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Executive summary

The Stock Identification Methods Working Group (SIMWG) met at the von Thünen Institute of Sea Fisheries in Hamburg, Germany, from 12–14 August 2013. It was attended by five delegates, plus one working by correspondence.

The agenda comprised three main Terms of Reference:

- a) Recent advances in stock identification methods, with a particular emphasis on technological and conceptual progress in tagging approaches;
- b) Reviews and advice on matters of Stock Identification, which specifically focused on the three tasks below:
 - i) Advice on stock structure of turbot, dab and brill in the Baltic Sea
 - ii) Evaluation of stock identity of anglerfish in ICES and adjacent areas and proposed new methodologies for future studies
 - iii) Considerations on the role of genetic markers under directional selection in stock identification analysis;
- c) A systematic appraisal of the terminology used in the field of stock identification.

On the back of the publication of the second edition of the book *Stock Identification Methods* (autumn 2013), a Theme Session proposal has also been submitted to the ASC 2014 committee, hoping to create an interdisciplinary forum on stock identification.

The second three-year term of the current SIMWG Chair has been fulfilled, so the EG has also come to the unanimous decision to propose Dr Lisa Kerr, of the Gulf of Maine Research Institute, USA, as the SIMWG Chair for the 2014, 2015, 2016 term.

1 ToR a) - Recent advances in stock identification methods, with a particular emphasis on technological and conceptual progress in tagging approaches

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, otolith research, and other approaches (e.g. tagging, morphometrics, etc.).

1.1 Genetics

In 2013, a sharp increase was recorded of papers focusing on "new" molecular genetic approaches, such as SNPs, functional genes, and transcribed regions-associated microsatellites. Most of the new findings still focus on "flagship" species, for which biological knowledge and genomic resources are substantial.

In cod (*Gadus morhua*), for instance, Bradbury *et al.* (2013) have identified 'genomic islands' in which SNP polymorphisms are most pronounced, suggesting that these regions may be associated with ecological adaptation in response to diversifying selective agents. Therkildsen *et al.* (2013) have also used SNPs to resolve fine scale cod population structure in Greenlandic waters, detecting different temporal changes in habitat use in different stock components, as well as pinpointing potential adaptive polymorphisms that may help examining future trends in stock movements in response to environmental changes. Ross *et al.* (2013) have furthered the understanding of haemoglobin sequence variation in relation to physiological traits and geographical structure.

Expressed sequence-associated microsatellites have also been used to determine substructure and potential diversifying selection in Baltic herring, *Clupea harengus* (Teacher *et al.*, 2013). Candidate gene-associated SNPs have been devised to study the genomic basis of variation in life history traits in sole, *Solea solea* (Diopere *et al.*, 2013).

One more significant finding, which is relevant to the stock perception of valuable resources in ICES areas, is the discovery of a depth-associated and phenotypecorroborated genetic break (at both nuclear and mitochondrial markers) in the south-Atlantic *Sebastes oculatus* group, which is suggestive of potential incipient speciation (Venerus *et al.*, 2013), and which strikingly mirrors recent, and highly debated findings in north-Atlantic *Sebastes mentella* (ICES, 2011).

An exhaustive review on population and evolutionary genetics applications to fisheries management has also just been published in the journal *Fish and Fisheries* (Ovenden *et al.*, 2013), which may be found very useful by a broad range of researchers and managers within the ICES community.

1.2 Otolith shape

The analysis of morphometric outlines of calcified structures in fish, such as otoliths and scales, continues to represent a standard stock identification method that has been widely used on a variety of species in several areas in the recent year.

In the ICES area, for example, Benzinou *et al.* (2013) used three otolith shape classification methods on striped red mullet (*Mullus surmuletus*) in the North Sea and Northeast Atlantic and found three geographical zones: the Bay of Biscay, a mixing zone composed of the Celtic Sea and the Western English Channel and a northern zone composed of the Eastern English Channel and the North Sea. Paul *et al.* (2013) investigated otolith shape of Baltic cod and reported on good separation of the Eastern and Western Baltic cod stocks.

The impact of genetic structure, environmental conditions and life history on otolith shape remains to be carefully studied. Vignon (2012) specifically addressed changes in otolith morphometrics during ontogenetic development and habitat shifts.

1.3 Otolith microchemistry and isotopes

Using otolith microchemistry, Heidemann *et al.* (2012) were able to separate the two Baltic cod stocks and North Sea cod. Further discrimination of individuals caught in three different spawning grounds of the eastern Baltic, however, was not possible.

Martin *et al.* (2013) analysed otolith elemental and strontium isotope signatures of Atlantic salmon (*Salmo salar*) in French rivers as natural tags for determining natal origins of juveniles and adults and relative contributions of natal sources to the population.

In the Pacific, Gao *et al.* (2013) used stable oxygen and carbon isotopes in otoliths to investigate stock structure of canary rockfish (*Sebastes pinniger*), suggesting a single stock along the Washington and Oregon coasts. For Pacific halibut (*Hippoglossus stenolepis*), however, Gao (2012) found significant differences between Puget Sound and the Washington coast by utilizing the same technique.

Woodson *et al.* (2013) examined the relationship between pelagic juvenile rockfish off California and their environment in an open coastal system, using a geospatial technique to relate water and otolith chemistries.

D'Avignon and Rose (2013) used growth rate and otolith elemental fingerprints to distinguish Atlantic cod from 4 spawning areas in Newfoundland and Labrador.

Tanner *et al.* (2012) utilized the chemical composition of otolith core and edge material of European hake to track movement of fish between local populations within the Atlantic and Mediterranean Sea.

Confounding effects on otolith chemistry still have to be studied carefully before drawing conclusions about elemental signatures attributable to stocks. Heagney *et al.* (2013), for instance, found significant effects of parasitism by a blood-feeding isopod on the otolith chemistry of the host fish.

1.4 Morphometry and Life History

Compared to otolith outline analysis, classic body morphometrics and meristics have been used to a much lesser degree, in recent times. In the ICES area, McAdam *et al.* (2012) analysed morphological descriptors of the head, fins and body of Icelandic cod, and found that these are correlated with sex, location, and genotype of the fish at the pantophysin (pan-I) locus. Their results suggest that morphology is more useful for distinguishing sympatric genotypes but less powerful at identifying genetically distinct geographic subpopulations, perhaps because counter-gradient evolution reduces phenotypic differences even with an underlying genetic cause.

Along the eastern coast of North America, Cronin *et al.* (2013) have shown that by using 10 morphometric descriptors, it is possible to rapidly and inexpensively identify alewife (*Alosa pseudoharengus*) from Maine or Massachusetts spawning stocks.

Life history traits continue to represent an insightful tool to pinpoint ecologically relevant features to corroborate stock subdivisions and investigate potential for local adaptation. McElroy *et al.* (2013) provide an interesting example, comparing fecundity and spawning strategies in three stocks of winter flounder (*Pseudopleuronectes americanus*).

1.5 Parasites

Among the most recent studies on parasites as biological tags of fish, the study of Cañas *et al.* (2013) examined a parasitic copepod in anglerfish (*Lophius piscatorius*) and reported on significant differences between areas in the Northeast Atlantic. The highest infestation levels were recorded in the West of Ireland and on the Porcupine Bank, and within these areas, the parasite load increased with latitude.

By studying endoparasites of horse mackerel (*Trachurus picturatus*) from the Madeira and Canary Islands, Costa *et al.* (2013) identified parasite species that are useful as population markers.

MacKenzie *et al.* (2013), investigated protozoan and metazoan parasite fauna of hoki (*Macruronus magellanicus*) in the Southwest Atlantic and Southeast Pacific, and found parasites of potential value as biological tags for stock identification and migrations. Oliva (2013) reported on *Anisakis simplex* s.l. as suitable biological marker for stock identification of Araucanian herring, *Strangomera bentincki*, from Chile.

1.6 Combination of techniques

The use of different stock identification methods in the same investigation is becoming an increasingly frequent approach, through true analytical integration of multidisciplinary data remains a largely unattained quest.

Trella *et al.* (2013) investigated pelagic beaked redfish (*Sebastes mentella*) through morphometrics, meristics and biological characteristics and reported on differentiation of shallow (300–450 m depth) and deep (550–800m) layers of the Irminger and Labrador Seas.

Papetti *et al.* (2013) integrated the analysis of fisheries data, population genetics and otolith chemistry to investigate the population structure of Atlantic mackerel (*Scomber scombrus*) in the Adriatic Sea (Mediterranean). Their results strongly suggest that Atlantic mackerel perform an autumn-winter migration from the northern to the central Adriatic Sea to reach a single spawning ground, and that a single population is present in this area.

A combined analysis of otolith chemistry and genetic diversity of conger eels in the northeastern Atlantic suggested a high degree of connectivity during the larval phase and limited connectivity during benthic life stages (Correia *et al.*, 2012).

Using geometric morphometrics, Pérez and Fabré (2013) studied the skull and otoliths of tiger catfish (*Pseudoplatystoma metaense*) to identify population structure in the Orinoco basin, Venezuela.

Zischke *et al.* (2013) combined morphometrics and parasite loads for the investigation of stock structure of wahoo (*Acanthocybium solandri*) in the western and eastern Pacific and eastern Indian Oceans.

1.7 Connectivity and migration

A recent paper by Frisk *et al.* (2013) highlights the need to consider the significant role of adult movements in determining population connectivity, using a skate and a flat-fish as case studies.

A couple of recent studies dealt with connectivity and migration of fish, using various markers. Ashford *et al.* (2012) used a multidisciplinary approach incorporating otolith chemistry, age data, and numerical Lagrangian particle simulations and indicated a single, self-recruiting population of Antarctic toothfish (*Dissostichus mawsoni*) in the Southeast Pacific Basin and Ross Sea, with a life history structured by largescale ocean circulation.

Hanson *et al.* (2013) reconstructed marine life-history strategies of wild Atlantic salmon from the stable isotope composition of otoliths. Otolith chemistry of sole (*Solea solea, S. senegalensis*) was used by Tanner *et al.* (2013) to determine the estuaries of origin off the Portuguese coast.

Moore *et al.* (2012) studied temporal and spatial patterns in parasite assemblages to evaluate the degree of movement and connectivity of post-recruitment life-history stages of king threadfin (*Polydactylus macrochir*) from northern Australia.

With regard to artificial chemical marking of otoliths, several publications reported on successful applications (e.g. Hobbs *et al.*, 2012; Huelga-Suarez *et al.*, 2012; Wood-cock *et al.*, 2013).

1.8 Tagging

The forthcoming new edition of *Stock Identification Methods* (Cadrin *et al.*, 2013) will include a substantial amount of new perspectives on tagging approaches, with contributions from David Hall, Greg DeCelles, Doug Zemeckis, Ben Galuardi, Tim Lam, Carl Schwarz, and Steve Cadrin. Here we provide a synopsis of the main topics examined.

Electronic and conventional tagging methods continue to advance at a rapid rate, and several new developments are promising for stock identification. Traditional tagging methods still offer new insights to basic life history and movement. For example a 45 cm and 3.7 kg Red Steenbras (*Petrus rupestris*) tagged in South African marine waters with a plastic tipped dart tag by Bruce Mann in 1989 as a young scientist was recaptured 21.3 years later in 2011 as a 115 cm and 17 kg specimen (Mann 2012). Similarly, a 50 cm southern bluefin tuna double tagged in 1990 by CSIRO was recaptured 21 years later as a 185 cm, 124 kg fish somewhere off Indonesia. New materials and coding methods for external and internal tag types include conventional plastic/metal tags, coded wire tags, visible implant tags and radio frequency identification tags.

Developments in acoustic and radio telemetry, including new tags, receiver array designs, triangulating technology and transmission of archival data have revealed new information on the behaviour and migration of fish and invertebrate species. For example, business card tags are capable of transmitting their own acoustic signal, as well as receiving and storing information from acoustic signals that were transmitted by other tagged individuals (Cooke *et al.*, 2011). Large-scale arrays enable fishery scientists to expand the geographic scope of their research beyond what would typically be possible under a single study's operating budget. For example, the Pacific Ocean Shelf Tracking network maintains an array of over 400 acoustic receivers that spans over 3,000 km along the west coast of North America from California to Alaska (Jackson, 2011). The development of passive monitoring systems has permitted inves-

tigation of fine-scale movements by calculating high-resolution positions of tagged individuals. Examples of such systems include Vemco's Radio Acoustic Positioning (VRAP) system (Klimley *et al.*, 2011) and the recently introduced VR2W Positioning System (VPS; Andrews *et al.*, 2011; Espinoza *et al.*, 2011).

Satellite telemetry and associated geolocation techniques also offer new insights into behaviour and movement patterns, including new hardware and software. Satellite tags are now being made much smaller. A recent example of pop-up satellite tagging was an investigation of spawning migrations of American eels (*Anguilla rostrata*; Béguer-Pon *et al.*, 2012). An example of the decreasing size of satellite tags is the tagging of hatchling loggerhead turtles (*Caretta caretta*), tracked from nesting beaches using solar powered satellite linked radio transmitters as small as 5g (Mansfield *et al.*, 2012).

New statistical models are also being applied to conventional and electronic tags to study movement, including hidden Markov models (e.g. Pedersen *et al.*, 2011), state-space models of individual trajectories based on continuous-positional information (e.g. McClintock *et al.*, 2012) and integrating movement and tagging observations into conventional stock assessment models (e.g. Goethel *et al.*, 2011).

2 ToR b) – Reviews and advice on matters of Stock Identification

2.1 Stock structure of turbot, dab and brill in the Baltic Sea

2.1.1 Turbot (Scophthalmus maximus)

The WKFLABA 2010 (ICES, 2010) concluded that turbot should be treated as several local stocks, despite there being insufficient data to accurately define the boundaries of these different stocks. New information for turbot was available at the WKFLABA 2012 (ICES, 2012). A study by Nissling *et al.* (2012) showed a significant difference in fecundity between ICES Subdivisions SD 25 and SD 28 with higher size-specific fecundity in the latter.

Based on the genetic differences along the salinity cline in the waters west of Sweden (Nielsen *et al.*, 2004), SIMWG concludes that there is reason to assume stock structure in Division IIIa, with a pragmatic separation line following the border between SD21 (Kattegat) and SD 20 (Skagerrak). Furthermore, differences in size specific fecundity coupled to salinity (Nissling *et al.*, 2012), and tagging studies showing high spawning site fidelity (Florin and Franzen, 2010), both point to potential stock substructure in the eastern Baltic, with another pragmatic line of population separation between SD 25/26 to the south and SD 27/28 to the north. The pattern of genetic differentiation between the Baltic Sea and the Kattegat, with a hybrid zone in SD 22 (Nielsen *et al.*, 2004), could not be reproduced by a similar study conducted three years later (Florin and Höglund, 2007). SIMWG therefore awaits further studies on turbot population structure in the Baltic and Div. IIIa; however, it seems parsimonious at this stage to follow the above-described delineations. In order to formulate more robust and definitive advice, there is a need for new, coordinated multidisciplinary studies (e.g. genetic markers + tagging); as well as rigorous comparative studies on fecundity.

2.1.2 Dab (Limanda limanda)

In WKFLABA 2010, three stocks of dab in the Baltic Sea were suggested; one in Öresund (SD 23), one in the Belt Sea (SD 22 plus western part of SD 24) and one in the Arkona and Bornholm basin (eastern part of SD 24 plus SD 25). The rationale for this was based on two studies. One by Temming (1989a), which showed that meristic characters and tagging experiments supported that dab in the Belt Sea and in the western part of the Arkona Sea, south of Mön, were differentiated from dab in the Bornholm basin. The second study revealed that salinity requirements for successful egg development, as well as neutral egg buoyancy, differed between dab from the Öresund straits and from the Bornholm basin (Nissling et al., 2002). Although there were no direct comparisons between Öresund and the Belt Sea, these were treated as separate stocks following the precautionary principle where it is assumed that merging of separate stocks can have a much more negative impact on preservation of the stocks than erroneous splitting of a continuous stock. In WKFLABA 2012 the number of stocks identified was reduced to two, merging the dab in Öresund and the Belt Sea. This was done based on the suggested stock structure of plaice (Pleuronectes platessa) by WKPESTO 2012 (ICES, 2012b).

SIMWG revisited the literature and found evidence of a previous eastern Baltic stock yielding up to about 2500 t annually from the Baltic proper in the early 1900s, and abundance maps from surveys showing a widespread population in SD 25, indicating a population maximum in the middle of the area (Figure 1).

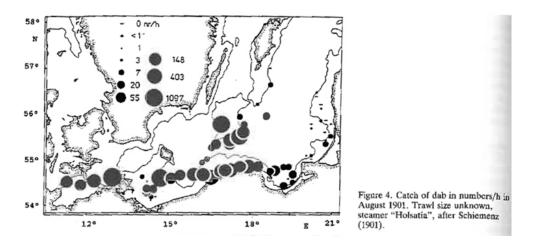


Figure 1. Dab catch data in the Baltic at the turn of the 20th century (from Temming, 1989b).

The mark-recapture study, with some meristic references (Temming, 1989a), shows possible differentiation, and no obvious connectivity, between SD 25 and the more western dab aggregations. The physiological studies by Nissling *et al.*, (2006) show indications of ecological adaptation to salinity for egg buoyancy and sperm activity, which, despite limited sample size and a sample stratification not ideally suited for population studies, could support the existence of a population component east of the island of Rügen. Furthermore, Trautner and Schmidt (2004) in a genetic study of dab population structure in the North Sea, western Baltic and the Norwegian west coast using AFLP methodology pooled their three stations from the western Baltic, two from SD22 and one from the area north of Rügen in SD24. The eastern station was close to the two western stations in the study by Nissling *et al.* (2006).

The SIMWG therefore support a dab population structure with a north–south separation line east of Rügen e.g. at about 13°30′E.

2.1.3 Brill (Scophthalmus rhombus)

In previous reviews by WKFLABA 2010 and 2012 (ICES, 2010; 2012) it was not possible to find any information on stock structure of Brill in the Baltic. Despite our efforts to identify studies targeting brill in the Baltic, we were unable to obtain any data; thus, SIMWG cannot provide any informed advice on the stock delineation of this species in this area.

2.2 Evaluation of stock identity of anglerfish in ICES and adjacent areas with proposed new methodologies for future studies

SIMWG was asked to evaluate the previous stock identity studies on anglerfish in the ICES and adjacent areas and the proposed new methodologies for future studies by the benchmark workshop on Flatfish species and Anglerfish (WKFLAT, 2012).

There are two species of Anglerfish co-occurring in the Northeast Atlantic, the black anglerfish (*Lophius budegassa*) and the white anglerfish (*Lophius piscatorius*). ICES assumes three different stocks for management and assessment for both of these species:

- 1) The northern shelf stock consisting of Anglerfish in Division IIa (Norwegian Sea), Division IIIa (Kattegat and Skagerrak), Subarea IV (North Sea), and Subarea VI (West of Scotland and Rockall)
- 2) The northern southern shelf stock consisting of Anglerfish in Divisions VIIb-k and VIIIa,b,d
- 3) The southern southern shelf stock consisting of Anglerfish in Divisions VIIIc and IXa

Advice is given for these three different areas for both species combined and with the exception of the northern southern shelf stock also the assessment is made on both species combined. However the biological support for these three stocks has been deemed insufficient (WKFLAT, 2012).

Several studies that potentially could be used to infer population structure for the *Lophius sp* exist. Crozier (1987) using allozymes found that white anglerfish could be treated as a panmictic unit within the Irish Sea but that they were different from Western Scotland. However the differentiation of a single sample could have been, even according to the author, driven by small sample size. Charrier *et al.* (2006) used mtDNA in both species and found evidence of a differentiation between Mediterreanen and Atlantic samples for the black anglerfish, and no substructure within the Atlantic samples for neither species. It might be argued that mtDNA is not sufficiently variable to detect fine scaled substructing.

Blanco *et al.* (2008) using the more variable microsatellites, in samples from a gradient spanning the British isles down to the Mediterranean, revealed a clear differentiation between Mediterranean and the rest, for the black anglerfish, and also a differentiation between Spanish and Portuguese samples but no differentiation within the rest of the samples and no isolation by distance pattern. For the white anglerfish there were no samples from the Mediterranean but among the rest, only the sample from the French Atlantic coast proved significantly different. The reason for the deviance is unknown but could, according to the authors, be due to chaotic genetic patchiness (Blanco *et al.*, 2008).

Another study using microsatellites in white anglerfish was focused on the Northern shelf, but also included samples from the Bay of Biscay and the Mediterranean (O'Sullivan, 2009). It revealed significant differentiation between the Mediterranean and the rest but not within the Atlantic samples. Overall, the genetic studies show no consistent population structure within the Northeast Atlantic for any of the species, but a clear differentiation between the Atlantic and the Mediterranean anglerfish.

The absence of clear, stable population structure of anglerfish within the Northeast Atlantic is also supported by a recent study using otolith shape analysis, to test for differentiation of white anglerfish from the three ICES units, represented by samples from the North Sea, western Ireland and southern Bay of Biscay (Canjas *et al.*, 2012), where no evidence of substructuring was found.

In the same way, meristic characteristics (number of fin rays) were not able to discriminate between samples in the southern shelf area for any of the species (Duarte, 2004). However, in the same study, morphometric variation showed for the white anglerfish a separation of samples in western Ireland, western France and northern Spain. For the black anglerfish, among samples from the same areas, plus southern Portugal and the Mediterranean, revealed that the largest difference between the southern Portugal and western France sample (Duarte, 2004). Anglerfish were previously believed to show a stationary behaviour, which would favour the existence of several subpopulations; however, tagging studies have shown that adults are capable of moving quite long distances and that movements occur between the three defined management units. The tagging experiment performed by Laurensen *et al.* (2005), in the Shetland islands, showed that only 35% of white an-**glerfish individuals were recaptured less than 25 km from the release positions, and** two individuals made a long distance movement - one to the Faroe islands and one to Iceland, nearly 900 km from the release locations. Tagging along the southern shelf area from western Ireland to southern Portugal of both white and black anglerfish between the years 1995 and 2004 (Landa *et al.*, 2008) showed movement between the southern and northern stocks for both species, as well as a movements between the northern south shelf stock and the northern shelf stock. Maximum displacement was 408 km by a black anglerfish from the south to the North of Biscay. The tagging was done in the feeding season and the longer movements could be part of a spawning migration to deeper areas (Landa *et al.*, 2008).

Additional factors that may contribute to population mixing is that anglerfish are highly fecund, and have a highly pelagic larval stage, with long durations (three months) and high dispersion (Hislop *et al.*, 2001).

In conclusion, the current management areas identified by ICES are not supported by any of the studies reviewed. In fact, overall, genetic studies, otolith shape and meristic characters suggest no population structuring within the Northeast Atlantic for either white anglerfish or black anglerfish. Considerable adult movement together with high dispersal of larvae are probable cause for the lack of population structure. Morphometric differences between areas may suggest a substructuring in the southern shelf area; however this needs to be confirmed by other markers.

SIMWG therefore recommends that:

- species should be recorded separately to allow for separate assessment.
- The current assessment units have no biological basis.
- In order to identify adequate units there is a need for future stock structure studies with:
 - Exhaustive sampling design covering the whole area, several seasons, and made during spawning time.
 - Collection fisheries and biological data such as species, sex, maturity, length, weight and age.
 - Use of a multidisciplinary approach, for example using powerful genetic markers, otolith chemistry and microstructure, parasites, artificial tags, hydrographic modelling, and a careful grounding of any morphometric data in explicit environmental characterization.

2.3 Considerations on the role of genetic markers under directional selection in stock identification analysis

WGAGFM (ICES, 2013) requested that SIMWG consider the role of genetic markers "under directional selection" in stock identification. As also pointed out in this report (see Section 1.1, page 2), novel markers of a putatively adaptive nature are becoming increasingly employed, and are offering new insights into population biology. SIMWG therefore sees these applications as valuable additional tools, to complement the array of methods available for stock identification analysis.

However, like every method, this approach also should be used with a full awareness of its powers and pitfalls, and, most importantly, should be matched with the appropriate questions. Here we highlight a few points that must be considered, in relation to genetic markers "under directional selection" (see Figure 2 for a graphical synopsis). A more extended discussion on this and related topics can be found in a forthcoming chapter of the new *Stock Identification Methods* book (Mariani and Bekkevold, 2013).

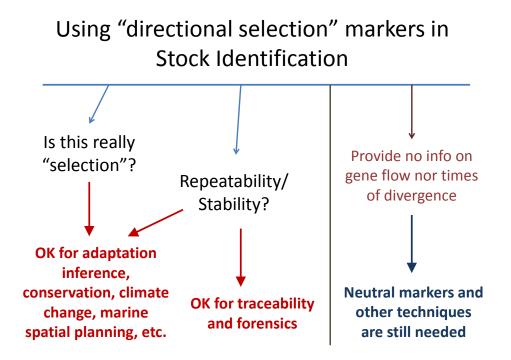


Figure 2. Summary diagram that synthesizes the applications and caveats of genetic markers under directional selection (see text for explanations).

- 1) A first key aspect is to test for repeatability and temporal stability of the patterns yielded through these markers. Since adaptive changes are less predictable than neutral evolution, this is a particularly important point; but if repeatability and temporal stability can be ensured (Nielsen *et al.*, 2012), these markers can be very powerful in population assignment and market traceability analysis.
- 2) The second key point relates to the presumed role of natural selection in determining such polymorphisms. Anonymous SNPs with a "non-neutral" pattern of variation can be identified on a statistical basis, but that does not

automatically imply that they truly reflect the action of natural selection. If additional functional genomic studies and quantitative genetic experiments are conducted to ascertain the adaptive role of these markers, then their application can be enhanced and expand to the arena of conservation biology (e.g. response to climatic changes, identification of evolutionarily significant units, etc.)

3) The final important consideration refers to the applicability realm of adaptive markers. Once the role of natural selection is established, these markers have no use in the investigation of gene flow and genetic drift; therefore other markers will be necessary to estimate degrees of connectivity, isolation, timing of coalescent events, effective population size, etc.

3 ToR c) - A systematic appraisal of the terminology used in the field of stock identification

Stock identification is an inherently eclectic endeavour, which draws strength from expertise of scientists with often remarkably different background and philosophies. As a consequence, much of the terminology used by certain researchers may sound obscure, or even ambiguous, to other practitioners,

Here we intend to present a first draft of a tool that we intend to develop in a more robust and exhaustive fashion, as part of a "multi-annual" term of reference. This "glossary" must, at this stage, be viewed as a 'draft', with ample possibilities of revisions. However, the longer-term aim is to resolve doubts and discrepancies in relation to terminology use, and eventually promote a more consistent and unequivocal language to assist effective communication among stock identification professionals, and the ICES community as a whole.

- <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>Colonization</u>: the process of establishment of a new subpopulation in a given spatio-temporally 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 linkage among biological units or habitat patches (for instance between life-history stages).
- **<u>Contingent</u>**: A group of fish that co-occur in space and time and adhere to the same behavioural pattern.
- <u>Deme</u>: A local randomly mating genetic subunit within a species or biological population.
- <u>**Dispersal**</u>: The movement of individuals between one place to another. It can take place either passively (mostly in early life stages) or actively (mostly in juveniles and adults).
- <u>Entrainment</u>: socially transmitted behaviours that have been suggested as a key factor to maintain spawning site fidelity.
- <u>Hardy-Weinberg Equilibrium (HWE)</u>: the condition under which the allele and genotype frequencies in a population will remain constant, assuming large random-mating 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.
- <u>Introgression</u>: 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 popula-

tions rather than from distant ones. This model is expected to result in a positive correlation between geographic distance and genetic divergence.

- <u>Local extinction</u>: the extirpation of a subpopulation.
- <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.
- <u>Member-vagrant model</u>: 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 subpopulations.
- <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.
- <u>Natal homing</u>: A return migration of sexually mature individuals to spawn upon the grounds where they were spawned. Natal homing behaviour is expected to result in population differentiation, as long as there is no change of spawning season.
- <u>Natural selection</u>: 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.
- <u>Open/closed populations</u>: Represent the degree of connectivity among biological populations, in a continuum between almost complete panmixia, to very low degrees of effective migration.
- <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>
- <u>**Philopatry</u>**: Fidelity to parental spawning sites either by natal homing and/or retention of early life stages.</u>
- <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 behavioural mechanisms through which early life stages are prevented from dispersing too far from the area of their release.
- <u>Spatial/temporal overlap</u>: 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, winter and/or spring-spawning populations).
- **Spawning component (group, aggregation)**: A group of individuals of a population that utilize a single spawning ground at the same time.
- <u>Spawning site fidelity</u>: 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.
- <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</u>: An exploited fishery unit. A stock may be a single spawning component, a biological population, a metapopulation, or comprise portions of these units. 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>Straying</u>: Occurs when individuals move to and join a spawning aggregation different from the one they had originated in.
- <u>Subpopulation</u>: A single, mostly self-sustaining unit within a metapopulation.

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Annex 2: Recommendations

Recommendations	For follow up by:
1. Submit ASC theme session (book)	ACOM, SCICOM
2. Turbot in the Baltic Sea should be parsimoniously treated as 3 stock units: one North of SD 21; one between SD 21 and SD 26; and one North of SD 26	WKBALFLAT,WGBFAS, SSGSUE, SCICOM ACOM
3. Dab in the Baltic Sea should be parsimoniously treated as 2 units, with a separation break at 13°30' East.	WKBALFLAT, WGBFAS, SSGSUE, SCICOM ACOM
4. No data are available to provide any advice on brill.	WGBFAS, SSGSUE, SCICOM, ACOM
5. The two species of anglerfish should be assessed separately. SIMWG finds no support for the currently existing 3 NE Atlantic groups. New robust data are required to formulate better advice.	AFWG, WGCSE, WHMM, SSGSUE, SCICOM, ACOM
6. SIMWG is in favour of the application of new genetic markers under directional selection, but also highlights the need to maintain and refine the use of neutral markers and other approaches to investigate population connectivity and genetic drift.	WGAGFM, SIMWG, SCICOM
7. SIMWG requests that the Secretariat communicate with advance about Benchmark processes, so that SIMWG advice can be provided in advance.	SSGSUE, SCICOM, ACOM
8. SIMWG proposes Lisa Kerr as new Chair.	SCICOM, ACOM

Annex 3: SIMWG terms of reference for the next meeting

The **Stock Identification Methods Working Group** (SIMWG), chaired by Lisa Kerr*, USA, is expected to organize a physical meeting, the details of which will be communicated after a brief consultation, and once the Chair will be officially elected by SCICOM.

SIMWG will report on the activities of 2014 (the first year) by Date, Month Year to SSGXX.

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 c) Regular communication 	Action 1.2.1	3 years (and continued)	EG report, and contribution to ICES ASC 2014
b	Build a reference database 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 	?	3 years	Web pages and downloadable ICES CRR
с	Develop a universal framework for consistent usage of terminology relevant to stock identification	a) Personnel commitment b) Feedback on usefulness of the task c) communicate "top" working terms	?	1 year	Perspective/Review paper in international academic journal
d	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 prioritize c) communication of new findings	?	2 years	EG report and contribution to ICES ASC 2014, and methodological paper in international journal

Year 1	Organize a physical meeting with the new Chair, trying to identify a period of the year that would allow best coordination with benchmarking processes. Attempt to work by correspondence towards the preparation of the "glossary" draft. Work on Theme Session for ASC2014, if approved.
Year 2	Establish working agreement with ICES web designers for delivery of ToR b. Strengthen and consolidate agreements for all tasks, even if working by correspondence.
Year 3	Focus primarily on ToR b.

Summary of the Work Plan

Supporting information

Priority	Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock level can be contemplated. SIMWG liaises with ICES expert groups and working groups on stock identification issues and con-tinues 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	WGNEW, WGDEEP, WGEF, WGAGFM, WKFLAT.
Linkages to other organizations	There are no obvious direct linkages, beyond the SIMWG members' affiliation and commitment to their own employers.