Theme Session on Stock Identification Methods (EE)

ICES CM 2004/EE:01

The role of stock identification in formulating fishery management advice

Cornelius Hammer and Christopher Zimmermann

It has been shown that there is a marked difference in the perception and the application of the "stock" -concept between fishery biologists and fisheries managers. In other words, both do not necessarily speak the same language. The TAC advice for a particular stock given from fishery biologists refers to biological entities, while the official TAC will in most cases refer to a management unit, and both do not necessarily match. This occasional mismatch exists ever since the stock and TAC-concept has been implemented, and it is clear that in order to avoid more misunderstanding the managerial units need to be adapted as far as possible to the biological realities. However, even if this was the case such management regime is not able to cope with the fact that in a number of cases the stocks migrate and mix with stocks from other management areas and are accordingly caught together. One has to acknowledge that the whole concept of stock separation and the idea of science supporting sensible management by defining biological entities has its principle limitations. Such a concept could only work if methods exist to identify members of different stocks in the catches of mixed aggregations. Science is in need not only to better define stock characteristics and boundaries but also to develop tools for the stock separation from the catches. This will not be possible without far more basic research and data collection on a routine basis, *i.e.* far better financing. This is where politicians join the game.

What is needed?

- 1. An agreement between the fishery management and fishery science what exactly both are perceiving as stock.
- 2. Management areas which match the natural stock boundaries.
- 3. More biological information about stocks in question. This can be broken down into major requirements:
 - a. Clear definitions of thresholds for genetic differences between stocks. Clear definition what a genetic difference between stocks is.
 - b. Regular biological sampling for stock specific parameters: age, length, weight, maturity, meristics.
 - c. Research and development of new stock separators: e.g. discrimination by shape analysis of otoliths, radiochemistry, trace elements.
 - d. Tagging experiments for migration analyses.
 - e. In some cases the utilization of the existing information

Keywords: Stock definition, stock identification, fishery advice, fishery management

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ICES CM 2004/EE:02

Analyses of calcified structures-texture and spacing patterns

Kevin D. Friedland and Steven X. Cadrin

Analysis of texture and spacing patterns found in hard body parts has been put to wide application in stock identification studies. The interpretation of texture patterns is partly dependant upon the correlation between the growth of the animal and the calcified structure to be analyzed. The variation of features from these structures throughout the species' range, as a product of both genetic and environmental influences, allows discrimination of groups with different growth patterns. Spacing patterns can be measured with conventional measurement techniques or with enhanced technologies such as image processing. Spacing patterns typically present a complex set of measurements necessitating the use of image processing techniques to achieve the desired accuracy and to process the large volumes of data associated with feature extraction. The texture of calcified body parts can be measured with physical probes or by the analysis of optical density profiles using transmitted light microscopy. Data reduction of texture data usually takes the form of the Fourier transform. Analysis of calcified structures can effectively reveal patterns in circuli spacing that correspond to the specimen's growth history. Therefore, phenotypic stocks that have significantly different growth rates can be discriminated using texture analysis.

Keywords: stock identification, pattern recognition, texture analysis.

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ICES CM 2004/EE:03

The use of genetic stock identification results for the assessment of wild Baltic salmon stocks

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Current assessment of the exploitation rates of wild Baltic salmon stocks is based on external tagging data. However, tagging data of wild Baltic salmon is limited and is geographically biased to two rivers located in the north-eastern rim of the Gulf of Bothnia. The current paper examines the use of genetic stock identification results within the probabilistic stock assessment of wild Baltic salmon stocks. Genetic stock identification results contain the same information as tagging data. In combination with the external tags, genetic stock identification results improve the estimation of the exploitation rate of wild Baltic salmon. The main uncertainties when using genetic stock proportion estimates stem from the uncertainty in the number of wild salmon smolts produced by the salmon stocks and the uncertainty in the representativeness of the catch sample to be used for genetic stock proportion estimation to the total salmon catch of the different fisheries. In addition to improving the assessment of wild salmon stocks for which tagging data is available, the genetic stock proportion estimates could also be used to improve the estimation of the abundance and exploitation of smaller wild salmon stocks. The river specific wild smolt production estimates in combination with the exploitation estimates for the assessment unit in which they are located, can result in a stock-specific assessment of management objectives.

Keywords: Atlantic salmon, Baltic, Bayesian, genetics, stock identification.

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ICES CM 2004/EE:04

Stock identification methods: from Working Group to book

Steven X. Cadrin, Kevin D. Friedland, and John Waldman

Stock identification is an interdisciplinary field that involves the recognition of self-sustaining components within natural populations and is a central theme in fisheries science and management. In 1992, ICES established a "Study Group on Stock Identification Protocols for Finfish and Shellfish Stocks," to review methodologies of stock identification and develop a protocol for the application of stock identification results. Over the next decade, the group expanded to the "Stock Identification Methods Working Group," and developed a volume of contributions that is aimed at synthesizing the many disciplines involved in stock identification. Methodological chapters review specific methods, with emphasis on recent advances, review of benchmark case studies, critique of strengths and weaknesses, and guidance for effective protocol. One theme that emerged throughout the development of the book is the strength of interdisciplinary analyses. When results from each approach are viewed in the context of what precise aspect of stock structure they reveal, a more holistic view with multiple perspectives is possible, providing more reliable information for resource management.

Keywords: stock identification methods.

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ICES CM 2004/EE:05

Morphometric stock identification

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Analysis of morphometric variables is a valuable tool that can indicate phenotypic stocks and complement other stock identification methods. Patterns of morphometric variation in fishes and invertebrates may indicate differences in growth and maturation rates, because body form is a product of ontogeny. The identification, discrimination and de-

lineation of phenotypic stocks are essential for population modeling, which generally assumes homogeneous ontogenetic rates within a stock. Morphometric analyses fall into two major categories: landmark methods and outline methods. Although the use of morphometric landmark characters to identify phenotypic stocks is more than a century old, imaging technology and analytical techniques have increased the power of morphometric analysis for stock discrimination and stock composition analysis. The development of affordable digital cameras and storage capacity offers the potential for collecting many images of specimens during routine fishery and research sampling. The technological advances and subsequent methodological advances that occurred in the last decade are expected to continue, enhancing the discriminatory and interpretive power of landmark morphometrics for stock identification.

Keywords: stock identification, morphometry.

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ICES CM 2004/EE:06

Parasites as biological tags

Ken MacKenzie and Pablo Abaunza

This paper provides a guide to the use of parasites as biological tags for stock discrimination of marine fish. Key literature is listed, and the following topics are covered: (1) the general principles involved in the use of parasites as tags in fish population studies and the advantages and limitations of parasites as tags compared to mechanical tags and genetic studies; (2) criteria applicable to the selection of tag parasites; (3) the two main approaches to the subject, one aimed at selecting a small number of the most appropriate parasite tags and examining a large number of host specimens for these parasites only, and the other based on analyses of entire parasite assemblages; (4) statistical analyses of data; (5) procedures and methods for the collection and preservation of host and parasite samples, and for the identification of parasites; (6) the interpretation of parasitological results in terms of host population biology, including examples of some typical life cycles of the major taxonomic groups of parasites infecting marine fish.

Key words: parasites, biological tags, fish stock discrimination, procedures, methodology.

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ICES CM 2004/EE:07

Stock identification and genetic variation of fishes in the Baltic Sea

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The stock identification project aims to identify different stocks of fish to improve the management of these stocks and to minimise the risk of loss of unique adaptations and genetic variation. We studied population structure and genetic differentiation of several commercially important fish species in the Baltic and North Sea. Two flatfish species, the turbot (*Psetta maxima*) and flounder (*Platichthys flesus*), are assumed to be divided into several local populations, but few genetic or ecological studies have confirmed this. The spawning behaviour of flounder differs between the southern and northern stocks with an overlap in behaviour around Gotland; southerly populations reproduce pelagically while the northern ones reproduce demersally. It is unknown if spawning behaviour is also reflected in genetical or morphological differences. Combination of tagging experiments with genetic studies using microsatellites and morphometric studies using computer image analysis are made to map the population structure and migration of flatfishes in the Baltic and in the Skagerrak/Kattegat area. In June 2003 915 wild-caught turbots were tagged in the area east of Gotland. The tagging will be repeated during 2004 and extended to include flounder. Baltic populations of whitefish (*Coregonus lavaretus*) were found to be genetically quite similar, whereas populations of pikeperch (*Sander lucioperca*) show clear differentiation in local sub-populations. Application of the results from the genetic analysis and tagging experiments in the local management of the stocks will be discussed.

Keywords: stock identification, genetic variation, Baltic Sea, population structure, turbot, flounder, tagging, microsatellites, whitefish, pikeperch, local management. Institute of Coastal Research, National Board of Fisheries, Box 109, SE 740 71 Öregrund, Sweden. [tel: +46-173-46460, Fax: +46-173-46490, e-mail: ann-britt.florin@fiskeriverket.se, teija.aho@fiskeriverket.se]

ICES CM 2004/EE:08

Changes in stock composition of annual Atlantic salmon catches in the Baltic Sea on basis of DNA-microsatellite data and Bayesian estimation

Marja-Liisa Koljonen

DNA level information, a 9-loci microsatellite baseline database of 27 Atlantic salmon (*Salmo salar L.*) stocks, and a Bayesian estimation method have been used to estimate stock and stock group proportions of Finnish catches in the Baltic Sea area. The proportions of seven stock groups important in terms of management were assessed in catch samples in three years (2000, 2002 and 2003). Genetic catch samples were drawn from the total scale sample of catches. In the Gulf of Bothnia area, catches are composed of three major units: wild fish, and Finnish and Swedish hatchery fish. The proportion of wild fish shows a rising trend, increasing from 43% to 76% in catches from the Åland Sea in 2000-2003, which was a result of decreasing amounts of hatchery fish. Contrary to previous assumptions and data from 2002, wild fish originating from rivers draining into the Gulf of Bothnia were also taken in catches in the Gulf of Finland. Half of the fish caught (51%) in these coastal trap-net catches were, from Finnish hatchery releases. Wild fish originating from the wild stocks of the Gulf of Finland were recorded only in the western part of the Gulf, with a 5% proportion.

Keywords: Atlantic salmon, stock mixture analysis, DNA, microsatellites.

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ICES CM 2004/EE:09

Maximum likelihood estimation of stock composition

Jon Brodziak

Stock composition can be a significant issue in the management of mixed-stock fisheries of highly migratory or transboundary resources. Stock composition analysis, the determination of the contributions of constituent stocks to a mixedstock fishery, uses differences in the frequency distributions of population characteristics among stocks to estimate the composition of a mixture of stocks. Two maximum likelihood estimators for stock composition analysis are developed, beginning with the formulation of a likelihood model for sampling population characteristics from a mixed-stock fishery. Maximum likelihood estimators of stock composition and computational methods are given for a standard likelihood model based on inherent population characteristics and an extended model that incorporates population characteristics and unique identifiers. Simulation experiments using allozyme frequency data for chinook salmon show that the standard model produces accurate estimates of stock composition. Simulation experiments also show that the extended model can improve estimation accuracy when constituent stocks have similar population characteristics.

Keywords: mixed-stock fishery, stock composition analysis, maximum likelihood estimator

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Multidisciplinary stock identification of North Atlantic fish species, with current examples of otolith analyses

Christoph Stransky and Cornelius Hammer

During the past few years, a growing number of multidisciplinary research projects have been undertaken to investigate the stock structure, boundaries and connectivity of commercially important North Atlantic fish species in order to improve the scientific basis for sustainable fisheries management. This study reviews the current knowledge on multidisciplinary approaches to stock identification and provides examples of recently completed work on redfish (*Sebastes* spp.) in the Irminger Sea and adjacent waters as well as horse mackerel (*Trachurus trachurus*) in the Northeast Atlantic and Mediterranean. These projects involved a large variety of techniques, such as body and otolith morphometry, otolith microchemistry, genetic markers, parasites and life-history parameters (growth, maturation) that were used concurrently

on the same material. With reference to the outcome of the otolith-based analyses of these case studies, the discriminatory properties of the applied stock identification methods and their contribution to improved resource management are evaluated.

Keywords: stock identification; otolith shape analysis, otolith microchemistry, morphometry; redfish, horse mackerel, herring; North Atlantic, Mediterranean Sea

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ICES CM 2004/EE:11

The genetic tools in stock identification

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The aims of most intraspecific genetic studies in fisheries are the determination of the population structure of exploited species and assessment of the relative contribution of such sub-specific groups to mixed population fisheries. In the genetic sense, stocks are equivalent to populations. For a stock to be genetically identifiable it must be a reproductively isolated population, with minimal gene flow. Genetic studies have shown much smaller differences in marine species between samples from geographically distinct areas, than for freshwater or anadromous species. One explanation for this finding might be that since marine spawning aggregations are very large, genetic drift, which is probably a major force in moulding the allele frequencies of freshwater and anadromous populations, would have a minimal role in altering gene frequencies. In the case of marine species, physical barriers to gene flow rarely exist, though different stocks may occupy distinct areas of the ocean or even different oceans, however, freshwater fish occupying rivers and also most anadromous salmonids, show a propensity to home to natal areas to spawn, thus, even though mixing of populations during reproduction is physically possible, it rarely occurs.

We present dates of the efficiency of genetics tools in some different specie cases: an anadromous –Atlantic salmonwith a strong homing conduct, a demersal fish - angler fish- with two sympatric species and a macrogeographical distribution in Europe, and a crustaceous specie –the Cuban white shrimp – with a life history divided between estuaries and the near-shore shelf environment.

Keywords: genetics, microsatellite loci, stocks, Salmo salar, Lophius budegassa, Lophius piscatorius, Litopenaeus schmitti.

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ICES CM 2004/EE:13

Experimental design and sampling strategies for mixed stock analysis

Mary C. Fabrizio

The precision and accuracy of stock composition estimates are affected by design and sampling issues that influence the performance of classification functions. These issues arise whether using classification models (e.g., linear discriminant functions) or mixture models for stock composition analysis. Proper sampling of the source stocks begins with an appropriate sampling strategy, which fully considers the total number of source stocks, sufficient sampling from each source stock, suitability of forming composite stocks, and verification that all source stocks were included in the base-line data.

Mixture sampling strategies need to take into account the geographic and temporal variability of the mixture, and adequate sample size of the mixture depends on many factors, including relative contribution of stocks, and the degree of stock differentiation. In most cases, the number of features necessary for a mixed-stock analysis is a statistical one, but a few pitfalls are associated with using too many features. The reliability of features for stock delineation depends on the consistency and accuracy of measurements, as well as the statistical properties of the set of features under investigation (e.g., statistical dependencies among features). Allometric and age relations, sex effects, and temporal stability of features should be fully investigated prior to application in stock composition analysis. Finally, consideration of the power to detect stock differences, particularly when stock differences are not supported by the data, is important when the desired outcome is the conservation of stocks.

Keywords: sampling design, stock mixtures, stock composition analysis.

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ICES CM 2004/EE:14

Fine spatial structure of Atlantic hake (Merluccius merluccius) stocks revealed by variation at microsatellite loci

Ana G. F. Castillo and E. Garcia-Vazquez

Gadidae biomass declined dramatically during the last decades, as occurred for other large predatory fish. The definition of their stocks is crucial in order to develop management plans for restoring fisheries to healthy levels. One of the problems for a scientific assessment of the population management of European hake is the scarce information about the genetic structure of the stocks. Genetic variation at five microsatellite loci was analysed for European hake *Merluccius merluccius* sampled from nine different regions in the Atlantic Ocean and the Mediterranean Sea. A significant genetic differentiation was found between samples that suggests a fine subdivision of Atlantic and Mediterranean hake stocks. For a more detailed analysis in a shorter spatial scale, pre-spawning hakes caught in eight locations around the Iberian Peninsula were also analysed. Their genetic variation suggests that the species follows a population model of isolation by distance in this geographical area. Three different areas can be identified, one corresponding to the Mediterranean Sea, another to the Portuguese coast and another to the Cantabric Sea. The lack of differentiation between samples caught in the VIIIabd and in the VIIIc ICES areas suggests that the boundary between the northern and the southern stocks of European hake should be reconsidered based on genetic information.

Keywords: Genetic variation, Merluccius merluccius, microsatellites, stock structure.

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ICES CM 2004/EE:15

Using artificial neural networks for the stock delimitation of horse mackerel (Trachurus trachurus)

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From January 2000 to June 2003 the EU funded project HOMSIR was carried out with the goal of defining horse mackerel stock units throughout this species distribution range. Samples were collected from 20 areas from Norway to Greece and Mauritania, during the 2000 and 2001 spawning seasons. All individuals from these samples were analysed using several stock identification techniques (morphometrics, parasitology, genetics and life-history traits), allowing to identify several probable stock units, and putting in evidence some probable mixing areas. Several results obtained with these techniques could be seen as individual characteristics (e.g. presence/absence of certain parasites, morphometric variables, presence of a certain allele, etc). These variables can be used to classify individuals to stock units, based on a priori knowledge, using artificial neural networks (ANN). ANN have been used for its versatility and for the capability of handling a large amount of data without problems of collinearity or any statistical assumptions. In this paper we investigate the usefulness of ANN for integrating several sources of data used for stock delimitation, and at the same time try to define mixing areas and to estimate the degree of mixing between the defined horse mackerel stock units.

Keywords: stock identity, Trachurus trachurus, neural networks.

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ICES CM 2004/EE:16

Blue whiting (*Micromesistius poutassou*) stock components in samples from the northern Norwegian Sea and Barents Sea, winter 2002

Rebekka Varne and Jarle Mork

Genetically distinct blue whiting has been found in the Barents Sea, which suggests a reproductively isolated population. It is also reported larvae and eggs near the northern Norwegians continental slope. This indicates that ripe individuals found in the Barents Sea in winter most likely belong to a local Barents Sea stock component and not to the main stock which spawns along the continental shelf west of the British Isles. In 2000-2001 it was reported of large amounts of young blue whiting in the Barents Sea. In 2002 a sampling scheme was designed to get material for a genetic investigation of a Barents Sea stock component and Norwegian-hebrido stock component in the Barents Sea. In total 693 individuals were assayed for the isozyme loci PGM-1* and IDHP-2*. Initial analyses showed no significant heterogeneity in allele frequencies among sampling locations. However, there was significant variation in allele frequencies for IDHP-2* among age groups when individuals were pooled into young fish and old fish (age <4 years and age >3 years). When tested for allelic homogeneity of age groups both loci had significant differences between age groups. Individuals at 4 years and older showed allele-frequencies that match the frequency found in samples grouped as a Barents Sea population in previous studies. These findings highlight the importance of considering the possibility that fish in different age groups need not be dominated by the same stock component.

Keywords: Blue whiting; Micromesistius poutassou; isozymes; population genetics.

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Population genetics of parasites as tags for stock identification of Herring (*Clupea harengus*) in the North Sea and North East Atlantic

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The use of parasites as biological tags for investigating stock identity has been widely applied in fisheries science. In more recent times the measurement of intraspecific variation of genetic sequences has been investigated as a means of discerning population biology. Lately it has been demonstrated that the genetic variability of parasite populations is closely related to the biology of the host. This discovery may have useful implications for future stock identification research projects. This study is part of a multidisciplinary stock identification project, which is examining herring stocks in seas to the west of the British Isles (WESTHER). The nematode Anisakis spp, metacercariae of the digenean Renicola spp. and adults of the digenean Hemiurus luehei, were selected for further investigation, based on the results of previous studies and their differing life-history strategies. Details of isolation of the cytochrome oxidase 1 (COI) gene from specimens of these parasites taken from sites in the Baltic Sea, the Atlantic Ocean and the Irish Sea are pre-

sented. The COI gene has been identified as a good indicator of intraspecific population variance in other parasites. Analysis of sequences was carried out to determine the utility of the COI gene to discriminate between parasites populations, and therefore their associated host populations. Preliminary results are presented here.

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Keywords: Herring, Stock Identification, Parasites as tags, Genetics.

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ICES CM 2004/EE:18

Fatty acid profiles as natural marks for stock identification

O. Grahl-Nielsen

A novel method of stock identification of individual fish is achieved by chemometric determination of the composition of fatty acids in selected tissues, mainly heart tissue. The determination is carried out by direct methanolysis/extraction of the fatty acids, as methyl esters, from the tissue, whereupon they are gas chromatographically separated and quantified, followed by multivariate, principal component analysis of the chromatographic results. The method has been used in stock identification of herring, *Clupea harengus*, in Norwegian waters; to distinguish Atlantic and North Sea mackerel, *Scomber scombrus;* to distinguish among striped bass, *Morone saxatilis,* from three American rivers; to identify farmed salmon, *Salmo salar*, escapees; to distinguish two Faroese stocks of cod, *Gadus morhua;* to distinguish four stocks of redfish, *Sebastes mentella,* in the North-Atlantic; and to detect the origin of harp seals, *Phoca groenlandica,* invading the Norwegian coast.

Keywords: Fatty acids, chemometry, individual fish, heart tissue.

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Stock discrimination of horse mackerel (*Trachurus trachurus*) in the Northeast Atlantic and Mediterranean Sea: integrating the results from different stock identification approaches

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The goal of horse mackerel stock discrimination was tackled by integrating both established and innovative approaches such as genetic markers (allozymes, mtDNA, microsatellite DNA and SSCP), morphometry, parasites, tagging experiments and life history traits (growth, reproduction and distribution), within the EU-funded HOMSIR project. The sampling covered almost the whole distribution range of horse mackerel through 20 sampling localities. 200 fish per sampling site were collected, taking into consideration the spawning season and temporal variation (two years of sampling). The results from genetic approaches (Multilocus Allozyme Electrophoresis, mtDNA sequencing and microsatellite DNA) showed that there was only slight genetic differentiation among sampling sites. Thus, there seems to be considerable gene flow along the entire area of distribution of horse mackerel species. However, sample homogeneity does not necessarily equate with population homogeneity. One genetic technique (SSCP), however, was successful in finding a genetic marker that demonstrated substructuring in horse mackerel populations.

Several approaches (SSCP, morphometrics, parasites) support the separation between the Atlantic Ocean and the Mediterranean Sea in horse mackerel populations, although the most western Mediterranean area could also be connected to the Atlantic populations. In the Northeast Atlantic three main stocks were distinguished: The west Atlantic coast of the Iberian Peninsula (southern stock); the western coasts of Europe from north Spain to Norway (western stock) and the North Sea stock. This information implies the revision of the boundaries of the so-called southern and western stocks as currently defined. Various results suggested that adult horse mackerel could migrate through different areas/or stocks in the Northeast Atlantic. Horse mackerel from the Mauritanian coast is distinguished by its high production parameters (growth and batch fecundity). The population of horse mackerel in the Mediterranean Sea is sub-structured roughly in at least three main areas: western, central and eastern Mediterranean. Horse mackerel from the Tyrrhenian Sea (Central Mediterranean) is particularly different from the rest of the Mediterranean areas. The holistic approach is the appropriate way to identify stocks in horse mackerel. Several markers have proved to be successful in delineating horse mackerel stocks, such as: the genetic marker based on SSCP technique; parasites, particularly anisakid nematode larvae, which allowed for example the clear differentiation of the North Sea population; body morphometrics and otolith shape analysis . In contrast, artificial tagging is very difficult to apply and further research is needed to reduce the mortality due to the method of catching and handling the fish. It was important to collect all the possible biological information to consider the influence of these covariables in the other approaches and to identify areas with homogeneous production parameters.

Keywords: Stock identity, Trachurus trachurus, genetic markers, biological tags, biological parameters.

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An approach to population homogeneity of hake *(Merluccius merlucius L.)* of the Portuguese continental coast attending to morphometric and physiologic characteristics

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Hake (*Merluccius merluccius* L.) is a high valuable fish species of the Portuguese demersal fisheries. In the present study, the morphometric and physiological variation along the Portuguese coast (ICES Division IXa) was analyzed in an attempt to define population homogeneity. Three geographical areas were considered which present certain oceanographic differences: north (in the northern area above Nazaré canyon), center (in the midle of the area between Nazaré canyon and cape of Sagres) and south (in the westhern area of Algarve). Results were compared with a genetic study realized in the same areas.

Keywords: Hake, Merluccius merluccius, portuguese coast, population homogeneity, morphometry, physiology.

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Parasite assemblages as a tool to establish harvest location of fish

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Parasites reflect the environment surrounding fish and potentially indicate whether or not fish are likely to have spent time in a given location. Most studies of parasites as biomarkers have concentrated on the characterization of stocks, focusing in establishing differentiation or mixing between populations. However, parasite information can also be used to establish the geographic origin of fish individuals. In fact, parasite data have been used in a court of law to prove the geographical origin of fish. The objective of this presentation is to illustrate with examples based on cod, *Gadus morhua*, from the NE Atlantic and bogue, Boops boops, caught off Spain that parasite assemblages can be useful predictors of fish harvest location. We applied several multivariate predictive statistics to datasets of parasite abundances and their predictive power ranged from as good as almost 100% of fish individuals correctly allocated to their origin in certain localities, to as bad as 60% in other localities. However, even the poorest classification rates can be useful in a legal context because we could set confidence intervals to both correct and incorrect classification rates potentially allowing the detection of fraud over the provenance of a catch. The legal implications of these results in terms of enforcement of fisheries regulations, with emphasis on the new Common Fisheries Policy of the EC, are discussed. We expect that similar approaches can contribute to set scientific standards acceptable for management and legal purposes to establish harvest location of individual fish.

Keywords: Parasites, fish, fisheries management, biomarkers, traceability.

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Morphometric and meristic study of white and black anglerfish (*Lophius piscatorius* and *L. budegassa*) from the south-west of Ireland to the south-western Mediterranean

Rafael Duarte, I. Bruno, I. Quincoces, A.C. Fariña, and J. Landa

Two species of anglerfish are found in the Northeast Atlantic and Mediterranean, white anglerfishes (*Lophius piscatorius*) and black anglerfish (*L. budegassa*). Both species are highly valuable in trawl and gill net fisheries. In the present study, the morphometric and meristic variation of both anglerfish species is analyzed along the Atlantic coast between the west of Ireland and the south of Portugal and also the south-western Mediterranean. In these Atlantic area ICES consider for assessment purposes two anglerfish stocks, northern and southern, with the geographical barrier between them in the Cap Breton Canyon. Results were not conclusive in determining whether or not the defined ICES stocks were differentiated, but they did allow for a reasonable classification of specimens in certain areas, namely between western Ireland, western France and northern Spain for *L. piscatorius* and between western France and southern Portugal for *L. budegassa*.

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Application of Baltic herring and cod stock identification results to fishery management

Robert Aps, H. Lassen, J. Rice, K. Andrejeva and J. Aps

Management of Baltic fishery resources is the responsibility of the International Baltic Sea Fishery Commission (IBSFC). The IBSFC has entered a period of difficult change during which it has to adjust its stock assessment units to the structure of fish populations and its management units to the stock assessment units. The optimal solution for implementation of the results of Baltic herring and cod stock identification seems to be in seeking a reasonable compromise between biological knowledge and practical constraints set by the availability of data, and require a new management system to be evolved based on management units that correspond as closely as possible with stock assessment units. At the same time, introduction of a revised management system will change the future perspectives of fishing nations sharing the Baltic fishery resources: in essence, there will be winners and losers. Zero- sum game was used to investigate possible the theoretical solutions to the problem of fishery resource re-allocation and to exemplify the issue by an analysis of the proposed split of the management areas for the herring and cod resources in the Baltic. As a basic principle it is proposed that any mismatch of allocation and fishing interests is solved through quota swaps and buying/selling of quotas among the countries. Role of the revised management scheme in conservation of population structure and relative abundance of the Baltic herring and cod is discussed.

Keywords: Baltic herring, Baltic cod, stock identification, zero-sum game, fishing quota allocation.

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Morphometric variation among anchovy (*Engraulis encrasicholus*, L) populations from the Bay of Biscay and Iberian waters

Bruno Caneco, Alexandra Silva, Alexandre Morais

For management purposes, the European Atlantic anchovy is separated in two distinct stocks, one distributed in the Bay of Biscay (ICES Sub-Area VIII) and the other occupying mainly the southern part of ICES Division IXa (Bay of Cadiz). However, spatio-temporal irregularities in the dynamics of the Sub-Area VIII stock as well as scant knowledge on the IXa anchovy biology lead ICES to recommend more studies on population dynamics and possible relationships between areas. The present work describes morphometric differences between the two stocks based on the analysis of 10 samples collected within the area from Bay of Biscay to the Bay of Cadiz during two consecutive years (2000 and 2001). Distances on a "Truss Network" were computed from 2D landmark coordinates obtained from digitized images of each individual and corrected from the effect of fish size. Multidimensional Scaling was applied to the mean individuals of each sample to visualise clustering and the significance of distances among samples was statistically tested. Finally, Artificial Neural Networks were applied to assess the robustness of sample groups highlighted in the previous analyses. Results indicate a separation between samples from the Bay of Biscay and those from Division IXa, which is stable on time, as well as a north-south cline along the Portuguese and Bay of Cadiz area. This variability is mainly caused by differences on the shape of the medium-posterior region of the body.

Keywords: Anchovy, morphometry, stock identification.

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Multiple stock identification approaches of anglerfish (*Lophius piscatorius* and *L. budegassa*) in western and southern European waters

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Anglerfish, *Lophius piscatorius* and *L. budegassa*, are valuable commercial species distributed throughout the Northeast Atlantic and Mediterranean. This paper examines multiple information (genetic, morphometric, growth and tag-recapture) on stock structure of anglerfish species from western and southern European waters, to evaluate the suitability of current stocks units (northern and southern). For both anglerfish species, genetic structure showed significant heterogeneity in gene frequencies among samples from different areas, but the proportion of total genetic variation between stocks was relatively small. Morphometric characters allowed an acceptable discrimination of samples from cer-

tain areas, but no from stocks as a whole. Differences in the growth parameters between stocks was significant, although uncertainties in the ageing criteria diminished the utility of this approach. Tag-recapture experiments proved displacements of anglerfish going through the boundaries of the two stocks.

Combined data from genetic, morphometric, growth and tag-recapture studies provide indications that the current geographic separation between the northern and southern stocks is not supported and suggest the existence of discreteness populations along the study area. Given the repercussion of the results in the assessment and management of the two species in the area, more research to improve our understanding of anglerfish stock structure is required.

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ICES CM 2004/EE:26

An investigation of stock structure in blue whiting (*Micromesistius poutassou*) using otolith microstucture and core morphometry

Deirdre Brophy and Pauline King

Blue whiting (*Micromesistius poutassou*) are widely distributed across the North East Atlantic and are likely to consist of several stocks. Spawning aggregations are thought to comprise two components, with one spawning to the north and a second to the south of the Porcupine Bank. However, there is currently very little evidence to support the proposed stock structure and the extent of overlap between the components is not known. For assessment purposes blue whiting are treated as a single stock.

This study investigates stock structure in blue whiting using otolith microstructure and core morphometry. Blue whiting were collected in 2003 and 2004 from across the main spawning grounds to the west of Ireland and Britain and also from feeding aggregations in the Norwegian Sea, the Celtic Sea and off the west coast of Ireland.

Transverse sagittal otolith sections were prepared and increment widths and morphometric measurements of the larval core were recorded. Otolith measurements were compared between areas, with variation due to age, size, sex and yearclass included as co-variables. The results show that blue whiting collected at certain spawning and feeding areas are of distinct larval origin suggesting that separate stocks exist to the north and south of the species' distribution. The implications of these findings for the proposed stock structure of blue whiting in the North East Atlantic are discussed.

Keywords: Stock identification, blue whiting, (Micromesistius poutassou) otolith microstructure, otolith morphometry.

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ICES CM 2004/EE:27

Phenotypic characteristics in genetically different populations in the Skagerrak

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In the Eastern North Sea, the Skagerrak and the Kattegat areas young autumn spawning North Sea herring mix with Western Baltic spring spawning herring during summer feeding migrations. In addition a number of local stocks have been identified that mix with the major stocks during their feeding migrations. For individual stock assessments a split-factor is applied to the catches in the area. From 1996 the split has successively been changed from a population based mean vertebral count to an individual based otolith microstructure analysis.

Otolith microstructure pattern has been shown to reflect environmental impact on fish physiology. Varying temperature regimes among different areas and hatch seasons are expected to determine the pattern of otolith increment width and transparency that make discrimination between different spawning stocks possible at the individual level.

Phenotypic characters like otolith morphology and vertebral counts in winter, autumn and spring spawners were examined and showed high degree of separation between possible population components. Molecular genetic analysis of spawning populations in the North Sea, Division IIIa and the Western Baltic has demonstrated geographical differentiations. The results from the phenotypic separation compared well with genetic mixed stock analysis based on a large number of spawning populations possibly contributing to the Skagerrak genetic composition. The combination of genetic and phenotypic markers for stock identification is discussed.

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Morphometric analysis of Sebastes mentella in the North Atlantic

Jákup Reinert and Hóraldur Joensen

In the summer and fall 1999, *Sebastes mentella* were sampled from 11 areas in the North Atlantic from the Irminger Sea and east wards to Iceland, Faroe Islands and the Norwegian Sea. The purpose of this was to apply different stock identification methods on the same samples in order to compare the methods and to contribute to the understandings of the stock structure of *S. mentella* in the area. The different methods were: Morphometrics, chemometry of the fatty acid profile, electrophoresis of proteins and DNA analysis. In this paper results from simple morphometric analyses will be presented and discussed in relation to the other stock identification methods mentioned.

Keywords: Sebastes mentella, principal component analysis, stocks, stock identification methods, North Atlantic.

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ICES CM 2004/EE:29

Conventional tagging methods in stock identification: internal and external tags

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This paper reviews the feasibility and practical use of conventional tags to identify fish stocks. There are many different types of tags and marks in use, external as well as internal, and many of them are used to estimate stock composition in mixed stocks and to follow their movements between different habitats. To obtain the best estimates, tagging and recovery of the fish must be representative. For the recovery of internally tagged fish, a systematic sampling program is required, whereas external tags can be recovered in sampling programs as well as by commercial fishermen. A tagging program should be carefully planned, taking into consideration effects of capture and handling of the fish, tag types to be used, retention ability of the tags, anaesthesia and recovery. We give examples of tagging studies of three pelagic species, Atlantic salmon, Atlantic mackerel, and Atlantic herring, and one deep-sea species, deep-sea redfish. Results from these studies show that conventional tagging can be used for estimating stock composition. The estimates, however, might be improved if used in combination with other stock identification methods.

Keywords: Tagging; internal tags; external tags; stock identification

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ICES CM 2004/EE:30 Poster

The population membership of the Baltic herring infected with Anisakis simplex larvae.

Magdalena Podolska, and Mirosław Wyszyński

The aim of this study was to evaluate the population membership of the Baltic herring infected with A. simplex larvae, caught in the Polish waters. So far, no major investigations have been conducted to show differences between infected

and non-infected herring in meristic and morphometric characters. The following hypotheses have been put forward and verified: infected herring belong to (1) Western Spring Spawners (2) Central Baltic Spring Spawners, (3) constitute a mixed group. Herring samples were collected during the spawning season in the selected regions of western and central Baltic. Morphometric and meristic measurements of infected and non-infected individuals as well as length, age and maturity stage were recorded. Multivariate statistical tests were used to compare the samples and discriminant analysis was applied for the separation of herring populations. Next, the fraction of herring populations in each area was estimated. Obtained results indicate, that infected fish represent a mixed group of western and central Baltic herring.

Keywords: herring, meristics, morfometry, Anisakis simplex, Baltic.

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ICES CM 2004/EE:31 Poster

Differences in spawning origins of juvenile whiting *Merlangius merlangus* (L.) inhabiting inshore waters on the west coast of Scotland inferred by otolith microchemistry

Suzanne Ware

Laser ablation inductively coupled plasma mass spectrometry (LA-ICPMS) techniques were used to investigate spawning origins of juvenile whiting inhabiting inshore waters on the west coast of Scotland. Multivariate analysis of the trace metal composition of the otolith nucleus suggested that juvenile whiting collected in the Clyde Sea originated from a different spawning area to juveniles inhabiting the Firth of Lorn and the Sound of Sleat. Multivariate comparison of elemental composition of spawning region (i.e. otolith nucleus) and juvenile region (i.e. otolith edge), in whiting collected from a given inshore area, further suggested that in all cases spawning occurs outside the inshore region where juveniles spend their post-settlement phase. All elements, excluding Mn, were shown to be significantly higher in the juvenile region of the otolith. Whilst mechanisms of uptake of trace elements into the otolith matrix are not fully understood differences in otolith microchemistry identified here are most likely explained by differential environmental histories experienced during the initial larval phase.

Keywords: Otolith microchemistry, Whiting, spawning areas, LA-ICPMS.

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ICES CM 2004/EE:32

Admixture analysis of herring feeding aggregations in the northern North Sea

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Analysis of microsatellite DNA offers a powerful genetic tool to examine population structure and dynamics in highly mobile species, and this approach is now being used to identify different commercial fish stocks genetically. On-going research on Atlantic herring (Clupea harengus) is revealing how herring populations are spatially structured in the North Sea and adjacent areas. This information can be used as a baseline to identify stock components in mixed fisheries. Here we present an initial analysis of herring mixed aggregations off Shetland. We sampled and genotyped five hundred fish from herring summer feeding aggregations, then we estimated the proportion of each baseline stock (western North Sea, eastern North Sea, English Channel, Skagerrak/Kattegat and Baltic) contributing to the mixed aggregation. Results are also presented taking into account age classes, showing that each baseline stock contributes differently to the age groups present in the mixed aggregation. Data form part of an EU-funded on-going multidisciplinary project on the genetics of the North Sea herring (HERGEN, EU Framework V).

Keywords: microsatellites, Atlantic herring, stock identification, fishery.

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