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First Interim Report of the Stock Identification Methods Working Group (SIMWG)

by correspondence



International Council for the Exploration of the Sea

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Executive summary

The Stock Identification Methods Working Group (SIMWG) worked by correspondence in 2014. The working group was chaired by Lisa Kerr (USA) with 13 members working by correspondence.

The work plan for SIMWG in 2014 comprised four main Terms of Reference, most of which, being multiannual, will require additional work over the next two years:

- a) Review recent advances in stock identification methods;
- b) Build a reference database with updated information on known biological stocks for species of ICES interest;
 - Technical reviews and expert opinions on matters of stock identification, as requested by specific Working Groups and SCICOM;
- c) Develop a universal framework for consistent usage of terminology relevant to stock identification;
- d) Review and report on advances in mixed stock analysis, and assess their potential role in improving precision of stock assessment.

ToR a) provides a comprehensive update on recent applications of stock identification techniques to ICES species of interest, summarizes new approaches in stock identification, and novel combinations of existing applications.

ToR b) provides advice on blue whiting (Micromesistius poutassou) in the NE Atlantic (as requested by WGWIDE) and on Atlantic cod (Gadus morhua) in offshore Greenlandic waters (as requested by NWWG). The advice is reported in a new format which will be developed further to build a reference database on known biological stocks for ICES species of interest.

ToR c) reports on the universal framework developed by SIMWG for consistent usage of terminology relevant to stock identification.

ToR d) briefly appraises work undertaken on mixed stock analysis and provides SIMWG's view on best practices in mixed stock analysis to improve stock assessment.

1 ToR a) Review recent advances in stock identification methods

In the last year, there have been several notable advances in stock identification methods and a proliferation of applications, with many results relevant to ICES science and advice. Here, we summarize advances and results accounting for research in genetics, otoliths, tagging, morphometrics, life history parameters, early life history stages, parasites, and interdisciplinary approaches.

1.1 Genetics

During the past year, the field of fisheries genetics has witnessed the consolidation of Single Nucleotide Polymorphisms (SNPs) as latest-generation markers for population identification. Mariani and Bekkevold (2013) provide an overview of their role and applications. Additionally, primary applications are becoming more frequent and offer direct evidence of the usefulness of SNP genotyping. In most cases, SNP applications focus on "outlying" markers potentially under selection, which show the greatest statistical power to distinguish individuals from specific areas. SNP applications to Atlantic cod continue to be highly influential (Bradbury *et al.* 2013; Ther-kildsen *et al.* 2013). SNP screening tools for salmonids are widely available and, in some cases, can be applied across species, such as the use of commercial SNP arrays for Atlantic salmon to discriminate sea trout populations (Drywa *et al.* 2013). Other recent examples of population identification and individual assignment using SNPs include Milano *et al.*'s (2014) study on European hake (*Merluccius merluccius*) and Abaina *et al.*'s (2013) contribution to resolve population structure of albacore (*Thunnus alalunga*) and Atlantic Bluefin tuna (*Thunnus thynnus*).

Reduced genomic representation techniques (e.g. RAD-type protocols) are becoming increasingly affordable and promise to provide rapid SNP development and screening for any species of interest. Although initial investigations still primarily focus on species with a long history and tradition in fisheries genetics (e.g. chinook salmon in Larson *et al.* 2014), there are also recent examples of application to species of more regional importance, such as the case of the Nassau grouper, *Epinephelus striatus* (Jackson *et al.* 2014). A feature of these new generation methods is their ability to produce a large amount of sequencing information, beyond the usual scope of stock identity studies. Thus, a challenge for the forthcoming years will be to map all the routinely used SNP markers on reference genomes, so that SNP panels generated as part of independent studies and using different methods, can be compared and understood in the context of the genome. For instance, SNP markers for Atlantic herring (*Clupea harengus*) used in Limborg *et al.* (2012) and in Corander *et al.* (2013) are used for the same fundamental purpose, but derive from different genome sections and are not directly comparable.

Other genetic markers continue to have an established role in fish stock identification (especially microsatellites), and are often used in conjunction with other methods (see *Interdisciplinary Analysis*). A novel approach is offered by Vandamme *et al.*'s (2014) study on turbot (*Scophtalmus maximus*), which employed gene-associated microsatellites in a "non-neutral seascape genetics" context "Seascape genetics" had previously been used as a spatially explicit causal model to understand the forces responsible for neutral population genetic variation (i.e. genetic drift and effective migration). In a novel application of this approach, Vandamme *et al.* (2014) interpret the spatial variation in selected EST-linked microsatellites on the basis of a multi-layered habitat map

of the seascape, and therefore locate the geographical dimension of the environmental drivers potentially responsible for local adaptation.

The application of genetics to assign individuals to population of origin has use in basic and applied research, providing information about population-specific life history and habitat use, ecotoxins, pathogen and parasite loads, and many other non-genetic ecological, or phenotypic traits. Although the origin of individuals may be of interest, the main objective can also be to infer the distribution of a non-genetic trait among populations (e.g., fecundity). Errors in individual assignment and the discarding of individuals that assign to populations below a minimum threshold can bias trait inferences. Moran *et al.* (2014) extended a Bayesian model for population mixture analysis that avoids bias from assignment errors by incorporating parameters for the phenotypic trait. This research extends the use of genetics in quantitative ecology.

1.2 Otolith structural analysis

Otolith structural analysis continues to be used in stock identification research worldwide; however this technique was not specifically applied to ICES species for this purpose in the past year. Here, we report on methodological advancements in the field. Although these are not papers explicitly focused on stock discrimination, they describe techniques/methods that may be used in the future for stock identification purposes.

Bouchard *et al.* (2013) used lapillar otoliths to discriminate between Polar cod (*Boreogadus saida*) and Ice cod (*Arctogadus glacialis*). Previous to this study, larvae and early juveniles of these two species were considered indistinguishable except via molecular analysis. Bouchard *et al.* found that Ice cod nuclei were 58% larger than those of Polar cod and were able to correctly discriminate 97% known-species fish that were not used to build the model. This technique is an adequate and frugal method to discriminate between these two ecologically important fishes.

Schulz-Mirbach *et al.* (2013) studied the texture and nano-scale internal microstructure of Atlantic molly *Poecilia mexicana* otoliths using the electron backscattered diffraction technique (EBSD). In this study, they found the otoliths from fish from two different ecotypes (surface dwelling and cave dwelling) exhibited different textures, with the sulcus of cave-dwelling fish being smoother than surface-dwellers, which were textured with large rod shaped crystals. Additionally, the authors determined that the cave dwelling fish have microincrements (assumed to be daily growth) in their otoliths despite there being no obvious environmental cues in that environment. This was only the second EBSD study to focus on otoliths.

1.3 Otolith shape

The investigation of stock-specific differences in morphometric outlines of otoliths, also termed 'otolith shape analysis' (see overview in Stransky 2014), was broadly conducted on several species in various regions across world oceans.

In the Northeast Atlantic, Tuset *et al.* (2013) and Vieira *et al.* (2014) applied otolith shape analysis to deep-sea fish species. Tuset *et al.* (2013) found no significant stock differentiation for two scabbardfish (*Aphanopus carbo* and *Aphanopus intermedius*), while Vieira *et al.* (2014) reported on a clear geographic separation of forkbeard (*Phycis phycis*) from mainland Portugal, Madeira and the Azores. Nearly complete separation of blue whiting (*Micromesistius poutassou*) from northern and southern spawning grounds was achieved by Keating *et al.* (2014) using otolith shape analysis.

Legua *et al.* (2013) were able to differentiate between South Atlantic and South Pacific stocks of southern blue whiting (*Micromesistius australis*) and their level of mixing. Other species that were analysed for otolith shape differences between stocks or areas were Pacific sardine (*Sardinops sagax*, Vergara-Solana *et al.* 2013), John's snapper (*Lutjanus johnii*, Sadighzadeh *et al.* 2014), white grunt (*Haemulon plumieri*, Villegas-Hernandez *et al.* 2014) and small yellow croaker (*Larimichthys polyactis*, Zhang *et al.* 2014).

In terms of methodology, however, the most interesting recent paper is the study of Franco *et al.* (2013) using electron paramagnetic resonance to measure the manganese concentrations in several fish species, which was found to be related to the elongation of otolith forms. Even area-specific consistent patterns were reported for two fish species from the Brazilian coast. This technique provides further insights into the biomineralization process and its impact on otolith shapes.

1.4 Otolith Chemistry

In the past year, otolith chemistry was broadly applied as a stock identification tool to discern stock structure of fish species around the world. Kerr and Campana (2014) provided a comprehensive review on the use of the chemical composition of fish hard parts (including otoliths, scales, vertebrae, fish rays and spines) in fish stock identification. Below is a summary of recent applications of otolith chemistry to fish stock identification on ICES species of interest and advances in the field.

Morales-Nin (2014) used otolith chemistry to evaluated connectivity of European hake in the western Mediterranean. No significant differences in otolith chemistry were detected across sampled locations within the western Mediterranean. This was attributed to either the high mobility of the juvenile hake in this region or to the relative homogeneity in the chemical composition of water masses.

Correia *et al.* (2014) used elemental fingerprints of juvenile and adult European sardine (*Sardina pilchardus*) to evaluate the population structure off the coast of Portugal. Currently sardine off the Iberian Peninsula are considered a single stock. The results of the otolith chemistry analysis suggest metapopulation structure for sardine in the region whereby adults form distinct aggregations, but individuals within aggregations are largely derived from a common northern juvenile recruitment area.

Wickström and Sjöberg (2014) reported on the use of strontium as a marker to identify stocked eels by Sweden. This complies with the EIFAAC/ICES Working Group on Eel (EIFAAC/ICES 2011) recommendation that all stocked eel should be marked and thereby separable from wild eel. It is currently unclear the degree to which stocked eels contribute to the spawning stock and marking of stocked fish will facilitate resolving this question.

Higgins *et al.* (2013) used trace element analysis to understand the population structure of two deep sea rockfish *Helicolenus dactylopterus* and *Pontinus kuhlii* from the Azores archipelago. *H.dactylopterus* and *P. kuhlii* are not directly managed in the Azores, but managed by default through limitations in place on *Pagellus bogaraveo* in the Azores region. A combination of trace element ratios provided reasonable discrimination of fish from different island groups in the region (East, West, and Central).

A recent experimental study on European plaice (*Pleuronectes platessa*; Sturrock *et al.* 2014) provided evidence that fish physiology can have a profound influence on the concentration of certain elements in the otolith. Based on these findings, the authors

strongly recommended controlling for age and sex of fish in studies using otolith chemistry to infer spatial population structure.

1.5 Life history parameters

Life history parameters continue to be used in stock identification research. McBride (2014a) provides an overview of historical uses and identifies recent advances. Examples are provided of using life history parameters for both data-poor and data-rich species, often within an interdisciplinary framework. McBride (2014b) includes life history parameters in an interdisciplinary review of stock structure for 25 species managed by the U.S. Atlantic States Marine Fisheries Commission.

Frisk *et al.* (2014) advanced the framework that for some species movement of adults is of paramount importance in structuring populations. They examine "adult-mediated population connectivity" with case studies of winter flounder and winter skate, both species whose adult movements are at a much larger spatial scale than the scale of larval dispersal, so that adult-stage processes heavily affect metapopulation structure for these species.

Jansen and Gislason (2013) describe evidence for 'twinning' by Atlantic mackerel (*Scomber scombrus*) in the North Atlantic Ocean, and along with other interdisciplinary data, they propose a new population structure model for this species. Twinning is evidence of strong year classes in one stock area spreading into another stock area. They also examine larval data and similarly conclude that such evidence is inconsistent with the view that the five spawning groups in this region are reproductively isolated. These life history data complement other, interdisciplinary data (i.e., tagging, genetic, parasites, otolith morphology, and blood types) that converge on the same conclusion.

Dolphinfish (*Coryphaena hippurus*) is a warm-water fishery species distributed globally, yet it has remained relatively data-poor in terms of information about its stock structure. Chang *et al.* (2013) developed growth models for the Kuroshio Current off of Taiwan, rejecting a two-stock model for this region. They expand this approach to develop growth performance indices from as many regions as possible, estimating at least five stocks the world's oceans. The example of dolphinfish is also reviewed with a more interdisciplinary perspective for the western Atlantic Ocean by McBride (2014a), where it appears four stocks may exist in this region alone. International cooperation and an interdisciplinary approach appear necessary to identify the stock structure and dynamics of this cosmopolitan, pelagic species.

Use of growth data can also have immediate practical use in discriminating stocks for stock assessment, as shown by Gröhsler *et al.* (2013) for herring in the Baltic Sea. Two stocks of herring overlap in the western Baltic which confounds stock assessments. Gröhsler *et al.* (2013) use known growth differences between these two stocks to discriminate between them in survey and commercial data and thereby improve the allocation of each stock in the assessment for this region.

Discrete spawning groups, in space, time or both, may not always be genetically distinct if mixing occurs at some other life stage (e.g., Atlantic herring metapopulation structure). Nonetheless, Beacham *et al.* (2014) show that distinct genetic populations of Skeena River sockeye salmon spawn in different tributaries with different spawning run times.

Ribeiro Santos *et al.* (2013) examine reproductive data for black scabbardfish to find evidence of panmixia in the eastern Atlantic. They found only immature black scab-

bardfish west of the British Isles, whereas all maturity stages were observed off Madeira, so they concluded this species is a single population that migrates between these geographic regions.

1.6 Early life stages

Early life history stages can be useful in stock identification providing insights on the scale of larval dispersal and mixing which, in part, defines the extent of stock structure for a species. Individual-based Models (IBMs) are particularly powerful tools for examining population structure and connectivity in marine fish species and can offer valuable insights into the stock structure of fishery resources. A number of recent studies highlight the potential for early life stages of fish to contribute to our understanding of stock structure.

Boucher *et al.* (2013) used an IBM to quantify interannual variability in the retention of haddock eggs and larvae on Georges Bank between 1995 and 2009. The authors concluded that above average retention on Georges Bank is necessary for large recruitment events to occur, although retention alone cannot explain the occurrence of large year classes. Their results also indicated that the vertical position of larvae had a substantial impact upon retention, and larvae at depths of >50m had a greater chance of being retained on Georges Bank.

Building upon a robust background of genetic stock identification research, Myksvoll *et al.* (2014a) simulated the dispersal of cod eggs from a number of spawning sites in fjords, coastal areas, and offshore waters along the Norwegian coast. Their results indicated high retention of eggs spawned in fjords, and the authors posited that fjord subpopulations could be described as a metapopulation. Retention was intermediate for eggs spawned in coastal waters, and no retention was observed for eggs spawned further offshore. The results indicated that dispersal patterns of early life stages differ between fjords and coastal waters, which could enhance population structuring among cod population along the Norwegian coast. In a subsequent modelling study, Myksvoll *et al.* (2014b) observed that changes in the seasonal cycle of freshwater discharge due to hydroelectric power plants may cause a reduction in the retention of cod eggs within a large fjord system on the Norwegian coast.

Cod in the Kattegat have been the subject of numerous stock identification studies. Building upon this research, Pacariz *et al.* (2014) employed the Baltic Sea Long-Term Large Scale Eutrophication Model (BALTSEM) to track the dispersal of cod eggs from spawning areas in the Kattegat and Öresund between 1971 and 2006. Their results indicated substantial interannual variability in egg retention. High retention was observed in years when winds were weak and variable, while strong westerly winds were associated with lower rates of egg retention. The model suggests high connectivity exists between the central and southern Kattegat, and regular exchanges between the Öresund and southern Kattegat basins, as well as between the Öresund and Arkona sub-basins.

Lacroix *et al.* (2012) employed a 3D IBM to examine the interannual variability of the transport of sole larvae that were spawned at six locations in the North Sea between 1995 and 2006. Using a series of sensitivity analyses, the authors sought to quantify the relative importance of both active (biological and behavioural) and passive (hydrodynamic) processes on larval dispersal. The study estimated retention at the six spawning grounds, and also quantified connectivity between spawning and settlement areas in the North Sea. The results suggest that retention rates on the Norfolk spawning grounds are high, and the Norfolk nursery received no larval subsidies

from other spawning grounds. Larvae in the Thames nursery primarily originate from local sources, but this nursery also receives larvae from the French, Belgian and Norfolk spawning grounds. The French, Belgian and Dutch nurseries appear to recruit a mixture of larvae that are produced both locally and from downstream locations.

Castaño-Primo *et al.* (2014) used an IBM to examine the dispersal of Northeast Arctic haddock eggs and larvae from locations along the Norwegian coast. Despite the commercial importance of this stock, the spawning grounds in this region are not well understood. The model results suggest that spawning north of 67°N would result in a greater likelihood of eggs and larvae successfully reaching nursery grounds in the Barents Sea.

Fish larvae do not float passively in the water column, but instead have the ability to adjust their vertical and horizontal position in response to biotic and abiotic factors. Staaterman and Paris (2014) provide an overview of recent advances in modelling the vertical and horizontal behaviours of fish larvae, and discuss the challenges that must be overcome to increase the realism of IBM's. The authors conclude that the inclusion of realistic three-dimensional larval behaviour will increase the utility of IBM's for addressing questions related to connectivity, recruitment variability, and stock structure.

1.7 Body morphometrics

Compared to other methods, classic body morphometrics and meristics have been used to a lesser degree, in recent times. There is however still some new scientific studies published yearly. In the ICES area, truss network analysis of Red striped Mullet, *Mullus surmuletus* using PCA and partial redundancy revealed no sexual dimorphism, but did find that juveniles were distinct from adults and fish from the eastern English Channel were distinguishable from fish in the Bay of Biscay (Mahe *et al.* 2014).

A caveat regarding the use of preserved samples for morphometric analyses is raised by Berbel-Filho *et al.* (2013). This study showed experimentally that preservation (both alcohol and freezing) changed the shape of fish. A new way of using body morphometrics is suggested by Farré *et al.* (2013). In their study, individual fish morphology was used to create geometric morphological indices for whole fish assemblages. These morphometric indices could turn out to be useful tools for comparing the diversity among fish assemblages when ecological information is absent or scarce.

1.8 Tagging

Contributions from SIMWG members as well as a brief abstract search demonstrate that tagging remains a common approach to describing and quantifying movement for application to stock identification. Several recent scientific meetings and resulting publications in the ICES community and beyond demonstrate recent tagging applications.

Tagging data is increasingly being used to inform tag-integrated stock assessment models that account for stock structure and mixing. For example, the World Conference on Stock Assessment Methods for Sustainable Fisheries (July 2013, Boston USA) had a session on spatial complexity, with several papers relevant to tagging and stock identification (<u>http://www.ices.dk/news-and-</u>

events/Documents/Symposia/WCSAM/ProgramDraft%20WCSAM2013-final.pdf):

- 3.03 Application of a tag-integrated stock assessment model to three interconnected stocks of yellowtail flounder stocks off New England (Goethel *et al.* 2014)
- 3.05 Evaluating benchmarks of biological status for Pacific salmon under temporal variability in stock productivity and meta-population dynamics
- 3.07 Evaluating the effects of mixing rates between Atlantic bluefin tuna stocks using simulation
- 3.09 Combining spatial sub-populations in a stock assessment is it a problem?
- 3.10 Modelling intermixing whitefish populations: a simulation study to evaluate alternative stock assessment methods (Li *et al.* 2014)
- 3.54 Central Baltic herring stock(s) together or separate? Evaluation of assessment units and management practices
- 3.62 A combined modelling approach for informing stock assessment with electronic tags

Electronic tagging is also leading to more fine-scale understanding of fish behaviour related to stock structure (e.g., seasonal movement patterns, spawning dynamics, spawning site fidelity, stock mixing). For example, the ICES/NAFO Symposium Ga-doid Fisheries: The Ecology and Management of Rebuilding (October 2013, St Andrews Canada) had a session on the effects of life history on productivity and stock rebuilding with several presentations on tagging applications for stock identification:

- O.1.6. Linking tagging experiments and molecular genetics markers to gain insight in the spatial dynamics of two stocks of cod in Northeast Atlantic waters (Michalsen *et al.* 2014)
- O.1.7. Gadoid subpopulations with distinct life history traits : management considerations in a changing environment
- O.1.8. Movement Patterns of Atlantic Cod (*Gadus morhua*) spawning groups off New England (Loehrke 2014)
- O.1.9. Fine scale movements of Atlantic cod on a spawning ground (Dean *et al.* 2014)
- O.1.10. Study of spawning ground of European hake (*Merluccius merluccius*, L.) from the southern stock (ICES VIIIc-west division). Attempted depm application
- O.2.4. Movements of Atlantic cod (*Gadus morhua*) spawning in the Western Gulf of Maine: Implications for population structure and rebuilding (Zemeckis *et al.* 2014b).
- O.4.3. Discrimination between northeast Arctic cod and Norwegian coastal cod on the spawning grounds as part of the recovery plan for coastal cod
- O.6.1. Review of Atlantic cod (*Gadus morhua*) population structure in U.S. waters: An interdisciplinary approach to stock identification (Zemeckis *et al.* 2014a)
- O.6.3. Impacts of inter-stock mixing on the assessment of Atlantic cod, *Ga- dus morhua*, in the Gulf of Maine (Cao *et al.* 2014).
- O.6.8. Consequences of a mismatch between biological and management units on our perception of Atlantic cod in the northwest Atlantic (Kerr *et al.* 2014)

The 2013 Tuna Conference "Back to Biology: The role of life history characteristics in tuna stock assessments"

(http://media.wix.com/ugd/ba25d2_6d6c9367d2332e03ebc89cb2992a86bd.pdf) also had a session on tagging:

- Movements and Oceanographic Associations of Bigeye Tuna (*Thunnus obesus*) in the NW Atlantic determined by popup satellite archival tags
- Seasonal movements and habitat utilization of white marlin
- Movements of Dolphinfish (*Coryphaena hippurus*) along the U.S. East Coast as determined through conventional mark and recapture data
- Tracking Sailfish from a Yucatan "hotspot"
- Evaluating post-release mortality of white marlin (*Kajikia albida*) caught in the recreational fishery: biochemical and physiological indicators of lethal stress
- Post-release survival of school-size Atlantic bluefin tuna (*Thunnus thynnus*) caught in the recreational trolling fishery
- Essential pelagic habitat of juvenile blue shark (*Prionace glauca*) in the North Atlantic
- Leatherback turtle movements, dive behaviour, and habitat characteristics in eco-regions of the Northwest Atlantic
- Movement Patterns of Blackfin Tuna (*Thunnus atlanticus*) in the Gulf of Mexico
- Demonstration of a Likelihood Framework for light based geolocation
- Ignorance of Stock Structure and Life History parameters contributes to uncertainty in tuna stock assessments Migration patterns of juvenile (AGE-0) Pacific Bluefin tuna (*Thunnus Orientalis*) in coastal nursery areas of Japan
- Migratory movements, depth distribution and temperature preferences of dolphinfish (*Coryphaena hippurus*) in the northwestern Mexican Pacific
- Transatlantic movements of juvenile Atlantic Bluefin tuna inferred from analyses of organochlorine tracers

1.9 Parasites

The past year saw the publication of two reviews dealing with the use of parasites as biological tags for marine organisms. Catalaño *et al.* (2013) reviewed the use of parasites as tags for marine fish and cephalopods, with the main emphasis on the latter group, and discussed new ways of incorporating parasite genetic data into population structure studies. MacKenzie and Abaunza (2014) updated their review of the use of parasites as biological tags for marine organisms for the 2nd edition of the book Stock Identification Methods. Both reviews proposed guidelines and recommended the multidisciplinary or holistic approach to studies of host population structure, with parasite tags being used in combination with other methods. A further eleven reviews of various aspects of the use of parasites as biological tags can be found in a Special Issue of the journal Parasitology (Timi and MacKenzie, 2014). Although this issue is not due to be published until later this year, the contents are available online now.

Two research papers on the use of parasites as biological tags for marine fish were also published. Alarcos and Timi (2013) analysed the structure and composition of parasite assemblages to identify stocks and reveal migratory patterns of the flounder *Xystreurys rasile* in the Argentine Sea, while Hermida *et al.* (2013) used five helminth parasites (one digenean, 3 larval nematodes and a juvenile acanthocephalan) to indicate the existence of three separate stocks of blackspot seabream, *Pagellus bogaraveo*, off the coast of Portugal and around Madeira and the Azores.

1.10 Interdisciplinary analysis

Stock identification and separation issues cannot be fully addressed by monodiscipline approaches (Cadrin and Secor 2009). Population units are by their very nature multidimensional phenomena and include spatial and temporal distribution characteristics and genetic and phenotypic variability. A population unit defined by genetic and phenotypic approaches is "a group of organisms whose demographic/genetic trajectory is largely independent of other such groups" (Waples 1998, Palsböl *et al.* 2006; Waples and Gaggiotti 2006).

The second argument for applying more than one stock identification method is naturally the enhanced likelihood of correctly identifying and describing population structures (Cadrin and Secor 2009). Technological advances in molecular genetics, otolith shape analysis and microchemistry, archival tagging and statistical tools improve the ability to detect and infer data on population structures. By involving interdisciplinary approaches, complex patterns of the spatial structure of many marine populations can be revealed (e.g., Stephenson *et al.* 2009).

Interdisciplinary approaches are not solely conducted for population identification purposes but also for predictions. For instance, information on genetics together with spatial modelling has been used for predicting the consequences of spatial variation in exploitation on population diversity of the North Sea cod (*Gadus morhua*; Heath *et al.* 2014). Likewise, differentiation in life history traits such as maturation rates (in this case maturation probability at length) has been attributed to cod subpopulations in the North Sea (Wright *et al.* 2011). Here, we report on interdisciplinary stock identification applications conducted in the past year.

Monitoring fish distribution in combination with other techniques

Fish distribution information can be a key piece of evidence and complement other techniques in stock identification. The spatial and temporal distribution of Atlantic cod spawning aggregations in the Gulf of Maine was studied by using synoptic acoustic and trawl surveys (Gurshin *et al.* 2013). Without this type of information, other studies including population genetics are curtailed in significance and may lead to spurious conclusions.

Population structure in North Sea mackerel was elucidated by means of data from the fishery, eggs surveys, hydrographical measurements, zooplankton abundance and wind stress as a proxy for turbidity (Jansen 2013). It was conjectured that the alleged depletion of the North Sea spawning component represents a pseudocollapse, as it was both environmentally driven and related to a high exploitation rate in the late 1960s. Decrease in temperatures in autumn and winter together with low temperatures in eastern North Sea during spawning in the 1970s changed the spawning distribution away from the North Sea.

Genetic markers, early life history stages, parasite load and tagging

In a review of cod population structure in New England waters (Zemeckis *et al.* 2014), the current management structure for cod in the region is confronted with information from several different stock identification methods. Genetic variation and

phenotypic variation, such as life history, parasite load, larval distributions are discussed in relation to spawning activity. Tagging studies provided additional information. The interdisciplinary approach indicated a much higher population diversity with for instance segregation between inshore and offshore stock units, a complexity yet to be accounted for by the management as continued neglect may "cause misperceptions of the magnitude and distribution of productivity and has potentially contributed to rebuilding difficulties and the depletion of spawning components."

Data Storage Tags (DST) and genetic markers

Reproductive isolation by fine-scaled differences in habitat selection was examined in Norwegian cod using the combination of tagging and genetic analysis (Michalsen *et al.* 2014). In this study, Michalsen *et al.* 2014 identified behavioural differences between Norwegian coastal cod and migratory cod (*skrei*) using genetic markers and DSTs.

Genetics and Otolith Chemistry

Tanner *et al.* (2014) used both otolith chemistry (including a suite of elemental ratios) and genetics (microsatellite DNA markers) to examine the stock structure of European hake (*Merluccius merluccius*). ICES manages Mediterranean and Atlantic population of hake as different stocks. Additionally, ICES divides hake in the northeast Atlantic into northern and southern stocks. Microsatellites provided evidence of a major genetic split in the vicinity of the Strait of Gibraltar, separating the Atlantic and Mediterranean populations. Together, genotype and otolith data increased the classification accuracy between northern and southern stocks within the Northeast Atlantic, however the misclassification of individuals between these regions provided evidence of movement between stock units. The results of the two techniques produced a complementary view of population structure with otolith chemistry providing insights over ecological time scales and finer spatial scale and genetics providing insights over evolutionary time scales and broader spatial scales.

Longmore *et al.* (2014) used otolith chemistry (trace elements and stable isotopes) and genetic (microsatellite DNA markers) analysis to evaluate the population structure of the deepwater black scabbardfish (*Aphanopus carbo*) in the Northeast Atlantic. *A. carbo* are currently managed as two stocks: 1) south (ICES subarea IX), and 2) north (ICES subareas V, VI, VII, and XII). Individually, and in combination, the otolith chemistry and genetic tools applied to *A. carbo* indicate a lack of population structure or differentiation throughout locations sampled within the NE Atlantic. Results do not support the distinction of this resource as two stocks.

Conclusion

The multidimensional aspects of stock separation issues, including the mechanisms leading to population integrity or connectivity between population units cannot be fully addressed by applying solely one method. This is due to the fact that behavioural and physical mechanisms important for stock separation cannot be extracted from just population genetics. However, very few examples so far exist whereby a range of stock identification markers have been applied consistently on the very same samples (Cadrin *et al.* 2013). A priority task for the future is to design sampling surveys with the prior expectation that individual fish may be subjected to a range of complementary analytical techniques for population characterisation. A further step will be to develop solid, verified statistical approaches that are able to use all the multi-disciplinary information in a coherent analytical framework. Although some of

these methods may already be available, there is no consensus as to what variables can be used together, and how they must be standardised and weighed in order to produce accurate and least-biased stock structure representation. One emerging option for combining data from different techniques is Bayesian modelling, which allows combination of all data types, if only the probability distributions are available.

2 ToR b) Build a reference data base with updated information on known biological stocks for species of ICES interest

SIMWG has a long-term aim to create a reference database that contains the most upto-date information on biological stocks for ICES species of interest. This year SIMWG was asked to provide technical advice on stock structure of blue whiting (*Micromesistius poutassou*) in the NE Atlantic and on Atlantic cod (*Gadus morhua*) in offshore Greenlandic waters. We have reported this advice is in a new format which will be developed further into an online format as we build toward a reference database. Next steps will include establishing a working agreement with ICES web designers for delivery of a SIMWG reference database on biological stocks for ICES species of interest.

2.1 Evaluation of blue whiting stock identity

ECOREGION: Widely distributed and migratory stocks

ICES STOCK(S): Blue whiting in Subareas I-IX, XII, and XIV

SIMWG FINDINGS: The perception of blue whiting in the NE Atlantic as a single-stock unit is not supported by the best available science. SIMWG recommends that blue whiting be considered as two units with the stock boundary defined at either the northern edge of ICES areas VIIk and VIIj or the northern edge of ICES areas VIIc and VIIb.

SIMWG Review

In 2014 SIMWG was asked by WGWIDE to provide our feedback on blue whiting stock structure given recent advances in stock identification that have occurred since SIMWG's 2009 review (ICES 2009). The 2009 review of blue whiting by SIMWG stated that the perception of blue whiting in the NE Atlantic as a single-stock unit was not supported by the best available science at the time and suggested blue whiting be considered as two units (north and south of ICES areas VIIk and VIIj; Figure 1).

In 2012, blue whiting underwent a benchmark review (ICES 2012*a*) and at that time the existing information on blue whiting stock structure was reviewed. The consensus from WKPELA 2012 was that evidence indicated there was only one stock which spawned together and was predominantly fished together. The conclusion by WKPELA 2012 that blue whiting exists as a single stock relied heavily on a review of past stock identity work by Keating *et al.* 2014 and otolith shape analysis by Oudard *et al.* presented as working documents in the benchmark review. (ICES 2012*a*). Upon review, SIMWG found the cumulative evidence detailed in the review document to support the existence of two or more stocks of blue whiting in the NE Atlantic. Additionally, detectable differences in otolith shape were identified between individuals collected in northern and southern areas; the working document authors suggested this as supporting evidence for the existence of a northern and southern subpopula-

tion. However, the mixture of otolith shapes found on the primary spawning ground for blue whiting (ICES Division VIa) was interpreted to support the hypothesis of a single stock of blue whiting. The collection of otoliths at different times of the year in this study may have influenced the composition of fish encountered. Recent research suggests northern and southern components share the same spawning ground, but may exhibit temporal separation in spawning time (Pointin and Payne, *In Press*).

The most recent results of otolith shape analysis by Keating et al. (2014) revealed two distinct otolith morphotypes from fish, one exhibited by fish that occupied a more northerly distribution (north of 54.25 N) and the other characterizing fish distributed south of 52 N, with limited overlap in between. This study targeted fish on the spawning ground and during the spawning period. These findings are consistent with previous findings from otolith microstructure (Brophy and King, 2007) and oceanographic modelling (Skogen et al. 1999), that support northern and southern components in the blue whiting population which may overlap to varying degrees in the centre of the spawning distribution. Additionally, recent examination of the extensive data series (1948 to 2005) of observations of blue whiting larvae from the Continuous Plankton Recorder documents two distinct spawning events, one slightly south at Porcupine Bank, almost a month earlier than the second, which occurs in the Rockall Trough (Pointin and Payne, In Press). This research supports the twopopulation hypothesis providing evidence of spatial and temporal separation in the spawning of northern and southern components whereby the southern component arrives at the spawning grounds (Porcupine Bank/Seabight area) between January and March, with a larger northern component arriving later (Feb-April) in the Rockall Trough (Keating et al. 2014; Pointin and Payne, In Press).

SIMWG confirms its earlier conclusion that the perception of blue whiting in the NE Atlantic as a single-stock unit is not supported by the best available science and should be revised. SIMWG finds that there is valid scientific evidence supporting the presence of distinct northern and southern spawning populations of blue whiting in the NE Atlantic with the boundary between 53-54 N. ICES subdivisions may be useful in delineating the stock boundary, although a decision will need to be made by species experts as to whether the most appropriate boundary is at the: 1) northern extent of ICES areas VIIk and VIIj, or 2) northern extent of ICES areas VIIc and VIIb. Additional samples and more genetic and phenotypic markers should be applied, outside of the spawning area and time to fully understand the spatial and temporal distributions of these components. SIMWG recommends that blue whiting be considered as two units with the stock boundary defined at either the northern edge of ICES areas VIIk and VIIj or the northern edge of ICES areas VIIc and VIIb.

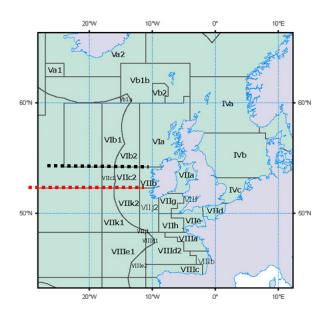


Figure 1 Proposed stock boundaries at the: 1) northern extent of ICES areas VIIk and VIIj (red broken line), or 2) northern extent of ICES areas VIIc and VIIb (black broken line).

2.2 Evaluation of stock identity of cod in offshore Greenlandic waters

ECOREGION: Iceland and East Greenland

ICES STOCK(S):

- I) Cod in inshore waters of NAFO Subarea 1 (Greenland cod)
- II) Cod in offshore waters of ICES Subarea XIV and NAFO Subarea 1 (Greenland cod)

SIMWG FINDINGS: SIMWG finds that there is a valid scientific basis supporting the presence of distinct eastern and western spawning populations of offshore cod stocks in Greenland waters. SIMWG recommends that ICES recognize the mixed-stock nature of the Atlantic cod fishery in offshore Greenlandic waters and the associated risks of managing the mixture as a single unit in their advice. Stock composition analysis would improve the scientific basis of advice and permit assessment and management eastern and western spawning populations as distinct stocks.

SIMWG Review

In 2014, SIMWG was asked by the North Western Working Group to consider the possibility that the offshore stock of Atlantic cod (ICES Subarea XIV and NAFO Subarea 1) in Greenland waters should be considered as separate eastern and western stocks. This information is relevant to and will be considered at the upcoming benchmark review for this stock in 2015. Previous work by SIMWG (ICES 2012*b*) includes an assessment of whether there are distinct inshore and offshore populations of cod in Greenland waters.

SIMWG found that new genetics work (Therkildsen *et al.* 2013) provides strong evidence that what is currently considered a single offshore Greenland cod stock is composed of distinct east and west spawning components. Therkildsen *et al.*'s (2013) analysis of Atlantic cod at its northern range indicated the presence of four genetically distinct components within their samples: 1) an inshore component in the fjords of west Greenland, 2) a west Greenland offshore component, and 3) an east Greenland offshore component, and 4) some influx of fish from Iceland. This study used SNPs to

resolve the fine scale cod population structure in Greenlandic waters, and by evaluating modern and historic (1930s-1950s) genetic samples from spawning fish, Therkildsen *et al.* (2013) were able to examine the temporal stability of cod population structure in this region. Interestingly, it appears that there has been a shift in the distribution of these components over time, with the eastern component currently distributed around the southern tip of Greenland to the southwest (Figure 2), whereas in the 1940s western fish were distributed in this area. This may relate to the current apparent lower biomass of cod to the west of Greenland compared to the east (ICES 2014*a*).

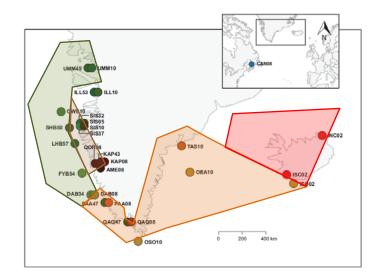


Figure 2 Map from Therkildsen *et al.* 2013 illustrating the sample location of cod during the spawning season (circles). The colors of circles denote the relative connectivity of spawning fish from each site (for further details see Therkildsen *et al.* 2013).

This view of offshore population structure is consistent with previous hypotheses about population structure based on egg distribution surveys, abundance records, and tagging data. Surveys of cod egg and larvae support the past and present occurrence of spawning on the banks off both the east and west coast of Greenland (Wieland and Hovgaard 2002). The Greenland shrimp and fish survey (Retzel and Post 2014) show distinctly different trends in estimated spawning stock biomass of cod off of east and west Greenland. This may reflect different responses of these groups to environmental variation. The results of tagging data suggest the eastern component may be more wide-ranging than the western component, moving into waters off west Greenland and returning to the east, or to Iceland. Although tagging reports indicate relative high rates of recaptures of fish tagged off west Greenland in east Greenland and Iceland, a recent review of this data indicated that these fish originated from southern and southwestern coast of Greenland (Buch et al. 1994; Storr-Paulsen et al. 2004; Hedeholm et al. 2012), and based on genetics data may be of eastern origin. It is clear from tagging that these components exhibit considerable spatial overlap and mixing outside of the spawning period. Recent stock composition analysis of cod collected off the west coast of Greenland indicate a mixture of samples in this region with eastern origin fish dominating around the southern tip of Greenland (Bonanomi et al., In Prep.) and increasing representation of western origin fish up the western coast.

SIMWG finds that there is a valid scientific basis supporting the presence of distinct eastern and western spawning populations of offshore cod stocks in Greenland waters. Recognizing these spawning groups as discrete may contribute to recovery of cod in the region, particularly for the western component which is currently at low biomass. However, genetic analyses of samples collected outside of the spawning season off the west coast of Greenland indicate spatial and temporal overlap of eastern and western components outside of the spawning period (Bonanomi *et al., In Prep.*). SIMWG recommends that ICES recognize the mixed-stock nature of the fishery in offshore Greenland waters and the associated risks of managing the mixture as a unit in their advice. Stock composition analysis would improve the scientific basis of advice and permit assessment and management eastern and western spawning populations as distinct stocks. Additional work should be done to understand the degree of connectivity between the eastern stock component and Icelandic stock.

3 ToR c) Develop a universal framework for consistent usage of terminology relevant to stock identification

Stock identification is an interdisciplinary field that is a critical component of effective fisheries science and management worldwide. The field is rapidly advancing and involves the synthesis of the more general disciplines of population biology and ecology, with more applied disciplines of fisheries science and stock assessment, as well as many specific fields of study (e.g., genetics, biometry, chemistry, oceanography, etc.). The terminology consists of some of the most basic, as well as most confusing, concepts in fisheries science (e.g., stock).

Here, we have worked to refine a glossary of terms relevant to stock identification, in order to resolve uncertainties and discrepancies in terminology use, and to promote consistent and unambiguous language for effective communication on the topic of stock identification among professionals, and the ICES community as a whole.

SIMWG will continue to develop this multiannual ToR, encouraging discussions among members of various experts groups and SCICOM, with the intention of ultimately producing a review-type publication to synthesize the terminology reappraisal, and minimise ambiguity.

Glossary

<u>Adaptive genetic markers</u>: genetic markers whose variation depends on the action of natural selection.

Biological population: A self-sustaining group of individuals, from a single species, whose dynamics are primarily determined by birth and death processes. A biological population may comprise a single or a number of different spawning components.

<u>Colonisation</u>: the process of establishment of a new sub-population in a given spatiotemporally defined habitat. It can take place either by dispersal of early life stages or by establishment of new spawning aggregations by roaming shoals of adult fish.

<u>**Connectivity**</u>: The degree of physical linkage among biological units or habitat patches (may or may not result in gene flow).

<u>**Contingent</u>**: A group of fish that co-occur in space and time and adhere to the same behavioural pattern.</u>

<u>Deme</u>: A local randomly mating genetic sub-unit within a species or biological population.

Dispersal: The movement of individuals from one place to another. It can be either passive (mostly in early life stages) or active (mostly in juveniles and adults).

Entrainment: Socially transmitted behaviours that maintain spawning site fidelity, although not necessarily fidelity to natal spawning site.

<u>Hardy-Weinberg Equilibrium (HWE)</u>: the condition under which the allele and genotype frequencies in a population will remain constant, assuming large randommating populations that experience no migration, no mutation and no natural selection.

<u>Hybrid zone</u>: an area where individuals belonging to different populations, or occasionally species, interbreed, to generate individuals of admixed genetic constitution. Sometimes referred to as admixture.

Indolence: limited movement by all life stages resulting in passive philopatry.

Introgression: Occurs when hybrid individuals back-cross with one of the populations (or species) of origin, and transfer part of the genome of the other population into the back-crossed population.

Isolation by distance: a mechanism of spatial structure according to which individuals are more likely to mate with individuals from nearby populations rather than from distant ones. This model is expected to result in a positive correlation between geographic distance and genetic divergence.

Local extinction: the extirpation of a species' population, or a subpopulation in the metapopulation framework.

<u>Management Unit</u>: A geographically delineated fishery resource that is based on practical or jurisdictional boundaries for operational stock assessment and fishery management, which may or may not reflect biological population structure.

Member-vagrant model: The hypothesis that explains the degree of cohesiveness of a population, whereby members remain associated during the various parts of the life cycle – especially during spawning – and 'vagrants' are lost from their population, and may stray to other populations, or form new aggregations.

<u>Metapopulation</u>: A system of interacting biological populations, termed subpopulations, that exhibit a degree of independence in local population dynamics as well as connectivity between sub-populations.

<u>Migration triangle</u>: A pattern that represents the life history circuit of a given population, and comprises a) the transport of planktonic stages to nursery habitats, b) the ontogenetic "recruitment" to adult habitat, c) and seasonal migrations to spawning grounds.

<u>Migration</u>: Active horizontal dispersal of individuals from one area/population to another. Ecologically, it may refer to change in habitat use during the life cycle (e.g. feeding migrations). In evolutionary biology, it refers to the movement of individuals between populations and underpins gene flow (effective migration).

<u>Mixed stock</u>: a spatio-temporally defined aggregation of individuals belonging to different biological populations.

Natal homing: A return migration of sexually mature individuals to spawn upon the grounds where they were spawned. Natal homing behaviour is expected to result in active philopatry and population differentiation, as long as there is no change of spawning season.

Natural selection: the non-random process by which phenotypic frequencies change in a population as a result of heritable variation in their fitness.

<u>Neutral genetic markers</u>: genetic markers whose variation primarily depends on the action of gene flow and random genetic drift.

Open/closed populations: Represent the degree of connectivity among biological populations, in a continuum between almost complete panmixia (open), to very low degrees of effective migration (closed).

<u>Panmixia</u>: is the status of a population within which mating is completely random and all adult individuals are potentially interbreeding. In population genetic terms, a 'panmictic' population is in Hardy-Weinberg equilibrium.

<u>**Partial migration**</u>: a phenomenon whereby individuals within the same population exhibit distinct lifetime migration behaviours (e.g. resident and migratory contingents).

Philopatry: Fidelity to parental spawning sites either by natal homing (active philopatry) or retention of early life stages coupled with residence of adults (passive philopatry).

<u>Reaction norm</u>: The pattern of phenotypic expression of a genotype across a range of environmental conditions. For instance, an individual of a given genetic constitution will grow at different rates, at different temperatures.

<u>Retention of early life stages</u>: Physical, environmental and/or behavioural mechanisms through which early life stages are prevented from dispersing too far from the area of their release.

Spatial/temporal overlap: Co-occurrence of two or more biological units in space and time. Spatial overlap can occur without temporal overlap. For instance, this can happen when spawning grounds are used at different times of the year (e.g., autumn versus spring spawning populations, or biennial populations spawning in alternating years).

Spawning component (group): A group of individuals of a population that utilize a single spawning ground at the same time.

Spawning aggregation: a repeated concentration of conspecific fish, gathered for the purpose of spawning, that is predictable in time and space. The density/number of individuals participating in a spawning aggregation is at least four times that found outside the aggregation. The spawning aggregation results in a mass point source of offspring (sensu Domeier 2012).

Spawning site fidelity: The repeated return of adult fish to spawn at the same location, irrespectively whether they were hatched at this location or not. The distinction between spawning site fidelity and natal homing is important because spawning-site fidelity may not necessarily lead to reproductive isolation if there is extensive egg and larval drift together with opportunistic and non-philopatric recruitment of juveniles to adult aggregations.

Stock: An exploited fishery unit. A stock may be a single spawning component, a biological population, a metapopulation, or comprise portions of these units (Figure 3). For management purposes stocks are considered discrete units and each stock can be exploited independently or catches can be assigned to the stock of origin.

<u>Stock identification</u>: the process of identifying groups of fish with some degree of biological independence from other groups, with the aim to inform the assessment and management processes. The identification of stock units involves different separation criteria and levels of complexity, depending on the management objectives and the nature of available information.

<u>Stock discrimination</u>: the process of using stock identity information and accepted identification technique(s) to discriminate fish in mixed-stock catches.

<u>Straying</u>: Occurs when individuals move to and join a spawning aggregation different from the one they had originated in.

Subpopulation: A single, mostly self-sustaining unit within a metapopulation.

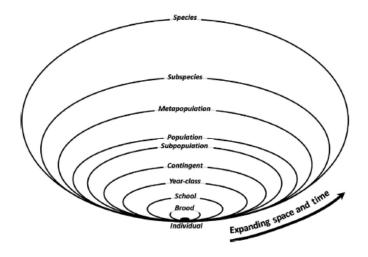


Figure 3. Levels of ecological organization relevant to defining a fish stock. Diagram concept from Secor 2014.

4 ToR d) Review and report on advances in mixed stock analysis, and assess their potential role in improving precision of stock assessment

Mixed stocks occur when stocks are not completely isolated and there is some spatial overlap in fish stocks for a period of time (Secor 2014). When a fishery focuses effort on a mixture of stocks this results in catch data that is composed of multiple stocks of fish which can introduce error into stock assessments. Likewise survey data from an area of overlap can produce biased estimates of stock biomass when incorporated into stock assessment. Oftentimes, the mixed stock nature of data is ignored in stock assessment. However, in some cases mixed stock data has been resolved through mixed stock analysis, which combines existing stock identity work and statistical analysis to estimate the relative contribution of each stock to the catch data (Prager and Shertzer 2005).

Successful mixed stock analysis requires a thoroughly tested 1) stock identification technique(s), that exhibits reproducibility over time, and 2) an estimation methodology to discriminate stocks. Several stock identification methods have been used to resolve the origin of species in mixed-stock fisheries, including genetic markers, otolith and scale growth patterns, etc. Once a reliable stock identification method(s) has been identified and tested for its temporal stability it is then employed in stock discrimination. Currently the primary statistical methods used in resolving the origin of individual fish based on stock identity data are 1) discriminant analysis (Pella and Masuda 2005), 2) maximum likelihood method for mixed stock analysis (Kalinowski et al. 2007), and 3) Bayesian hierarchical methods for mixed stock analysis (e.g., Pella and Masuda 2001). Discriminant analysis may not be the best method to classify samples of unknown stock origin because it performs poorly when the stock markers are similar and requires prior knowledge of stock proportions in the mixture (i.e. development of a classification rule; Campana 2005). Maximum likelihood is a standard tool for stock composition analysis that can provide good discriminatory power in mixed stock situations. Increasingly, Bayesian methods are being used in mixed stock analysis due to advantages that include 1) greater realism in model assumptions, 2) better flexibility to deal with shortcomings (e.g. missing data; Pella and Masuda 2001). Additionally, these models allow for simultaneous analysis of multiple data sources (e.g., otolith and genetic data; Smith and Campana 2010) and enable one to account for and analyse several sources of uncertainty (Pflugeisen and Calder 2011).

A prime example of the implementation of mixed stock analysis to improve fisheries stock assessment and management is the case of western Baltic spring spawning herring (WBSS) and North Sea autumn spawning herring (NSAS). In this instance, herring catches within mixing areas (Division IIIa (Skagerrak and Kattegat) and parts of the Eastern North Sea) are made up of a mixture WBSS and NSAS which are identified using vertebral counts and otolith microstructure (ICES 2012*c*). In the biological advice, the level of mixing between the stocks is measured and used to calculate a total TAC for herring in the separate areas (ICES 2012*c*). Atlantic salmon is another example of a species for which mixed stock analysis has been used to improve assessment. Atlantic salmon in the Baltic Sea is a species of ICES interest and a database of 36 salmon stocks around the sea is available as baseline dataset and is annually used for mixed stock analysis of international catches in the sea. Results are reported by WGBAST (ICES 2014*b*). Michielsens *et al.* 2004, have combined results of genetic

mixed stock analysis into the Bayesian Baltic salmon assessment model and an improved certainty level was reached with that analysis. However, it is not used systematically for annual assessments.

The International Commission on the Conservation of Atlantic Tunas (ICCAT) is taking a somewhat different approach to the challenge of addressing stock structure and mixing in the assessment and management of Atlantic Bluefin tuna. Decades of conventional tagging and more recent deployments of electronic tagging have documented considerable mixing between eastern and western Atlantic stocks, and recent analyses of otolith chemistry have informed stock composition analysis. However, movement estimates from stock assessments that integrate information from tagging and otolith chemistry are not well estimated (e.g., Taylor *et al.* 2011). In addition to the conventional approach of estimating stock composition for stock-specific assessments, ICCAT is also applying a Management Strategy Evaluation (MSE) approach in which a spatially-explicit operating model will account for seasonal movement and stock mixing to evaluate the performance of simpler management procedures (e.g., assessments assuming no mixing and robust harvest control rules). The MSE will be developed for the 2015 stock assessment (ICCAT 2013).

SIMWG will continue to work on this ToR to address the issue of how mixed-stock analysis can be best utilized to improve stock assessment and management. Furthermore we will try to address critical questions regarding how mixed-stock component estimates can affect reference points (e.g. MSY) of assessed stocks.

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Annex 2: Recommendations

Recommendations	For follow up by:
 Establish working agreement with ICES web designers for delivery of a SIMWG reference database on biological stocks for species of ICES interest. 	SIMWG, ACOM, SCICOM
2. Blue whiting in the NE Atlantic should be considered as two stock units: northern and southern.	WGWIDE, SSGSUE, SCICOM, ACOM
3. The mixed stock nature of Atlantic cod in offshore Greenlandic waters should be considered in ICES advice.	NWWG, SIMWG, SCICOM
4. Plan an in-person SIMWG meeting for June 2015 in the US.	SIMWG

Annex 3: SIMWG terms of reference for the next meeting

The **Stock Identification Methods Working Group** (SIMWG), chaired by Lisa Kerr, USA, plans to organise a physical meeting in the USA in 2015 (venue and dates in June 2015 to be confirmed).

ToR descriptors

ToR	DESCRIPTION	Background	Science Plan topics addressed	DURATION	EXPECTED DELIVERABLES
a	Review advances in stock identification methods	a) Personnel commitment b) Regular communications	Action 1.2.1	3 years (and continued)	EG report
b	Build a reference data base with updated information on known biological stocks for species of ICES interest	a) Advances in stock knowledge for more species b) provision of Secretariat and HQ support c) communication of new findings		2 years (and continued)	Web pages and downloadable ICES CRR
c	Review and report on advances in mixed stock analysis, and assess their potential role in improving precision of stock assessment	 a) Personnel commitment b) Advice on key stocks and species to prioritise c) communication of new findings 	?	2 years	EG report and contribution to ICES ASC 2015, and methodological paper in international journal

Summary of the Work Plan

Year 1	Organise a physical meeting for SIMWG for summer 2015, trying to identify a period of the year that would allow best coordination with benchmarking processes. Establish working agreement with ICES web designers for delivery of ToR b.
Year 2	Focus primarily on ToR b and assess personnel commitment and feasibility of ToR c.
Year 3	Complete the first version of ToR c.

Supporting information

Priority	Understanding stock structure is a fundamental requirement before any assessment or modelling of a stock level can be contemplated. SIMWG
	liaises with ICES expert groups and working groups on stock identifica-
	tion issues and continues to review new methods as they develop.
Resource requirements	SharePoint website and clear feedback from expert groups, SCICOM and SSGSUE is pivotal for the efficacy of SIMWG.
Participants	The Group is normally attended by some 10-12 members and guests.
Secretariat facilities	Access to SharePoint to all members and Chair-nominated guests.
Financial	As per previous years.

Linkages to ACOM and groups under ACOM	As per previous years.
Linkages to other committees or groups	NWWG, WGWIDE, WGDEEP. WGAGFM, WGNEW, WKFLAT, WGSPEC, WGBAST, WKPELA
Linkages to other organizations	There are no obvious direct linkages, beyond the SIMWG members' affiliation and commitment to their own employers