the maintenance of local population structure in coastal Atlantic cod.

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Linking natural and electronic data records to assess population dispersal and lifetime migration in North Sea Plaice

Current fisheries management advice is limited by a lack of knowledge on the spatial dynamics of commercially important fish stocks. To describe the lifetime movements of plaice (*Pleuronectes platessa* L.) in the North Sea, we combined two state-of-the-art techniques: fish tagging with electronic data storage tags (DSTs) and otolith microchemistry. DST data allowed detailed reconstruction of the geographical movements of more than 160 free-swimming adult plaice and provided continuous records of ambient temperature for periods of up to 18 months. By matching DST data with seasonal growth-ring composition in the otoliths of 40 of these fish, we attempted to establish the retrospective positioning of these fish in space and time throughout their adult lives. Otoliths obtained from juveniles sampled from the main nursery areas of the English Channel and North Sea were also analyzed for differences in trace element composition. By matching the chemical signatures obtained for each nursery area with the elemental composition of otolith core in DST tagged fish, we attempted to link pre- and post recruitment behaviour in plaice. By providing information on population structure and dynamics that would be unattainable using conventional methods, the results from this study have the potential to significantly improve the parameterisation of assessment methods currently applied in fisheries management.

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Assessing the evidence for cod sub-stock separation between the English Channel and southern North Sea

Cod in the North Sea (ICES area IV) and eastern Channel (VIId) have been assessed as one stock since 1996. The stock is currently at historically low levels and subject to a 'Recovery Plan'. However, evidence that a single stock exists over this large region is limited. To test the hypothesis that cod in ICES IVc and VIId move as one stock, we evaluated movement and behavioural data using conventional and electronic tagging studies. First, we evaluated archived conventional tagging data (1964 to present day) to test the assumption that there is no exchange of cod between VIId and IVc. Second, we used electronic data storage tags to assess the behaviour and environmental experience of cod in VIId and IVc. The results of conventional tag analysis show that small (<50 cm) cod tagged in VIId during autumn and winter sometimes move into southern North Sea where they remain until capture. In contrast, cod in IVc show a clear pattern of seasonal northward movement. Analysis of electronic tag data show similar behaviour patterns occur within each area of release but not between them. These results provide evidence that the population of cod in VIId is not supplemented by post-spawning cod from IVc, and that cod in these different areas can be characterised by different behaviours. Our findings are a step towards modelling and simulation studies to evaluate biological and management implications of cod movement between the southern North Sea and eastern Channel.

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A biologically-based movement model for plaice in the North Sea

In spite of increasing evidence of complex population structure and varying rates of exchange of commercially exploited marine fish stocks between different management areas, the stock assessment methods currently used by ICES to advise on total allowable catches

(TACs) and technical conservation measures still take only limited account of seasonal migrations and movements. As an example, plaice, *Pleuronectes platessa* L., is currently managed as a single stock in the North Sea. However a combined experimental approach using conventional tagging data, and the release of hundreds of plaice tagged with electronic data storage tags, have allowed the identification of population substructure and the characterisation of annual migration routes and spawning areas. More recently, otolith microchemistry has been used to determine the contribution of larvae from different spawning areas to different nursery grounds, and the input from the nursery grounds to the adult population subunits. Here a biologically-based population movement simulation model is presented which utilizes data from each of these sources. The effects of a range of area and seasonal closures were tested in terms of reduction in overall fishing mortality. Results from this study illustrate the value of high-quality biological data to improve current advice on biologically and technically interacting fish stocks and fisheries.

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Adaptive morphological divergence vs. neutral genetic divergence in sympatric morphs of rainbow smelt, *Osmerus mordax*

Two freshwater populations of rainbow smelt (*Osmerus mordax*) in eastern Canada present an unusual opportunity to study the interplay of neutral gene flow and adaptive morphological divergence. In Lochaber Lake (Nova Scotia) and Lake Utopia (New Brunswick), smelt have independently diverged from a common marine anadromous ancestor into small planktivorous and large piscivorous morphs. In addition to differing in body size, the morphs differ in a variety of morphological traits, including gill raker number and length, eye diameter and jaw length that are consistent with the dietary specializations of the two forms. In both lakes, morphologically divergent smelt spawn at overlapping times in the same streams, creating the potential for gene flow between forms. We carried out morphometric analyses on both trophic morphs in both lakes, and compared morphological divergence to levels of genetic divergence determined from analyses of 10 microsatellite markers. The results revealed differing levels of morphological and genetic divergence between morphs in the two lakes, and also varying genetic divergence among years. Collectively, the results strongly suggest a dynamic balance between gene flow and disruptive natural selection that may be influenced by variation in the abundance of the piscivorous morph.

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Spatial variability of multiple paternity in a naturally spawning population of Atlantic salmon, *Salmo salar*

Genetic variation in Atlantic salmon populations can be maintained by the mating of many males with a single female. Males of this species can mature at a young age and small size as parr, or as large, migratory individuals. Large individuals form dominance hierarchies and compete for access to females, while smaller mature male parr “sneak” fertilisations by releasing sperm simultaneously with the large male as the female releases her eggs. Simultaneous spawning of both male maturation phenotypes, or many males with a single female, increases the genetic variability of the offspring. We undertook a field study in Catamaran brook, New Brunswick, Canada to determine the average number of males fertilising eggs in a single spawning event and how this varies within a system. In autumn, 2003, redd surveys were conducted along a 12 km stretch of the brook. Sixty eggs from 18 of a total of 62 egg nests were sampled, with almost equal numbers of nests sampled from three major sections of the brook. Kinship analysis was performed using

microsatellite markers to assign offspring to parents. Preliminary results suggest that up to eight males successfully fertilised eggs in some nests, though this varied greatly among egg nests, as well as spatially along the brook. We also relate incidence of multiple paternity to variability in mature male parr distribution. This study has implications for determining effective population size, as well as assessing genetic variation at early life stages in Atlantic salmon.

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Phenotypic variation and population structuring in Atlantic salmon in fluctuating environments

We used historical data to examine population structuring and phenotypic variation in neighbouring Atlantic salmon populations over several decades. We also used published sources to compare phenotypic variation among salmon populations and temporal stability within populations at larger geographical scales. Our results indicate that the environment inhabited by Atlantic salmon tends to vary more from year to year than either the genotype or the phenotype, suggesting that there must be considerable adaptive resilience. Fitness-related phenotypic traits tended to differ more between populations than they differed from year to year within populations. Freshwater traits varied the most among populations while marine traits varied the least, when corrected by the degree of temporal stability. Our study suggests that population structuring in anadromous Atlantic salmon is probably adaptive and that local adaptations are perhaps more likely to occur in freshwater than in the sea.

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Two size classes of 0+ perch: is phenotypic plasticity based on food resources?

0+ perch were caught in a gravel pit lake in June (unimodal size distribution) and in July and September (bimodal size distribution) to analyse differences in morphology. Independent of size, perch developed a deeper body and a shorter tail during ontogenesis (June to July/September). Perch of the large size cohort had an even deeper body and smaller tail than perch of the small size cohort. This supports the hypothesis that 0+ perch of the small size cohort were malnourished and individuals of the large size cohort showed the regular ontogenetic development. In a second step, we excluded the assumed factor "food quantity" of the field investigations, to focus on the influence of different food resources on morphology. Two groups of 0+ perch were fed for 40 days in mesocosms with the same biomass of either plankton or cyprinid fishes. At the end of the experiment, the two experimental groups of 0+ perch did not differ in size but in some morphological details. The mouth of the piscivorous 0+ perch became larger, the pectoral fins and the centre of mass of the posterior abdomen were shifted backwards. The results suggest that the factor "food quantity", and due to this the state of nutrition of 0+ perch is the major factor influencing growth and morphology. The type of food, however, is although important and might lead to further functional adaptations in morphology.

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Genetic differences in life history reaction norms among populations of Atlantic cod (*Gadus morhua*)

Common-garden experiments were undertaken to disentangle the genetic and environmental contributions to population differences in larval growth, larval survival, and phenotypic plasticity for growth and survival in Atlantic cod. Adults were captured immediately prior to spawning from 4 spatially distinct regions of the Northwest Atlantic: Southwest Nova Scotia (Northwest Atlantic Fishery Organisation [NAFO] division 4X), Southern Gulf of St. Lawrence (NAFO division 4T), Placentia Bay, Newfoundland (NAFO division 3Ps), and Bonavista Bay, Newfoundland (NAFO division 3L). Subsequent to their collection, groups of 40–70 adults were allowed to spawn undisturbed, producing egg batches that were transferred to a controlled environment prior to hatching. Offspring were reared at 2 levels of food (1500 and 4500 prey per litre) and at 2 temperatures (7 and 11 °C). Size at, and survival to, 43 days post-hatch differed significantly among populations, with growth generally increasing with latitude, as predicted by the counter-gradient selection hypothesis. Reaction norms, which describe the way in which genotypes alter their phenotype along an environmental gradient, also differed among populations, providing evidence of a genetic basis to plasticity. Importantly, genetic differences in fitness-related traits were evident at spatial scales at which genetic variation at selectively neutral loci detected no population substructure. Genetic differences in traits directly linked to reproductive success are consistent with the hypothesis of adaptation to environmental conditions at comparatively small scales in Atlantic cod.

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Sexual size dimorphism in blennies: variation among populations and the role of interspecific competition

The extent of sexual size dimorphism is usually determined by the intensity of sexual selection, and often regarded as a fixed trait within species. Using Mediterranean blennies as a model system, we show that interspecific competition can also be a powerful force promoting size differences between males and females and large variation among populations in intensity of interspecific competition occurs. In blennies male territoriality is essential for reproduction and fierce competition takes place for breeding holes. We found that males of several species used virtually identical nest sizes and interspecific nest takeovers occur frequently in the wild. In this study we test the prediction that variability in interspecific competition intensity among populations relates directly to variation in sexual size dimorphisms. We studied three blenny species, for each we compared 22 populations in one breeding season. Populations showed striking variation in body sizes of males, females and in the extent of sexual size dimorphism, the latter ranging from no dimorphism to males being one and a half times the size of females. For some species, there was a strong relationship between the intensity of interspecific competition and the extent of sexual dimorphism although for others intraspecific competition proved to be of greatest importance. This study provides a unique example of how interspecific competition can mediate selection for large male body size and how differences in the intensity of interspecific competition can generate large-scale variation in sexual size dimorphism among populations.

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Interpopulation variation in body form, fins and feeding structures in pumpkinseed populations introduced into Catalanian lakes and reservoirs

The pumpkinseed (*Lepomis gibbosus*), introduced into Spain in 1910, is now widely distributed throughout the Iberian Peninsula, where it has become a dominant species in streams, lakes and reservoirs. To assess its adaptations to the introduced environment, we examined the morphology of pumpkinseed populations in five Catalanian water bodies, and compared these to a native North American reference site that contains two morphological variants of this species, as well as a central European reservoir containing another introduced population (Požeg Reservoir, Slovenia). The morphological traits examined in this study were those known from previous studies to be functionally related to foraging mode and prey type. Study populations exhibited significant differences in morphometric measures related to fin location, body depth, caudal peduncle length, gill raker spacing and pharyngeal molar size. All of the study populations could be discriminated on the basis of external and internal morphology. The main axis of separation was geographical rather than functional; however the secondary DFA axis did separate populations that fed primarily on zooplankton from those that were primarily benthic invertebrate feeders. A pumpkinseed population from a steep-sided Catalanian reservoir with an unstable littoral zone showed similar morphological adaptations to the native limnetic morphological variant, supporting previous studies showing that pumpkinseed morphology is strongly affected by prey type and feeding mode. The high degree of morphological and life history plasticity in this species may partially explain why they are so successful in areas where they have been introduced.

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Morphological divergence in the cyprinids *Abramis brama* and *Blicca bjoerkna*

It has been long postulated that competing species evolve to reduce competition. Such evolution could result in a greater difference in e.g. resource use, and in features associated with that. Sympatric populations of two species can differ more than allopatric populations in their resource use, and the difference may be reflected in their morphology. To investigate whether interspecific competition between two cyprinid species resulted in morphological differences five lakes with sympatrically occurring *A. brama* and *B. bjoerkna* and five lakes with only *A. brama* were sampled in Uppland county, Sweden. Morphology was quantified using landmark-based geometric morphometric methods. Differences in shape were found between sympatrically occurring *A. brama* and *B. bjoerkna* as well as between sympatrically and allopatrically occurring *A. brama*. Removing the effect of length, the differences in shape between the above named groups persisted. However, no differences were found among *A. brama* populations from allopatric lakes. Analyses of stomach content and otoliths gave additional information on the life-history of these species. Differences in resource use were found between the sympatric and allopatric populations. Among the sympatric populations no such differences were found. Estimated length-at-age growth models revealed that hybrids were intermediate in size but had the same growth rate as *B. bjoerkna*. Comparisons of genetic differentiation for neutral markers (F_{st}) and quantitative traits (Q_{st}) revealed diversifying selection for the sympatric populations and stabilizing selection for the allopatric populations. The results suggest that interspecific interactions can be important for the evolution of shape in fish populations.

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Population variation in life history traits and thermal responses of cod

Atlantic cod occur over a wide range of thermal environments and exhibit a rich population structure. This study reports on a series of experiments from egg, through juvenile to adult maturation, in which population specific responses to temperature were investigated. Two cod populations from Scottish waters were selected on the basis of their differing annual thermal regimes. Wild caught post-settled juveniles from the East and West coasts of Scotland were taken into controlled laboratory conditions. The effect of temperature on growth and maturation was investigated at an individual level in these two populations. Juvenile growth rate was a parabolic function of temperature. The two populations differed when temperatures exceeded 9° C with East coast cod maintaining higher growth rates at higher temperatures. This evidence of local adaptation will enable more reliable predictions of population level responses to environmental change.

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Natural selection and adaptation of the deep-sea redfish *Sebastes mentella*

The deep scattering layer, comprising of plankton, squids and mesopelagic fish, extends from 300–400 to 550–750 meters depth within the North Atlantic in the area where our fish were sampled. This layer was used to define two zones within the Irminger Sea: shallow (<550 m) and deep (>550 m). Genetic analysis revealed a clear signal of two genetically distinct groups associated with the shallow and deep-zones indicating depth as barrier to gene-flow within the Irminger Sea. Natural selection favouring adaptations to local environmental conditions can lead to genetic differentiation of populations in the presence of restricted gene-flow. As light intensity decreases with the ocean depth, head parameters ($n = 1111$) were measured that are important in the foraging and the feeding of the species under different light conditions. The results showed that regression residuals of head features against body length were larger for the deep-zone fish, when compared to the shallow-zone fish above. These results demonstrated the occurrence of a selection pressure upon larger head features of redfish that dwell in the deep-zone, leading to adaptation to the darker environment.

Stefánsson, M. Ö., Pampoulie, C., Þorgilsson, B., Ragnarsdóttir, A., Gíslason, D., Danielsdóttir, A. K. & Sigurðsson, Þ. (*Marine Research Institute, Skúlagötu 4, IS-101 Reykjavík, Iceland*)

Genetic effective size and conservation/management of exploited and endangered species

Two central issues in the conservation and management of exploited and endangered species are whether the species is subdivided geographically into different populations (stocks) and whether the populations have sufficient genetic resources to ensure long-term adaptability and genetic integrity. The former is assessed typically by a variety of homogeneity tests of allele/genotype distributions at selectively neutral genetic markers, while the latter is assessed via estimates of genetic effective size (N_e). These issues are discussed in relation to the Gulf red snapper, a highly exploited lutjanid fish found primarily in the northern Gulf of Mexico, and the Cape Fear shiner, a critically endangered cyprinid fish now found in only two localities within the same river drainage in North Carolina. Allele/genotype distributions of red snapper are homogeneous across the northern Gulf of Mexico; estimates of short-term N_e , however, differ significantly among geographic samples, indicating occurrence of distinct 'demographic' assemblages (stocks). The hypothesis of different

demographic assemblages is supported by significant geographic variation in life-history traits. The demographic assemblages likely experience partially independent dynamics, but appear to be connected by sufficient gene flow to homogenize selectively neutral markers. Allele/genotype distributions between the two remaining, geographic populations of Cape Fear shiner are heterogeneous. A coalescent approach indicated a one-two order of magnitude decline in N_e , with current effective sizes on the order of 100–500. Both the genetic heterogeneity and the decline in effective size may have been precipitated by a water-diversion dam constructed in the early 1920s. These studies illustrate a significant role for estimates of effective population size in the conservation and management of both exploited and endangered fish species.

Gold, J. R. (*Center for Biosystematics and Biodiversity, Texas A&M University 2258, College Station, Texas, 77843-2258, U.S.A.*)

Biocomplexity in a highly migratory pelagic marine fish, Atlantic herring

The existence of biologically differentiated populations has been credited with a major role in conferring adaptive potential in fish. Management regimes that ignore the existence of such complexity can lead to the erosion of genetic diversity by inadvertently depleting spawning components. This problem is especially acute in highly abundant and widely distributed marine fish exhibiting diverse population components that migrate and intermingle seasonally, yet are often managed under the assumption of panmixia. Based on information describing genetically distinguishable (9 microsatellite loci) spawning assemblages of herring in the North Sea, Skagerrak, and Kattegat and western Baltic, along with information on otolith morphology (proxy for spawning season), we identify the proportional contributions by North Sea, Skagerrak and Western Baltic to mixed aggregations targeted by the North Sea fishery. Our study suggests that sustainability may be compromised if such complex patterns of intraspecific diversity are reduced through generalized management (e.g., area closures) that overlooks population differences in spatial use throughout the life cycle.

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Genetic imprints of quaternary spatial and demographic expansions in Atlantic herring

The high diversity in phenotypic traits and life-history strategies in Atlantic herring (*Clupea harengus*) have long stimulated the debate as to the most realistic population model applicable to the species. To examine the evolutionary history of Atlantic herring, we sequenced a 558 bp portion of the mitochondrial ND3/4 gene in 113 herring individuals

from locations spanning the whole present-day distribution range of the species (NE Canada, Iceland, English Channel, North Sea, Baltic and Barents Seas), and one Pacific herring sample from the Canadian west coast.

Using Phi-st and AMOVA computations, we found no significant differences in haplotype frequencies among geographic locations. Parsimony haplotype networks, for both Atlantic and Pacific herring, showed the starburst phylogeographic pattern typical of expanding populations. Unimodal mismatch distributions together with negative values of Tajima's D indicate herring may have undergone a demographic and spatial expansion, after a mid-Pleistocene bottleneck event.

The data represent valuable information on the recent evolutionary trajectories that led to the current Atlantic herring distribution and population structure. Our results provide grounds for better interpreting recent microsatellite studies, by suggesting the relatively recent colonisation of present-day habitats from possibly one single glacial refugium, followed by rapid demographic expansion.

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The genomic architecture of population differentiation: neutrality, adaptation and the evolution of quantitative traits in Atlantic salmon

From Mendel's first experiments with peas, biologists have tried to understand the genetic basis of heritable differentiation between individuals and populations. Effective fishery management depends upon the quantification of these differences, such that populations can be reliably defined, traits of interest identified and conserved, and genetic diversity maintained. Investigations into the genetic basis of differentiation can also elucidate the processes and components of local adaptation and the evolution of population-specific life-history traits. A common approach in recent studies is the use of genetic markers, such as microsatellites, to define measures of inter-population structuring (e.g. FST) and/or intra-population relatedness (e.g. FIS). This approach is particularly informative if comparisons are made between selectively 'neutral' markers and markers linked to genes under selection: it is, after all, the genes under selection which underpin adaptive diversity and which are the main focus of biological and conservation interest. To take this approach, however, markers linked to adaptive loci, or the loci themselves, must first be identified. Molecular markers for adaptive variation, underlying adaptive traits in Atlantic salmon, and the approaches used to identify them, are discussed; these include markers for sex, growth, smoltification, sexual maturation and parasite resistance. The results of population investigations using the identified markers are described.

Gilbey, J.¹, Verspoor, E.¹, Thompson, C.¹, Noble, L.², Jones, C.², McLay, A.³ & Houlihan, D.² (¹*FRS Freshwater Laboratory, Faskally, Pitlochry, U.K.*; ²*The University of Aberdeen, Zoology Building, Tillydrone Avenue, Aberdeen AB24 2TZ, U.K.*; ³*Fisheries Research Services, P. O. Box 101, 375 Victoria Road, Aberdeen, AB11 9DB, U.K.*)

The genetic structure of Icelandic cod

Marine fisheries are often managed under the assumption of panmixia without consideration of often suspected or known life history or genetic differences among components of a stock or population complex. Icelandic cod is one example. Management of this fishery is conducted under the assumption of a single panmictic unit, despite suggestions that the complex may indeed comprise a number of distinguishable spawning units distributed around the country. Here, we examine the genetic structure of Atlantic cod around Iceland using

nine microsatellite loci and the Pan I locus along with information from tag recaptures. A total of 2533 cod collected from 24 spawning locations in 2002 and 2003 were examined genetically and 6536 cod were tagged within the same regions of which a total of 240 were recovered. Genetic structure was significant but low with microsatellites ($F_{ST}=0.003$) and high for the Pan I locus ($F_{ST}=0.277$). This analysis revealed a clear and significant differentiation between the group of samples from the Northeast and those from the Southwest of Iceland. The tagging experiment revealed that over a period of 12 months following tagging 95% of the individuals marked were recaptured in the same or adjacent areas to those where they were marked. This study indicates that Icelandic cod from the Northeast and Southwest regions are genetically distinguishable, a finding that is likely to influence the management of this stock in the future and is consistent with the notion that oceanographic fronts in Northeast and Southwest Iceland likely limit gene flow among these regions.

Pampoulie, C., Ruzzante, D. E., Chosson, V., Jörundsdóttir, Þ. D., Taylor, L., Þorsteinsson, V., Danielsdóttir, A. K. & Marteinsdóttir, G. (*Marine Research Institute, Skulagata 4, 101 Reykjavik, Iceland*)

Small scale genetic differentiation between ecotypes of Eurasian perch from Lake Mälaren, Sweden

Many species of fish inhabiting lakes of glacial origin show repeated patterns of intraspecific divergence in morphology associated to the littoral and pelagic habitats of lakes. The occurrence of different resource based morphs (i.e. ecotypes) within a species has been hypothesized to be of great evolutionary significance, for example as an initial step during speciation. However, a prerequisite for this to happen is the evolution of reproductive isolation between ecotypes. Here we show evidence that littoral ecotypes in perch could be genetically differentiated from pelagic ecotypes. This pattern was found on two sampling occasions, in May (spawning period) and August the same year. We also found genetic differentiation between littoral ecotypes from two closely situated sites (separated by less than 500 meters) as well as differentiation within littoral and pelagic sites between sampling occasions. The different sites seemed to have hosted different sub-populations over time since we found indications of kin-structures within sites and sampling dates. Our results suggest more fine scaled genetic structuring in perch than previously acknowledged, and that non-random mating between ecotypes might have evolved in perch. The temporal genetic differentiation and indications of kin-structures within sites suggest that perch in this lake aggregate in kin-structured schools that are mobile in time and space. Our results imply that small-scaled spatial and temporal sub-structuring of fish populations needs to be incorporated into conservation practices if we are to preserve genetic variation in nature.

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Combining microsatellites and geometric morphometrics for the study of redfish population structure in the northwest Atlantic

An approach combining genetics and geometric morphometrics has been used to define the population structure of two redfish species, *Sebastes mentella*, and *S. fasciatus*, in the Northwest Atlantic. The genotype at 13 microsatellite loci, and body shape—defined by 10 anatomical landmarks—were determined on 1121 specimens representing 36 fishing aggregations of redfish (19 *S. fasciatus*, 16 *S. mentella*, and an additional *S. marinus* sample for comparison purpose). An overall good concordance was observed between the two data sets, based on a Mantel test on the matrices of pairwise genetic and morphometric distances ($r_S = 0.71$, $P < 0.001$), suggesting that shape has a strong genetic basis. A model-based clustering method, using a Bayesian algorithm, detected introgressive hybridization between

S. fasciatus and *S. mentella*. The overall genetic structure was weak within species (mean $F_{ST} = 0.010$), with only three *S. mentella* and four *S. fasciatus* samples presenting significant pairwise F_{ST} values. Multidimensional scaling analyses (MDS) performed separately on the genetic and the morphometric data both indicated large scale geographic population structure. This structure was in agreement with the member-vagrant hypothesis and suggested adaptive selection of body shape in fish experiencing different environmental conditions. Smaller scale genetic heterogeneity was superimposed on the large scale structure. Introgressive hybridization played a role in shaping the large scale population structure, and contributed to the small scale heterogeneity, which remained in part unexplained. In some cases, the apparent contradiction between the genetic and the morphometric results revealed the complementarity of the two approaches in describing population structure and connectivity.

Valentin, A. E., Sévigny, J.-M., Chanut, J.-P. & Penin, X. (*Institut des sciences de la mer de Rimouski, Université du Québec à Rimouski, 310, Allée des Ursulines, Rimouski (Québec) G5L 3A1, Canada*)

Genetic differentiation at a small geographical scale in the perch (*Perca fluviatilis*)

Gene flow is one of the factors that maintain genetic diversity and thus hinder differentiation between populations. The effect of gene flow depends on the ability of migration between populations and has been related to geographical distance. Recently it has been shown for a highly mobile species the perch (*Perca fluviatilis*), that one lake may not represent a single panmictic population, but instead are substructured into smaller populations. In this study, perch from nine locations ($n = 266$) in lake Erken, Upland county, Sweden, were genotyped by using eight microsatellite DNA loci. Both differentiations of pairwise comparisons and overall populations resulted in significant F_{ST} values. Bayesian assignments resulted in structuring nine populations, corresponding to the sampled populations. Very low migration rates and low effective population sizes were detected between locations within the lake, supporting the idea that substructure is a result of local random genetic drift. Significantly high inbreeding values indicate that the subpopulations consist of relatives forming shoals based on kin preferences which could explain the persistence of population structure found. The sample locations in this study are within a small spatial scale and thus distance is unlikely to be the explanation, supported by the lack of isolation by distance pattern. Hence, in this study we have shown that populations can become differentiated within a small spatial scale, in a continuous environment without physical barriers.

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Genetic structure of blue whiting (*Micromesistius poutassou*) in the north-east Atlantic Ocean

Blue whiting is a pelagic gadoid fish that is found throughout the North Atlantic Ocean and Mediterranean Sea. It is a commercially important species with over 2 million tonnes landed in the Atlantic Ocean per year. Despite this, scientists are predicting that collapse may be imminent unless pressure from fishing is decreased, and have appealed for international action on rational management of this straddling-species, which passes through several Exclusive Economic Zones to complete its life cycle. Meristic, morphometric and parasite load data support a subdivision of the species into a number of populations. In contrast, published genetic data only support differentiation at the extremes of the range, i.e. Barents Sea and Mediterranean with no support to date, for further subdivision of the spawning population to the west of Ireland. On his basis, ICES has recommended that the species be managed as a single stock. This study analysed genetic variability at six polymorphic microsatellite loci (*MpouBW7*, *MpouBW8*, *MpouBW13*, *MmerUEAW01*, *Tch6*

and *Tch10*) in ten spawning samples of blue whiting collected in the Spring of 2003 and 2004 50°20' N–60°33' N latitude and 4°18' W–17°35' W longitude. Genetic structure was analysed using Fisher's exact tests, F_{ST} estimates and distance methods. The results indicate three genetically differentiated groups: one to the north of 50° N latitude, and two to the south of this line in the Celtic Sea.

Was, A., McCrann, K. & Gosling, E. (*Molecular Ecology Research Group, School of Science, Galway-Mayo Institute of Technology, Ireland*)

Genetic population structuring of Atlantic salmon within the subarctic Teno river system

An important issue for designing any conservation program aimed at preserving genetic diversity is determining the scale at which genetic structuring occurs. For species such as Atlantic salmon, which have a tendency to home to their natal river to spawn, the scale of genetic structuring can be at the within-river level. Due to its remote location, one of the most productive wild salmon river systems in the world, the river Teno, in northeastern Finland/Norway, has only been minimally affected by human activities and thus provides an ideal system for studying the natural within-river population genetic structure of Atlantic salmon. We studied the genetic structuring of Atlantic salmon sampled from 15 distinct sites, each representing putative independent breeding units from main channel or tributaries of the Teno river system using 30 microsatellite markers. Preliminary analyses indicated that significant genetic differentiation between tributary samples was commonly observed and the level of pairwise F_{ST} values within the river system was comparable to that normally observed between Atlantic salmon populations from different rivers. These and more recently generated results, as well as their conservation implications will be discussed.

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The genetical architecture of outbreeding depression in Atlantic salmon

Reduced fitness in offspring caused by the breeding between individuals from genetically distinct populations is known as outbreeding depression. If populations derived from different species, fitness reductions can be severe and lead to reduced offspring viability and fertility, something which increases with increasing taxonomic divergence between species. These reductions are often asymmetric, and differ depending on which species is the maternal parent, something explained by cyto-nuclear incompatibilities. Outbreeding depression among conspecific populations is less well understood. Reduced offspring viability and fertility is not generally observed in the F1 generation, but may occur in the F2 or backcross generations. The expectation is that it should, as seen for interspecific crosses, increase with increasing genetic divergence between the populations of Atlantic salmon. We investigated whether there was evidence for differences in viability in backcrosses. Egg viability was studied in F1 and backcross generations constructed for two genetically similar and two highly divergent populations. The former involved two divergent populations from different tributaries of the same Scottish river and the other, a non-anadromous population from Canada and an anadromous population from Scotland. Our results show outbreeding depression associated with backcrossing and that the effect is expressed as asymmetric viability. This asymmetric viability increases with increasing genetic divergence. The observations are explained by dominance effects increasing with increased genetic divergence.

Cauwelier, E., Jones, C. S., Noble, L. R. & Verspoor, E. (*FRS Freshwater Laboratory, Faskally, Pitlochry, PH16 5LB, U.K.*)

Temporal stability of population genetic structure of Atlantic salmon (*Salmo salar*) in Newfoundland

Although genetic relationships between populations of Atlantic salmon have been well documented, less is known about the temporal dynamics of these patterns. In particular the relationship between population genetic structuring and demographic changes, such as experienced by Atlantic salmon over the last few decades, remains poorly understood. Here, we genetically characterize Atlantic salmon populations from Newfoundland and Labrador using 14 microsatellite markers. We investigated temporal stability by analyzing scale samples ($n = 3100$) dating back as far the 1950s. Pairwise F_{st} values, analyses of molecular variance (AMOVAs) and isolation-by-distance analyses, considering spatial and temporal samples, indicate a stable pattern of spatial differentiation. We found no apparent loss of genetic diversity in any of the populations sampled. This is further supported by absence of significant temporal genetic differentiation between samples from the same river. No strong pattern of isolation by distance was observed for populations at this geographic scale. Rather a population model where some rivers function as source of migrants and other as sinks seems more appropriate. Our results provide a basic framework for studying local adaptation in these Newfoundland populations.

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Mitochondrial dna analysis of the cape hakes, *Merluccius capensis* and *M. paradoxus*: a panmictic population for one species and not the other?

Cape hake species, *Merluccius capensis* and *M. paradoxus* form the most important part of the Namibian and South African (SA) demersal fisheries. It is unclear whether there is a shared trans-boundary stock of both species between these countries; as such they are currently managed separately with three stocks of 'Cape hakes' recognised. In addition, there is little external morphological differentiation between the two species and they are caught and managed jointly. In order to test whether there may be genetic differentiation between Namibian and SA fish, we obtained samples ranging from Lüderitz (S26°55' E14°49') in Namibia to south of Cape Point in SA (S35°10' E18°53'). We analysed the variable 5' end of the mitochondrial control region for 311 *M. capensis* and 333 *M. paradoxus*. Our results reveal 107 haplotypes within *M. capensis* and only 8 within *M. paradoxus*. Haplotype and nucleotide diversities were 0.88 and 0.006 for *M. capensis* and 0.51 and 0.0013 for *M. paradoxus*. AMOVA and Pairwise F_{st} analyses between southern Namibian and one to four SA 'populations' revealed no structure in *M. capensis*; significant genetic differentiation between Namibian and three SA 'populations' was detected for *M. paradoxus*. Mismatch distributions and Fu's F_s statistics reveal that *M. capensis* has undergone population expansion ($F = -26.65$, $P < 0.001$), but not *M. paradoxus*. Although further, extensive analyses on northern Namibian and south coast SA hake are required our work highlights the use of genetic tools to address management issues within regions where commercially valuable stocks may be shared between nations.

von der Heyden, S., Lipinski, M. & Matthee, C. A. (*Evolutionary Genomics Group, Department of Botany and Zoology, Stellenbosch University, Stellenbosch, South Africa and Marine Coastal Management, Cape Town, South Africa*)

Comparative estimates of effective population sizes in three species of wolffishes (*Anarhichas* spp.)

Effective population size (N_e), in particular the ratio of effective population size to census size ($N_e:N$), can be critical in determining the conservation status of exploited or depleted

marine populations where numbers may still be large, but effective population size may have become severely reduced. Unfortunately, estimates of N_e based on temporal variance in allele frequencies are difficult to obtain when age structure is poorly known, population structure is ill-defined, and large population samples are difficult to obtain because of the species scarcity or remote habitat. Such difficulties attend the estimation of N_e via allele frequency changes for the three species of wolffish (genus *Anarhichas*) that occur across the North Atlantic Ocean. All three species have suffered severe declines since the 1970s, and have been listed by the Species at Risk Act in Canada as either threatened or special concern. N_e estimation in wolffishes may provide an interesting contrast to other studies of marine fishes due to their relatively unusual life history and mating behaviour. They seem to form monogamous mating pairs, they exhibit paternal care of young, and the larvae are thought to have a very limited pelagic stage. Using mitochondrial DNA and microsatellite loci, we assessed genetic variation in all three species, and used the data to obtain estimates of both long-term and contemporary N_e . We discuss differences in estimates of N_e among marker types, estimation methods and species, and compare the various N_e measures to relative estimates of contemporary species and population abundance.

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A simulation model of population genetic to unravel the panmictic nature of European eel

Here we propose a model to simulate the population genetics of the European eel by explicitly taking into account the continental phase and the oceanic-reproductive phase of *A. anguilla*. The model is used to investigate alternative hypotheses on the panmictic nature of eels and, specifically, to test which amount of time/spatial segregation (i.e. lack of perfect synchronization among eels migrating to the spawning area for reproduction from different continental sites; not perfect overlapping of spawning areas among eels coming from very geographically distant continental sites) is required to produce a value of "Fst" index similar to those reported in literature. Given a certain amount of spatial or time segregation, the model is finally used to assess which is the minimum sample size of two distinct subpopulation that would be required in order to obtain values of Fst significantly different from zero. A sensitivity analysis is carried out to test the sensitivity of the model to uncertainty in demographic parameters estimations. A MonteCarlo stochastic approach allow us to replicate simulations in a large of number times so as to explicitly include both environmental variability and uncertainty in parameter estimations.

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Consequences of spatial structure in biology to the dynamics of a reef fish population subject to various levels of effort

Fish populations may comprise several spatially or temporally distinct stocks that exhibit different demographic parameters. It is believed that stocks may respond differently to fishing pressure and failure to take demographic variation into account could result in unsustainable harvest strategies. Little is known, however, of the magnitude of difference required in the demographic parameters between stocks to warrant separate management strategies, and whether some parameters are more sensitive than others in maintaining exploited populations. We examined these questions using a spatially-structured simulation

model developed for the common coral trout, *Plectropomus leopardus*, population and the Great Barrier Reef (GBR) line fishery, Australia. The model was used to simulate the effects of four potential harvest strategies on the *P. leopardus* reef metapopulation subject to different demographic regimes. The different harvest strategies involved shifting the distribution of effort between four regions of the GBR, a potential response to weather, social, economic or regulatory factors. The demographic regimes involved simulating the coral trout population with or without regional differences in individual growth and mortality rates. Performance indicators such as spawning biomass and the biomass available to the fishery were compared between the different combinations of harvest strategies and demographic regimes. The difficulties in managing coral reef populations with a complex spatial structure are discussed.

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Does age diversity in population structure buffer environmental effects on recruitment of Northeast Arctic cod?

The population structure of the Northeast Arctic (NEA) cod stock has changed considerably due to fishing pressure. The Shannon age diversity index (H) can be used to describe the relative contribution of different age/length groups to the spawning stock age/size composition and the uniformity of fish distribution among these groups. Over the period investigated (1946–2001) the H for NEA cod varied from 0.93 to 0.49 with maximum H values occurring at the beginning of the 1960's and minimum values at the end of 1980's. H values were stable at the 1940–1950-s then declined throughout the mid-60's to the mid-70's. Thereafter large and rapid fluctuations in H were observed due to the influence of abundant year-classes dominating the age distribution and reducing H in certain years. The long-term trend towards increasing fishing mortality resulted in year-classes failing to attain older ages resulting in a decreasing trend in H which was consistent with the overall reduction in stock size. The time period before 1980 showed a weak, positive correlation between H and recruitment ($R^2 = 0.12$), whereas, the time period after 1980 showed no relationship between H and recruitment. This difference between the two time periods possibly reflects a change in the reproductive behavior of the stock. Currently, there are fewer age classes (1–3) contributing significantly to the spawning stock which could result in shortening of spawning duration and relocation spawning grounds. Resilience to environmental conditions is likely greater in a population with high H because more complex behavior is a form of bet-hedging that would buffer the stock against poor environmental conditions.

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Using cohort-specific values of r to describe the stock dynamics of Northeast Arctic cod

Stock dynamics are partly determined by r, the intrinsic rate of population increase. Estimating r is data intensive, consequently indirect estimation methods have been developed which use the stock/recruit relationship or life history correlates of r. Recent interest in quantifying stock reproductive potential has resulted in improved databases for traits (sex ratios, maturation, and fecundity) that are required for estimating r directly. Using these data, cohort-specific estimates of r were estimated for Northeast Arctic cod (1946–1988 cohorts). In this calculation the probability of survival included natural mortality but not fishing

mortality (F). Thus, r represents the intrinsic rate of population increase in the absence of a fishery. Values of r (% increase per year) ranged between 7 and 57% and were significantly, positively correlated with cohort-specific F but uncorrelated with the age at which 50% of the cohort matured. On the other side of the ledger, fishing removes a substantial portion of mature females that contribute to annual production of eggs. The annual removal of eggs by the fishery was approximated by converting the catch at age into the corresponding egg production, summing across age classes and dividing that sum by the total egg production for that year. The proportion of total egg production removed by the fishery annually ranges from 22 to 63% and is strongly correlated with F . Comparing the intrinsic production of eggs, as represented by cohort-specific r , to the annual removal rates shows that the longterm sustainability of the stock depends on relatively few cohorts that occur irregularly.

Marshall, C. T. (*School of Biological Sciences, University of Aberdeen, AB24 2TZ, Scotland*)

Regional variability in cod dynamics in the North Sea and west of Scotland and its implications to management

Whilst cod in the North Sea and ICES division VIa are assessed as single units, recent research suggests that these stocks are comprised of a number of reproductively isolated populations. This study aggregated research vessel trawl survey data into putative areas of high spawner fidelity and then fitted the resultant abundance indices with a separable model to obtain time series for three stock indicators of total stock biomass (TSB), spawning stock biomass (SSB) and recruitment. Regional variability in these stock indicators lend support to the hypothesis of distinct inshore, resident populations and larger offshore populations. These indices also indicate that recruitment in the southern North Sea population collapsed prior to that seen in the total stock. The degree to which the results support the idea that the cod stocks in the northern shelf and North Sea regions are metapopulations is discussed as is the implications for the present level of aggregation in stock assessments.

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A life-cycle based fisheries model for broad whitefish, *Coregonus nasus*, of the lower Mackenzie River: a solution to management of a trans-boundary migratory species in the Canadian Arctic

Broad whitefish and related coregonid species are harvested in small scale community fisheries along the lower Mackenzie River. However, the life cycle of these species involves extensive migrations between spawning, rearing and over-wintering areas located 100s of kms apart. Fisheries are co-managed by the Department of Fisheries and Oceans and three aboriginal land claim management boards. Due to the nature of the migrations stocks may be harvested repeatedly by communities under different land claims. The consequences to the long-term health of the resource are not accounted for in the localized management structure. We present an interactive model of the population dynamics based upon the unusual life cycle of broad whitefish and the fisheries along the Mackenzie River. The model is useful for fishery managers to explore harvesting options. Simulations identified that research on the early life history of broad whitefish is needed for improved management of the resource.

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Considerations of population structuring in Atlantic herring, *Clupea harengus* L. assessment and management in the North Sea, Skagerrak, Kattegat and western Baltic

Herring are caught throughout the North Sea (ICES Sub-area IV), Skagerrak and Kattegat (ICES Division IIIa) and into the western Baltic. In the assessment of herring from these areas two units have been considered, the North Sea Autumn Spawners (NSAS) and the Western Baltic Spring Spawners (WBSS). In area IV the southerly Downs component is managed separately on the basis of geographical area. Both the NSAS and WBSS have historically been considered to comprise several population components mixing as juveniles and adults within areas IIIa and IV at various stages of the life cycle. Results of the EC funded project HERGEN, using microsatellite DNA markers and otolith microstructure techniques, have demonstrated a strong cline of genetic differentiation between the North Sea and the Baltic. Among the NSAS herring the Downs component is best differentiated using otolith techniques; within IIIa and the western Baltic there was strong genetic differentiation between local Skagerrak spawners and herring spawning in the Kattegat and western Baltic. Within this region herring from different year classes, spawning components, or areas dominate the population in different periods. These findings facilitate a more detailed analysis of the stock dynamics of the different components within the system and suggest the potential for fishery management that considers these factors. We discuss the implications of these findings to the assessment and management of NSAS, WBSS and IIIa local spring spawners and present scenarios for monitoring the presence of the various population components throughout the area of study.

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