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Report of the Working Group on the Application of Genetics in Fisheries and Mariculture (WGAGFM)

5–7 May 2010

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Executive summary

The Working Group on the Application of Genetics in Fisheries and Mariculture (WGAGFM) met in Cork, Ireland, 5–7 May 2010. The meeting was very well attended; with a total of 19 representatives present from 8 countries. In addition a number of master and PhD students were attending parts of the meeting

Due to the very difficult situation with the volcano eruption in Iceland, some of the proposed attendance were not able to get to Ireland, and this had a big impact on the meeting as several of the ToRs had to be postponed to next year. The group did focus on the request from OSPAR (2010/3) – ToR(f), as well as discussing the other ToRs even though the leads were absent.

It was decided that three of the ToRs (a–c) could not be presented in this report, and will be transferred to 2011meeting in Bangor, while a report on ToR d) is included in the report despite the absence of the "leaders".

The value of creating a meta-database to catalogue species-specific data on fish and shellfish population genetics relevant to conservation and fisheries management was identified in the 2006 and 2007 ICES WGAGFM reports. The benefits from such a web-based meta-database arises from the large number of scientific research projects on fish and fisheries genetics that have been carried out in Europe and worldwide whose data sets are not widely known or accessible. This means these data sets are often less than optimally exploited something that constrains the realisation of the potential for exploiting molecular genetic tools in fish stock conservation and management. To make a significant advance over existing meta-data gathering tools the meta-database will have to provide a comprehensive, accurate listing of published, unpublished and in-progress data sets and allow the meta-data on these sets to be explored quickly and efficiently. The existence of such a database would do much to ensure a wider and more comprehensive exploitation of existing research by ensuring that existing information is taken into account in new research programmes and available for new types of analyses. It will also make it easier to generate wider ranging and potentially more informative population genetic analyses with existing data by facilitating data access and research collaborations. Furthermore, a properly implemented meta-database would facilitate the uptake of genetics into marine fisheries management, which only currently occurs to a very limited extent. In previous WGAGFM reports, a potential institutional framework for developing the meta-database, incorporating the web-crawler (JRC), hosting it (ICES), and running it (WGAGFM) have been identified. What is now required is to identify the human resource to carry out the final database design, implement it, and carry out the initial populating with the meta-information. Such a resource is unlikely to be realised at the national level and will most likely be able to be accessed through the funding of international bodies such as the EU, the IASRB (International Atlantic Salmon Research Board), or an international philantrophic organization.

The over-exploitation of traditional coastal stocks, the rising demand for seafood and technological advances in fisheries, have all combined to result in the shift of commercial fishing towards less-known, deep-sea species in many parts of the world. ICES define the term deep-sea fisheries as those fisheries that occur in depths greater than 400 m. The ToR e) summarize the available information about basic population genetics of deep-sea fish (such as population structure, effective population sizes and connectivity), suggests potential sources of present and future threats to these species, and identify research priorities and needs in relation to recent and future trends

in deep sea fisheries. Conservation measures are necessary and ignorance should not be used as an excuse for causing long lasting, even irreversible, degradation of the deep-sea ecosystem. Prior to any deep sea resource exploitation or dumping of waste (including CO_2 sequestration) rigorous environmental and genetic impact studies should be undertaken. As any conservation measures established for the deep-sea ecosystem could be slow to demonstrate significant results, appropriate initiatives, including the establishment of large no-take marine protected areas (to protect both habitat, target species, and non-targeted species) must not be delayed, and any lack of instant results should not be justification for discontinuing conservation initiatives. As most of the deep-sea is in international waters and not under national regulations it will be complex to establish regulatory frameworks that can be enforced. This lack of regulatory frameworks is a significant impediment to successful management and conservation of deep-sea resources, but it is paramount that efforts are made to establish such frameworks.

OSPAR requested that WGAGFM and other WG's provide the current state of knowledge on the interaction of finfish mariculture on the condition of the wild fish populations (both salmonids and non-salmonids) both at a local and regional scale. The WGAGFM concentrated on escaped fish and how interactions with escapees might change as result of an expansion of mariculture activities. OSPAR also suggested that this should be addressed through a risk analysis approach.

Potential risks associated with translocation of marine finfish arise from introduction of pathogens and parasites new to an area, and genetic shift in natural populations through hybridization with reared individuals. With increasing threats to natural populations, more focus is put on the possible importance of genetic differences among populations, especially differentiation between reared and wild populations. However, presently we have little data and the models are not robust enough to be able to evaluate the vulnerability and eventual limits for such anthropogenic changes. The possible effect from an interaction between farmed and wild individuals are dependent on a number of different parameters, such as genetic diversity, local adaptation, and the relationship between the number of farmed escapees and the wild conspecifics.

In order to perform a risk analysis of possible genetic interaction between farmed and wild conspecifics the models require information of at least four factors, However, most of the factors are species specific factors, making it virtually impossible to standardize a risk assessment tool for possible genetic interaction between farmed and wild fish. The recommendations made are general and should be carried out for any marine finfish put in farms in the marine environment. For the risk assessment each species must be treated separately but the issues are the same for each species. Reproductive sterility (all-female or triploids) is recommended as a future key to eliminating the genetic potential of escaped fish. This might be the only way to reduce the genetic impact from escapees to its wild conspecific. At the same time maintenance of robust populations of wild fish is recommended as a key to minimizing the effects of escaped fish on wild populations.

The WGAGFM is also proposing a theme session at the ASC in Poland 2011, Advances in the traceability of fish and fish products: from species to populations (see 2.7)

1 Opening of the meeting

The Working Group on the Application of Genetics in Fisheries and Mariculture (WGAGFM) met in Cork, Ireland from 5–7 May 2010. The ToRs were decided in the Council Resolutions adopted at the ICES Statutory meeting held in Berlin, Germany in 2009. Dr. Geir Dahle (Norway) chaired the meeting, which opened at 09:00 on Wednesday, 5 May and closed at 12:30, Friday, 7 May 2010.

1.1 Attendance

Nineteen persons from eight countries (Belgium, Canada, Denmark, France, Iceland, Ireland, Norway, United Kingdom) attended the meeting (Annex 2). The meeting was also attended by master and PhD students from University College Cork

1.2 Venue

The meeting was held at the Department of Zoology, Ecology and Plant Science, University College Cork, Cork, Ireland. The WG wishes to express their appreciation to the local host Dr. Tom Cross and the rest of his staff at the University and Department for their kind hospitality and assistance. The meeting venue was ideal with accommodation available in walking distance from the accommodation for the meeting. The venue had a big room with projector and also small meeting room for any group meetings.

1.3 Meeting Format

WGAGFM has an established framework for completing its ToRs. Prior to the meeting, small *ad hoc* working groups, under the leadership of one person, are established to prepare position papers related to specific issues in the Terms of Reference. The leader of the ToR is responsible for presenting the position paper in plenary at the meeting and chairing the discussion. Thereafter, volunteers undertake the task of editing and updating position papers according to points raised in the plenary discussions. The ToR leader is responsible for preparing the final report text from their sessions. Prior to the meeting an agenda is circulated to all members.

2 Adoption of the agenda

2.1 ToR a) Report on how to utilise genomic approaches to the study of adaptation of marine organisms in changing environments: what can populations tell us about genes underlying phenotypic and demographic changes and what can genes tell us about adaptive evolution of populations

Postponed to WGAGFM meeting in 2011

2.2 ToR b) Define genetic data needs and explore opportunities and requirements for the integration of genetic data resulting from the implementation of the EU data collection regulation (DCR 199/2008)

Postponed to WGAGFM meeting in 2011

2.3 ToR c) Review the issues and challenges associated with the utilization of SNPs as markers in population genetic studies with special attention to data handling and statistical tools

Postponed to WGAGFM meeting in 2011

2.4 ToR d) Pursuing the establishment of a meta-database cataloguing molecular data in the field of fish and shellfish population genetics

Eric Verspoor, Antonella Zanzi, John Gilbey and Jann Th. Martinsohn.

2.4.1 Rationale

The value of creating a meta-database to catalogue species-specific data on fish and shellfish population genetics relevant to conservation and fisheries management was identified in the 2006 and 2007 ICES WGAGFM reports. These highlighted the increasing recognition of the importance of intraspecific genetic diversity, to fisheries character and abundance, and of the potential for using molecular genetic information in fish management and conservation to help achieve sustainable exploitation. Recognising this, the reports argued that there were considerable benefits that would be realised of having a public website for facilitating rapid accessibility to such data by the research community and stakeholders in support of advancing understanding and the application of this body of knowledge in support of fisheries management.

The benefits from such a web-based meta-database arises from the large number of scientific research projects on fish and fisheries genetics that have been carried out in Europe and worldwide whose data sets are not widely known or accessible. This means these data sets are often less than optimally exploited something that constrains the realisation of the potential for exploiting molecular genetic tools in fish stock conservation and management. Currently, data produced by research projects are primarily exploited at the time of a study, to address specific questions or hypotheses by the groups involved, and results emerging from data analysis are to varying degrees published to address the specific study objectives. However, the primary data generated will often be highly valuable beyond the original research mandate (e.g. Verspoor *et al.*, 2005). This is particularly true as regards addressing new questions or facilitating the optimal development of new studies, future (fisheries management) applications, and innovations, as well as for providing historical reference data for assessing temporal change or when a species is examined with new markers or analytical technologies. The latter point becomes increasingly relevant with the current genetic and genomic technological revolution which is also entering fish genetics and conservation research (Primmer, 2009). Unfortunately, at present, when research projects are concluded, generated primary data tends to be forgotten and difficult to obtain, discouraging the integration of old and new data sets, and making it less likely new projects will be built on the foundations of existing work. The lack of a comprehensive catalogue of existing work increases the risk of data loss and is an impediment to the development of a more coherent approach to genetic fish and fisheries research.

These data management and access issues can to a large extent be remedied by the existence of an easily and publically accessed meta-data base for the research and fisheries management community, provided it is comprehensive, appropriately focused, and kept up to date. The value of a genetics meta-data base will be determined by the type, quality and comprehensiveness of the information it makes available relative to other meta-data gathering tools such as web based search engines, as well

as the ease with which it can be accessed relative to alternatives for obtaining the same information. Data provided must address the needs of the user community. Currently, as most data sets are associated with research and development work, this will largely be confined to scientists working on a particular species. However, applications for molecular markers in management emerge, data sets will become of increasing value to managers in support of fish stock monitoring and assessment, and assessing exploitation or tracking fish products.

2.4.2 Progress since 2009

Progress on the development of a meta-data base of fish population genetic data has been slow and hindered by the lack of resources. However, the value for research, fisheries management, and policy of having a fish and shellfish genetic meta-database is recognised by the research community and led the WGAGFM in 2009 to recommend continued efforts toward its development and implementation. In particular three key actions toward this end were set out:

1) Exploitation of a web-crawler tool under development as part of the EU **FishPopTrace** project (https://fishpoptrace.jrc.ec.europa.eu/home) by the ICES WGAGM should be considered

2) Identification of projects to be included in the Crawler development and consideration of using information generated as part of the ongoing EU **SALSEA-Merge** project, focused on the population genetics of Atlantic salmon, (http://www.nasco.int/sas/salseamerge.htm) as a single species meta-data model which could be used as a prototype for a future multi-species version; as part of this, a list of the type of data to be included in a future meta-database should be established;

3) Monitor developments in relation to the EU Marine Observation and Data Network (**EMODNET**) initiative and explore the possibilities of integrating fish and shellfish genetics at some stage into **EMODNET**.

The development of a practical data base prototype that has potential for application to a wide range of species requires focusing on two key issues:

- the information to be delivered and how it is accessed;
- the mechanisms for gathering, managing and updating information;

To make a significant advance over existing meta-data gathering tools the meta-database will have to provide a comprehensive, accurate listing of published, unpublished and in-progress data sets and allow the meta-data on these sets to be explored quickly and efficiently as to existing genetic information delivery systems such as GENBANK. It needs to do everything but provide access to the data itself though, where possible, it should provide links to web based data sets.

The viability of the meta-database will be determined by the efficiency and comprehensiveness, of the data gathering process, by the currency, and quality of the data, as well as by the degree of support from researchers in the field and other potential users. The former will to a large degree be dictated by available resources, which are at present limited, but also by the approaches taken to data gathering and entry, with the latter determined by the issues discussed in the previous paragraph. Significant resources are needed for setting up and hosting the database, and these will need to be found. In contrast, the resources needed for running and updating the database are likely to be less onerous, at least in the early stages until it becomes an established resource routinely exploited in support of national or transnational management

programmes. Thus in the early stages of development, the day to day running may be able to be sustained by the voluntary support of members of the user community; indeed, this will probably be essential given that funding for such activities is often difficult to obtain. As such, at this point, it will be important to ensure that there is the potential for a useful return on people's investment of their time from the database. This represents a significant challenge. One such return to contributors would be the increased possibility for developing intergroup collaborations (e.g. new projects or publications) using information gleaned from the integration of different data sets. Another is the increased visibility of projects, as well as their principals and stakeholders. These would be clearly indicated in the meta-database, and it would naturally serve as a dissemination platform for such information. However, as many approaches as possible will need to be developed to motivate contributors and these returns will need to be real and obvious to users and contributors.

2.4.3 Data types and Access

The focus of the meta-database needs to be efficiently providing comprehensive and sufficiently detailed information on existing and in-progress data sets for species of interest to fisheries scientists and managers. Most, if not all, genetic data sets will be molecular rather than dealing with quantitative trait variation, and focusing effort in this area is likely to be of greatest value and deliver the biggest return for the resources invested. However, where molecular data is linked to other types of biological information, this will be of considerable interest and enhance its value and should be catalogued as well.

In the fish and shellfish genetics field different molecular markers have been employed over the years (Kochzius, 2008) and various markers are used to address different questions (e.g. population genetics- microsatellites and increasingly SNPs; species identification-mitochondrial DNA), and sometimes genetic markers are used in combination with other markers (otolith microchemistry, protein analysis, fatty acid profiles etc.). Thus the key variables defining data sets will be the species and the type(s) of molecular data. However, the meta-data for each data set that will help users determine their value to them and are identified as being indispensible for inclusion in a prospective database are:

Data Set Designation					
Who	Institutions involved	Consortium Name (if applicable)	Contact	Country	Date of Entry/Update
What	Project Designation	Project Acronym	Project carried out from to	Project Website	Summary of Project Content
Target Species	Common Name	Scientific Name			
Sampling	Geographical Area Covered	Sampling Locations	Sample Sizes	Archived Yes/No	
Genetic Markers	Mitochondrial	Nuclear	Genetic Loci Screened		

Methods/Technologies	Length Polymorphisms; SSCP; Real Time PCR; Sequencing; DNA barcoding; microarrays; etc.			
Additional Markers	otolith microchemistry; fatty acids; proteomics; etc.			
Data Set Used	Publications	Projects		
Database	Available Yes/No	Format (SQL; MS Access; .xls, etc.)	Accessible via public webpage Yes/No	Database accessible via public webpage & password protected user account: Yes/No

This meta-data should be readily accessible through a public web site using a basic search engine. Ideally, the geographical locations to which data pertain should be able to be visualised, using GIS-applications or at least a link to Google Earth, It should also be possible to download or email the results of searches, or to cut and paste them into user defined files.

2.4.4 Gathering and Updating Meta-data

Different strategies can be considered for gathering meta-data and populating the data base. These include web-based data entry by individual researchers, employment on a paid or voluntary basis a database manager to carry out regular data searches using tools such as Web of Science, or internet search engines. Additionally, there is considerable scope for automating searches, at least in part, using IT tools such as a Web-crawler, and this approach is a focus of consideration in this ToR (see below). However, it should be noted though from the start that while the crawler tool can be very powerful for meta-data search and compilation of meta-data, it cannot substitute a true meta-database, since it relies on the availability of databases which are accessible through the Web. Additionally, as documented below, its efficacy is constrained by the fact that many projects have not been supported by web-based databases.

2.4.5 Web Crawler

The basic principle of this IT tool is explained in the WGAGFM report 2009. In short the project-crawler accesses databases of selected projects via their web pages each night and acquires as well as updates available information, which is than stored on a designated server. The end-user can query the information using a web-based menu. While the crawler development was initiated by Luca Arnaudo, who has in the meantime left the JRC team, it has been continued by Antonella Zanzi. The crawler is available online on https://fishpoptrace.jrc.ec.europa.eu/crawler. At the time of the writing the project-crawler includes two projects (www.fishtrace.org; www.pescabase.org), and the search menu just allows selecting a species of interest. The information displayed includes:

- Direct link to the project website
- Biology resume available
- Specimens used [number]
- Genetic markers used [number]

- Bibliographic references [number]

The current implementation is rather basic but demonstrates the principal feasibility. The next projects to be included are **Fish and Chips** (http://www.fish-and-chips.uni-bremen.de/); the **FishBol** database (www.barcoding.si.edu) and **SALSEA-Merge** (www.nasco.int/sas/salseamerge.htm). **Fish and Chips** has been chosen because it is an example of a project supported by a web-page accessible database, which however is password protected. It will be shown that the project-crawler can deal with such a scenario. The **FishBol** database which is fully integrated into the **CBOL** database has been selected since it is professionally curated and, thus, an ideal target to develop and test new applications. In parallel the JRC plans to improve the query menu (free text search, further search criteria) and the output display (more items and more detail).

Ultimately it should also be possible for end-users to add information manually (e.g. availability of historical archives: where/what/by whom). However any improvements will greatly depend on the availability of other projects, which can be included. This is a challenge as shown by Table 2.4.6.1, which lists a panel of research projects related to fish(eries) genetics. The minimal condition for a project to be included in the targets of the project-crawler is that the project database is accessible through the world-wide-web. This unfortunately does not appear to be the standard situation. Rather databases in all kinds of formats are stored locally, which exacerbates the data dispersal and loss problem. This highlights the importance of creating an incentive for academic institutions and research centres to strongly support projects on the IT level.
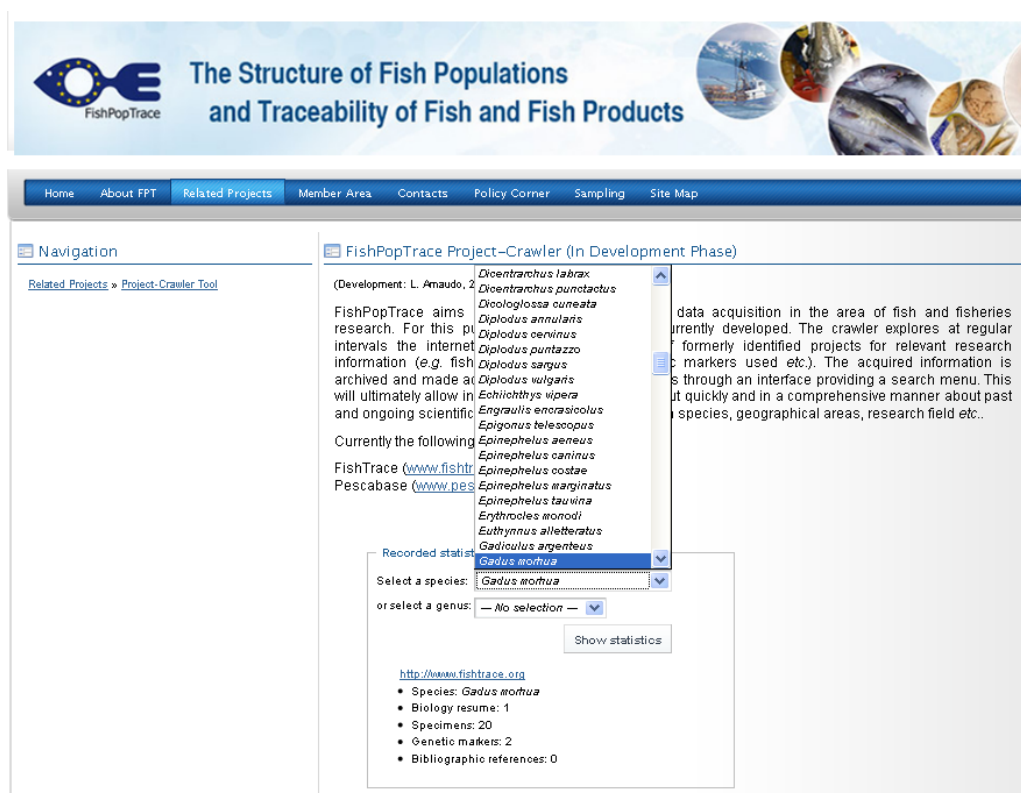
Figure 2.4.5.1. The Project-crawler Interface. The menu allows someone to select a species of interest for which meta-statistics on a variety of data in relation to identified projects are displayed. The underlying IT technology was explained and illustrated in the WGAGFM report 2009. For details see text.

2.4.6 Project Web-sites

A general "project inventory" is an indispensible first step to assess the current situation as regards crawler development and to identify challenges as well as identify solutions, of which one would possibly be an inclusion in the EU Marine Observation and Data Network initiative EMODNET (see below). Table 2.4.6.1 below lists a number of academic projects with content and potential to be accessed by the crawler tool. As described above the focus is currently on projects which have a potential to be included in the project-crawler. Unfortunately, the scope at present is limited with many databases not being accessible via the web and, ideally, non-academic databases from the industry should also be included. The latter tend to be intentionally excluded from public access. This could, however, be addressed by the EMODNET initiative as discussed below.

Table 2.4.6.1. Projects with relevance to fish and shellfish population genetics and their potential to be included in the web-crawler tool.

PROJECT	SUBJECT	DATABASE	FUNDED FROM/ TO	STILL SUP-PORTED	DB Accessible by Web-Interface	DB Accessible by Crawler	Contact
FishPopTrace https://fishpoptrace.jrc.ec.europa.eu	Fish population structure + traceability.	YES (Microchemistry, Gene Expression, Fatty Acids, SNPs, Proteomics)	2008-2011 (FP7)	YES (Last update: 2010)	YES	YES	Jann.martinsohn@jrc.ec.europa.eu
FishTrace www.fishtrace.org	Genetic Fish species identification	YES (CytochromeB Rhodopsine Biology)	2002-2005 (FP5)	YES (Last update: 2009)	YES	YES	Jann.martinsohn@jrc.ec.europa.eu
PESCABASE www.pescabase.org	Biological information useful for authentication and traceability of marine species	YES (Cytochrome b Biological data Species distribution)	Not Stated	YES (Last update: 2010)	YES	YES	info@pescabase.org solea@iccm.rcanaria.es
FishBol www.fishbol.org	Fish Barcode of Life Initiative. DNA barcodes, for species identification.	YES (at www.dnabarcodes.org)	Not Stated (Managed under the Barcode of Life remit).	YES (Last update: 2010)	YES	YES	bob.ward@csiro.au rhanner@uoguelph.ca
Fish & Chips www.fish-and-chips.uni-bremen.de	DNA chips for marine species identification.	YES 16S rDNA Cytochromeb	2002-2005 (FP5)	YES	YES	YES	dhb@biotec.uni-bremen.de
FinE, www.iiasa.ac.at/Research/EEP	Fisheries-induced Evolution	Not Stated	2008-2011 (FP7)	Not Stated	Not Stated	Not Stated	Not Stated

PROJECT	SUBJECT	DATABASE	FUNDED FROM/ TO	STILL SUP- PORTED	DB Accessible by Web- Interface	DB Accessible by Crawler	Contact
/FinE							
UNCOVER www.uncover.eu	Understanding the Mechanisms of Stock Recovery.	Content proba- bly not relevant – no genetic data	2006-2010 (FP6)	Not Stated	Not Stated	Not Stated	Not Stated
SeaFood Plus www.seafoodplus.org	Promoting safe seafood products of high eating quality.	Content proba- bly not relevant – no genetic data	Not stated	Not Stated	Not Stated	Not Stated	Not Stated
TraceFish www.tracefish.org	Bring together companies and research institutes to establish common views with respect to what data should follow a fish prod- uct through the chain from catch/farming to consumer	Content proba- bly not relevant – no genetic data	2000-2002 (FP5)	Not Stated	Not Stated	Not Stated	Not Stated
SALSEA-Merge www.nasco.int/sas/salseamerge.htm	To advance understanding of stock specific migration and distribution patterns and overall ecology of the marine life of Atlantic salmon and gain an in- sight into the factors re- sulting in recent increases in marine mortality	SQL, web ac- cess uncertain (microsatellite data for rivers across Europe)	2008-2011 (FP7)	Yes (now populated and being ex- tended as project progresses)	NO	NO	John Gilbey j.gilby@marlab.ac.uk Bernt Drange bernt.andreas.drange@ imr.no

PROJECT	SUBJECT	DATABASE	FUNDED FROM/ TO	STILL SUP-PORTED	DB Accessible by Web-Interface	DB Accessible by Crawler	Contact
CODTRACE www.ucd.ie/codtrace	Develop the methodology to establish the location of spawning and of harvest of individual cod	Local MS Access DB (Genetics, micro-chemistry)	2002-2005 (FP5)	Yes (functional)	NO	NO	Ruth M. Higgins ruth@uac.pt
HERGEN www.hull.ac.uk/hergen	Herring genetics and otolith traits. Provide guidelines for the conser-vation and management of biodiversity of Atlantic herring in the North Sea and adjoining waters	Local MS Exel DB: (Genetic and otolith data)	2002-2005 (FP5)	Website (func-tional and last update 2002)	NO	NO	db@aqua.dtu.dk
The Marine Genomics Project www.marinegenomics.org	Web-based interface for public transciptomic and genomic data and analysis tools.	Web Interface (ETSs Tran-scriptomics)	Not stated	Website (func-tional update in 2008?)	YES	YES	Not Stated
The Redfish Project www.redfish.de/	Two commercially ex-ploited redfish species: investigation of the ge-netic relation across these redfish; reproductive strategy of the viviparous redfish species; dynamic demography of the redfish stocks including scientific and commercial fleet data.	Password protected MS Access DB (downloadable as ZIP file)	1998-2002	Website func-tional	YES	NO	hans-joachim.raetz@ish.bfa-fisch.de

2.4.7 EMODNET (EU Marine Observation and Data Network initiative)

In its green paper on maritime policy (Commission, 2007a), the European Commission expressed concern that currently most marine data collection is focused on meeting the needs of a single purpose - as part of a regulatory requirement, for operational purposes or to further scientific understanding, and is therefore highly fragmented. As a countermeasure the Commission suggested to develop a system that will allow a better identification of what is being collected, that will facilitate access to coherent data sets, that will permit the recognition of data gaps and that will shape a data collection and monitoring infrastructure directly suited to multiple applications, which is ore encompassing but nevertheless very similar to the WGAGFM proposal for a fish/fisheries genetic meta-database. In its EU's Maritime Policy Blue Book, adopted in October 2007, the European Commission, elaborated concrete steps towards EMODNET in order to improve availability of high quality data (Commission, 2007b); this was further specified in 2009 by an EU action plan to make progress in this area on the basis of a road map (European Commission, 2009).

Basic design principles of EMODNET have been formulated by the Commission together with the Marine Observation and Data Expert Group (MODEG; http://ec.europa.eu/maritimeaffairs/eu-marine-observation-data-network-members_en.html). These are

1) collect data once and use it many times;

2) develop standards across disciplines as well as within them;

3) process and validate data at different levels; structures are already developing at national level but infrastructure at sea-basin and European level is needed;

4) provide sustainable financing at an EU level so as to extract maximum value from the efforts of individual Member States;

5) build on existing efforts where data communities have already organised themselves;

6) develop a decision-making process for priorities that is user-driven;

7) accompany data with statements on ownership, accuracy and precision; and

8) recognise that marine data is a public good and discourage cost-recovery pricing from public bodies.

The feasibility of EMODNET is currently being tested through preparatory actions and pilot projects started in 2009, and should lead to first results end of 2010. Portals for a number of maritime basins are being set up for hydrographic, geological, biological and chemical data as well as functional habitat maps. These portals will provide access to marine data of a standard format and known quality and identify gaps in coverage. The projects will identify the main challenges in moving to a fully operational EMODNET.

ENDOMET is clearly a highly ambitious endeavour and of great relevance and only if well prepared would it be possible to uptake genetic data in EMODNET. This makes it essential that the cataloguing and documentation of available fish and shellfish genetic data independently of EMODNET would be required for it to be included in this portal. To explore this possibility, in 2009 the WGAGFM, through its membership, participated in the EMODNET public consultation process (http://ec.europa.eu/maritimeaffairs/consultation_emodnet_en.html), and responded

to a catalogue of pre-defined questions to assess data needs of stakeholders and general dis-/agreement with the EMODNET initiative at the conceptual level. The response of the more than 300 stakeholders that replied in two month consultation period was mostly positive and the response statistics can be found on: http://ec.europa.eu/maritimeaffairs/emodnet/consultation/IPM%202_3.htm. The WGAGFM response is provided in Appendix I.

2.4.8 EU SALSEA–Merge (EU SALmon at SEA – Merging genetics and ecology)

In 2008, the EU SALSEA Merge FP7 project (N$^{\circ}$212529) was initiated. The overall objective of SALSEA-Merge is, by merging genetic and ecological investigations, to advance understanding of stock specific migration and distribution patterns and overall ecology of the marine life of Atlantic salmon and gain an insight into the factors, resulting in recent significant increases in marine mortality. This objective was to be achieved by the development of a genetic tool of the identification of the region/river of origin of Atlantic salmon captured at sea and combining this with information on the location of capture, biological metrics on individual fish, and oceanographic conditions, to gain insights into stock-specific ecologies and migration patterns.

Recognition of the potential for the development of this genetic tool was made possible by the prior development of a comprehensive population genetic meta-database as part of SALMAN (Atlantic SALmon Microsatellite Network), an informal network of government and academic researchers working on the molecular genetics of this species. This network emerged out of the EU FP5 SALGEN Accompanying Measure (Q5AM-2001-00200 – Review of Genetic Studies on Atlantic Salmon to Increase Understanding and Improve the Effectiveness of Wild Stock Conservation and Rebuilding Programmes in Europe (Verspoor *et al*., 2007). The development of a comprehensive overview of available information made possible the thorough evaluation of the implications of existing research for genetic stock identification in this species which was needed to ascertain the potential for the development of a molecular genetic assignment tool. It also led to the development of a common strategy for co-ordinating and integrating data sets across research programmes, and to the identification of and agreement on set of common markers to facilitate the linkage of work across projects to gain a broader trans-range perspective. Building on this, it was possible to ascertain and demonstrate the potential for developing such a tool to achieve the project objectives, allowing the science to advance much more rapidly than would otherwise have been possible.

Now, as part of the SALSEA Merge project, a comprehensive integrated database of molecular genetic data for microsatellite DNA loci on Atlantic salmon from across the species' European range is being built. This involves the integration of existing and new genetic data from 12 government and university laboratories across Europe, and will encompass more than 20,000 salmon from over 250 rivers as well as data on salmon caught at sea, and is the first purpose-built integrated and full inter-calibrated molecular genetic data set for this species that spans the entire European range of the species. However, while the most extensive and comprehensive, there are other microsatellite DNA data sets both for Europe and North America, as well as large numbers of data sets related to variation at allozyme loci, nuclear and mitochondrial restriction enzyme and SNPs (single nucleotide polymorphisms), as well as sequence variation. No publically accessible catalogue of all these data bases and the research findings arising from them is available, that could be used by the research community to build new research projects and to develop further insights into the popula-

tion genetics of the species from data integration. Yet, for Atlantic salmon, this could be achieved at this point in time with relative ease by building on the data bases developed under SALSEA Merge, and the institutional collaborations it has spawned. This could also serve as a structural and operational meta-data base model for other species and, if appropriately implemented, provide a platform that could be extended to deliver equally useful population genetic meta-databases for other fish species, which is why we focus on SALSEA Merge in this ToR.

2.4.9 Conclusions and next steps

The merit of developing a publically accessible, up to date and appropriately focused meta-database on molecular genetic information related to the population genetics of fish species is acknowledged and accepted by the research community. The existence of such a database would do much to ensure a wider and more comprehensive exploitation of existing research by ensuring that existing information is taken into account in new research programmes and available for new types of analyses. It will also make it easier to generate wider ranging and potentially more informative population genetic analyses with existing data by facilitating data access and research collaborations. Furthermore, a properly implemented meta-database would facilitate the uptake of genetics into marine fisheries management, which only currently occurs to a very limited extent (Waples *et al.*, 2008) and, beyond that, contribute to improved conservation efforts and ecosystem assessments as, for example, foreseen in the EU Marine Strategy Framework Directive (European Commission 2008a). Finally the use of public funding resources would be greatly improved. However, constructing and maintaining such a database presents particular institutional challenges as regards to resourcing and maintenance. Benefits to individuals and institutions inputting information or hosting and managing websites will not often be direct and immediate. Benefits will be diffuse and maximised if the databases are in the public domain and can be widely accessed and exploited. Also, while not sufficient, it would be advisable to considerably improve IT support within academic institutions for research networking and the development of properly managed and Web-accessible local project databases, as this would facilitate the development of a meta-database. Alternatively this could be achieved on the national level. Interestingly European Union member states already collect much data for fisheries management and in some cases are legally obliged to do so European Commission 2008b, which invites the question whether and how genetic data could be included in these national efforts.

In most cases, the transnational distribution of species means that databases will also need to be transnational to be of greatest value, meaning that finding supporting resources at national levels will often be difficult. Furthermore, at least initially, when their greatest value is in respect of advancing general understanding and research, benefits will not be well defined and easy to justify in terms of practical returns in relation improved implementation or monitoring of fish conservation and fisheries management measures. These considerations do not diminish the overall value of setting up such a meta-database in support of fish and fisheries research and management, but they do mean that will not be easily achieved, particularly given the general resource constraints likely to be faced by most governments and institutions.

This situation makes it particularly important to have a working demonstration of a data base that can be used to fully explore the set-up and operational issues as well as to accurately evaluate the benefits and resource requirements. The relatively advanced state of research into the molecular population genetics of the Atlantic salmon and the existence of the current EU SALSEA Merge project provides a unique oppor-

tunity to develop a working demonstration model for such an evaluation. Much of the meta-information can be easily assembled, building on work already done as part of the EU SALSEA Merge project and exploiting the network of researchers working on this project, who collectively will be aware of the data sets existing for non-SALSEA molecular markers.

In previous WGAGFM reports, a potential institutional framework for developing the meta-database, incorporating the web-crawler (JRC), hosting it (ICES), and running it (WGAGFM) have been identified. What is now required is to identify the human resource to carry out the final database design, implement it, and carry out the initial populating with the meta-information. As indicated, such a resource is unlikely to be realised at the national level and will most likely be able to be accessed through the funding of international bodies such as the EU, the IASRB (International Atlantic Salmon Research Board), or an international philantrophic organization. With regard to the EU, the required human resources could potentially be obtained through Marie Curie fellowships such as "Early Stage Research Training", "Intra European Fellowships", or "International Incoming Fellowships".

Action in the coming year is essential to ensure the initiative to develop the data base does not lose momentum and to ensure it is in place as quickly as possible to support rapidly evolving developments in marine science and management.

2.4.10 References

European Commission. 2007. Towards a future Maritime Policy for the Union: A European vision for the oceans and seas. 58 p.

European Commission. 2007. Communication from the Commission: An Integrated Maritime Policy for the European Union. 14 p.

European Commission. 2009. Building a European marine knowledge infrastructure: Roadmap for a European Marine Observation and Data Network. Commission Staff Working Document.

European Commission. 2008a. Directive 2008/56/EC OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL of 17 June 2008 establishing a framework for community action in the field of marine environmental policy (Marine Strategy Framework Directive). Official Journal of the European Union L: 19.

European Commission. 2008b. Council Regulation No 199/2008 of 25 February 2008 concerning the establishment of a Community framework for the collection, management and use of data in the fisheries sector and support for scientific advice regarding the Common Fisheries Policy. Official Journal of the European Union L 60/1. pp. 12.

Kochzius M. 2008. Trends in fishery genetics. In: R.J B, J. RB, editors. The Future of Fisheries Science in North America, Springer, pp 451-491. 1 ed: Springer. pp. 453–494.

Primmer C. R. 2009. From conservation genetics to conservation genomics. Annals of the New York Academy of Sciences, 1162: 357–368.

2.4.11 Recommendations

The authors of this ToR recommend:

a) A working demonstration meta-database of molecular population genetic information be developed for the Atlantic salmon, building on the EU SALSEA Merge project, to assess the benefits, feasibility and practical operational issues of developing a full, multi-species meta-database

b) An attempt, led by the EU SALSEA-Merge consortium and JRC, be made in 2010 to exploit the opportunities available in the EU Marie Currie Fellowship and Training programmes to acquire the human resources required to achieve a).

c) An attempt be made by JRC to achieve further development and extension of the project crawler tool for populating the fish genetics meta-data base

d) A further report on progress in relation to the recommended actions a), b) and c), be presented at the 2011 meeting of the WGAGFM.

2.5 ToR e) Review the genetic effects of exploitation on deep-sea fishes

Sarah Helyar, Jens Carlsson and Jann Martinsohn.

2.5.1 Introduction

The aim of this ToR is to summarize the available information about basic population genetics of deep-sea fish (such as population structure, effective population sizes and connectivity), suggest potential sources of present and future threats to these species, and identify research priorities and needs in relation to recent and future trends in deep sea fisheries.

The over-exploitation of traditional coastal stocks, the rising demand for seafood and technological advances in fisheries, have all combined to result in the shift of commercial fishing towards less-known, deep-sea species in many parts of the world (the term deep sea, or deep water, is defined as the waters below the continental shelves. That is all the water deeper than about 200 meters. ICES defines the term deep sea fisheries as those fisheries that occur in depths greater than 400 m. The deep water in the ICES area covers the deep parts of ICES Subareas I, II, III, V-X, XII, and XIV. This review is based upon the ICES definition). By 2000, 40% of the world's trawling grounds were classed as deep sea (Roberts 2002), and in the North Atlantic, the mean fishing depth has increased steadily since 1990 at a rate of 32.1 m per decade (Morato *et al.*, 2006).

The expansion of deep sea fisheries and the improvements in fishing technology have increased concern over the vulnerability of deep-sea species both to overexploitation and to loss as by-catch (Koslow *et al.* 2000; Roberts 2002). The deep-sea constitutes vast areas of the oceans and is a cold, low nutrient environment with a slow turnover, and deep-sea fishes tend to have a greater longevity and later sexual maturity than fish found in shallower, more nutrient rich waters (Moore *et al.*, 1999; Koslow *et al.*, 2000; Devine *et al.*, 2006). These properties make deep-sea fish unsuitable candidates for fishing, because stocks are highly vulnerable, and show very slow recovery after depletion. As a result, dramatic declines have been seen in many targeted species (see Figure 2.4.5.1) with numerous stocks collapsing to <20% of their pre-exploitation abundance in just a few years. As a majority of deep sea fishing uses non-selective technologies such as trawling, there is an inevitable capture of species other than those targeted, and these fisheries therefore cause significant by-catch mortality (Gordon *et al.*, 1995; Clark *et al.*, 2000; Piñeiro and Bañón, 2001). It is therefore reasonable to expect that deep-sea species other than those targeted may also qualify as species-at-risk.
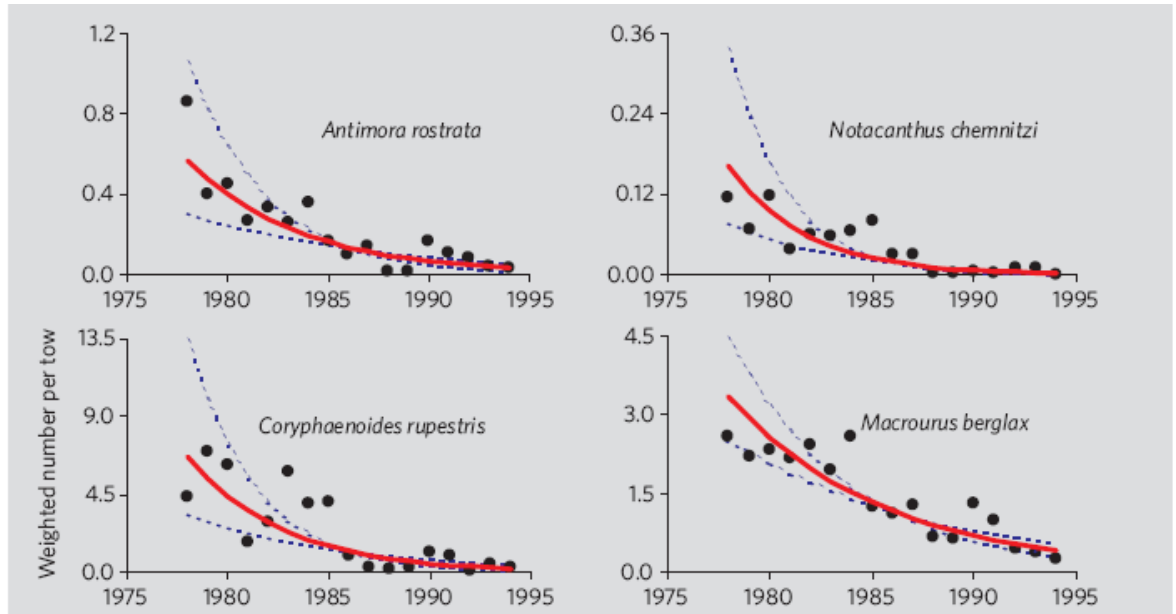
Figure 2.5.1.1. Trends in relative abundance of four species of deep-sea fish. Weighted relative abundance (number per tow) over time from research-survey data, showing the estimated exponential decline (red line) and 95% confidence projections of the estimate (dashed lines) for five deep-sea species in the Canadian waters of the northwest Atlantic, 1978–94. Taken from Devine *et al*. (2006).

Fisheries are not the only activity that has benefited from the rapid advances in submersible technology; huge new areas have also been opened up for resource extraction. While the deep-sea has traditionally been underexploited in comparison to terrestrial and shallow water areas, the advances in technology have allowed access to these previously economically unviable resources. Deep-water commercial oil, gas and mineral (e.g. ore and diamonds) extraction as well as waste dumping and CO_2 sequestration are just some of the activities taking place or under development that will influence the deep-sea habitat, and will affect ecosystems that may already be under pressure due to fishing activities (e.g. Thiel H, 2003). While technologies for the exploitation of the deep-sea have advanced rapidly, our understanding of its biology and the effects of these activities on deep-sea ecosystems are insufficient. For this reason, although this review will mainly focus on commercially important fishes, we feel that there is an urgent need to put considerably more emphasis on the comprehensive study of the deep-sea environment and to introduce an 'Ecosystem Approach' to deep-sea fisheries management.

The term 'Ecosystem Approach' found formal acceptance at the Earth Summit in Rio in 1992 where it became an underpinning concept of the Convention on Biological Diversity (CPD; CPD 2009). It is in line with the precautionary approach (FAO 1996, ICES 2001) which is a further important principle in current fisheries management that can be directly linked to this approach. The term 'Ecosystem Approach to Fisheries' (EAF) was adopted by the FAO Technical Consultation on Ecosystem- based Fisheries Management in September 2002 (FAO, 2003). The concept delineates a way of taking ecosystem considerations into more conventional fisheries management (Garcia *et al*., 2003). The Reykjavik FAO Expert Consultation (FAO, 2003) agreed that the "*purpose of an ecosystem approach to fisheries is to plan, develop and manage fisheries in a manner that addresses the multiplicity of societal needs and desires, without jeopardizing the options for future generations to benefit from a full range of goods and services provided by marine ecosystems.*" Therefore, "*an ecosystem approach to fisheries strives to balance*

diverse societal objectives, by taking account of the knowledge and uncertainties about biotic, abiotic and human components of ecosystems and their interactions and applying an integrated approach to fisheries within ecologically meaningful boundaries."

However the management of deep-seas faces considerable challenges as the majority of deep-sea habitats lie in international waters. - While in coastal areas, the coastal states are empowered to take action to guard against the impact of bottom fishing on fragile ecosystems, the situation is more ambiguous and intricate with respect to monitoring, control and surveillance (MCS) in international waters. Regional Marine Conventions have general responsibilities for the protection of the marine environment, and Regional Fisheries Management Organisations (RFMOs; Lugten (2010)) adopt measures for the conservation and management of living marine resources and regulate the impacts of fishing on vulnerable ecosystems (see Figure 2.5.1.2). While RFMO's have been criticised as being inefficient (e.g. Cullis-Suzuki and Pauly, 2010) under the UN Convention on the Law of the Sea (UNCLOS), they are endowed with full authority to take concrete and binding legal measures, and to assure compliance by applying control and enforcement. UNCLOS is also central to the governance of the deep-sea, as it lays down the fundamental principles governing the freedoms and duties of the high seas, and requires the adoption of internationally agreed measures for the conservation of marine living resources in waters beyond national jurisdiction (United Nations Division for Ocean Affairs and the Law of the Sea - Office of Legal Affairs, 1997). To date, 158 countries and the European Community have joined the Convention. However in addition to the general difficulty of efficient high-sea governance there also persist areas where there is no regulatory body yet in place, leaving a loophole for uncontrolled and destructive fishing practises. This issue was addressed in 2007 by UN General Assembly resolution 61/105, which called for additional installations of RFMOs in zones not covered yet (United Nations General Assembly, 2007).
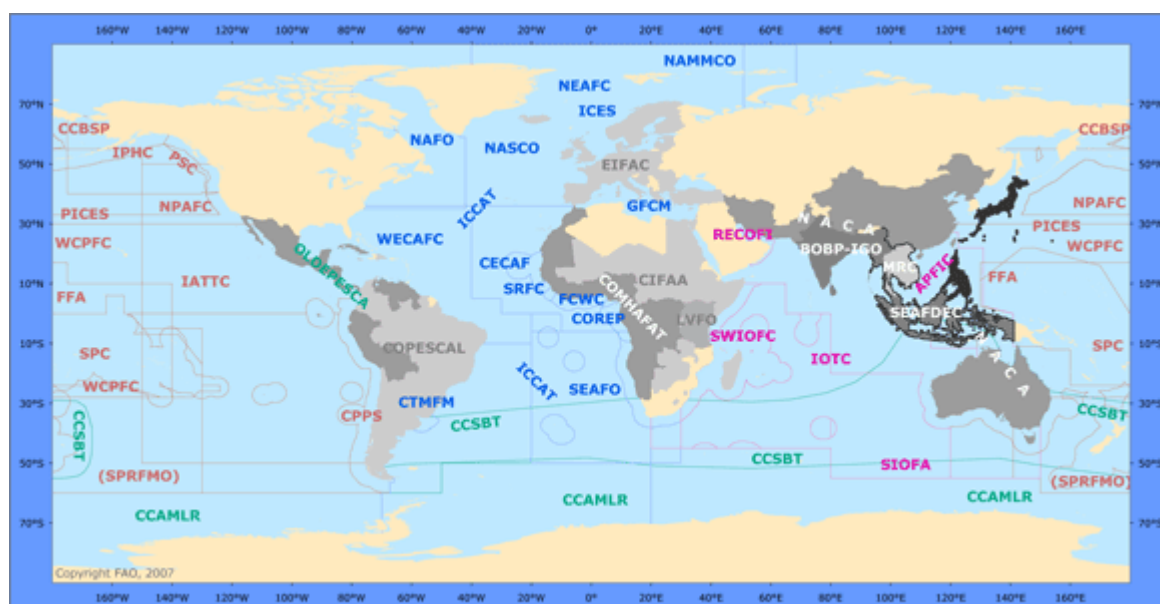
Figure 2.5.1.2. Map showing the areas covered by each of the Regional Fishery Management Organisations (RFMOs). These bodies are comprised of a group of States or organizations that are parties to an international fishery arrangement, and work together towards the conservation and management of fish stocks. (All boundaries on this map are approximate and are indicative only). Taken from the FAO website: http://www.fao.org/fishery/rfb/en.

Moreover international resolutions and legislation further address governance and fisheries management of the deep-seas. For example the Food and Agriculture Organisation (FAO) has developed technical guidelines for deep-sea fisheries within the framework of the Code of Conduct for Responsible Fishing (FAO, 1995), and in 2004 UN General Assembly Resolution 59/25 issued a call for urgent measures to eliminate destructive fishing practices in the high seas and committed to review in 2006 what action had been taken by States and RFMOs in response to such call (United Nations General Assembly, 2005).

In 2004 and 2006 the UN Convention on Biological Diversity, which has been negotiated under the auspices of the United Nations Environment Programme (UNEP), recognised the serious threats to biodiversity in marine areas beyond national jurisdiction and stressed the need for rapid action to address these threats (Conference of the Parties to the Convention on Biological Diversity, 2004; 2006). Particularly in Decision VII/21 the Conference of the Parties;

1) Notes that deep seabed ecosystems beyond the limits of national jurisdiction, including hydrothermal vent, cold seep, seamount, coldwater coral and sponge reef ecosystems, contain genetic resources of great interest for their biodiversity value and for scientific research as well as for present and future sustainable development and commercial applications;

2) Recognizes that given the vulnerability and general lack of scientific knowledge of deep seabed biodiversity, there is an urgent need to enhance scientific research and cooperation and to provide for the conservation and sustainable use of these genetic resources in the context of the precautionary approach;

3) Concerned about the threats to genetic resources in the deep seabed beyond national jurisdiction, requests Parties and urges other States, having identified activities and processes under their jurisdiction and control which may have significant adverse impacts on deep seabed ecosystems and species in these areas, as requested in paragraph 56 of decision VII/5, to take measures to urgently manage such practices in vulnerable deep seabed ecosystems with a view to the conservation and sustainable use of resources, and report on measures taken as part of the national reporting process.

(Quote taken from the Conference of the Parties to the Convention on Biological Diversity (2006), emphasis of genetic resources in the text is by the authors.)

Acknowledging that sound deep-sea fisheries management is an urgent requirement in EU-waters and worldwide, the European Union contributed to and endorses the above mentioned conventions and rules. In 2007 the European Commission came forward with a proposal for a Council Regulation on the protection of vulnerable marine ecosystems in the high seas from the adverse effects of bottom fishing gears (European Commission, 2007). The proposal seeks to eliminate the destructive fishing practices that threaten vulnerable marine ecosystems in the high seas. It also envisages requiring Community vessels using bottom fishing gears to obtain a special permit. This applies to vessels operating in the high seas in areas not regulated by a Regional Fisheries Management Organisation (RFMO). In 2008 this led to Council Regulation No 734/2008 on the protection of vulnerable marine ecosystems in the high seas from the adverse impacts of bottom fishing gears (European Council, 2008).

2.5.2 Summary of available information

Many of the basic life-history characteristics needed to manage fish populations are not yet known for deep-sea fishes and although most species are not targeted by directed fisheries, research has shown that many non-target species are also affected (Baker 2009).

2.5.2.1 Species level studies

The need for clear knowledge of the true taxonomic status of species is a basic requirement for good management. This is particularly true of chondrichthyans, as the sharks and rays are particularly vulnerable to depletion, due to their low reproductive potential compared to teleosts. Although not an exclusively deep sea species, an example of the importance of species identification has been recently highlighted by a study on the European common skate (*Dipturus batis*) which has been described as the first clear case of a fish species brought to the brink of extinction by commercial fishing. Its listing was upgraded to Critically Endangered in the 2006 IUCN Red List of Threatened Species. The study by Iglesias *et al.* (2010) used a combination of morphology and genetics and showed that the scenario was actually more serious than had been realised as five species were actually being mislabelling under only two landing names. This implies that official fishery statistics were masking species-specific declines, and a dramatic decline and collapse of the spawning stock, preventing the recovery of relict populations (also see Griffiths *et al.*, 2010).

The technical hurdles and high economical costs associated with deep-sea research limits our knowledge about the number and biology of fish species inhabiting these habitats and many species are probably still unknown to science. Recent studies that have concentrated on refining the systematics of deep sea species include some that are unique enough to warrant new orders (Danielsdottir *et al.*, 2008; Miya *et al.*, 2007; 2010; Johnson *et al.*, 2009), demonstrating that the classification of many deep sea species is still in its infancy compared to terrestrial or coastal regions. Very few deep sea taxonomic studies incorporate molecular techniques, which are particularly important with cryptic species. For example, the two species of scabbardfish (*Aphanopus carbo* and *Aphanopus intermedius)* are morphologically indistinguishable but were thought to have different latitudinal distributions. However, closer investigation by Stefanni and Knutsen (2007) using molecular barcoding demonstrated that these two species are sympatric in the Azores, Madeira, Canaries and the north-western coast of Africa, some of the areas where exploitation is concentrated. Molecular barcoding has also been used to aid the species identification of the Atlantic deep-sea sharks. There are morphology-based identification problems among and within the deep-sea shark genera, and landings of processed shark products further prevent an objective assessment of the exploitation levels of these species. (Moura *et al.*, 2008). In this case, molecular barcoding provides a fast and inexpensive strategy to resolve within genera identification problems, and is an important tool for the assessment and implementation of management policies for hard to identify species.

2.5.2.2 Population level studies

Among studies of the population genetics of deep-sea fish, some species, such as the slender armourhead *Pseudopentaceros wheeleri* (Martin *et al.* 1992), and the alfonsino *Beryx splendens* (Hoarau & Borsa 2000; Akimoto *et al.* 2006) appear to show panmixia within the North Atlantic. Both of these species are associated with seamounts; and have high fecundities and an extended pelagic larval duration (up to 2 years), so a panmictic population structure fits with biological expectations. However, studies of

the orange roughy *Hoplostethus atlanticus*, have also found no evidence of population structure, although significant differences were found between the North Atlantic and populations from the west coast of Africa (White *et al* 2009). Population structure has been demonstrated within other ocean basins (e.g. Elliot and Ward 1992; Smith and Benson 1997; Smith *et al* 1997). Unlike the previous two species, the orange roughy has a short pelagic larval stage, and it is not known if this lack of structure is due to the orange roughy demonstrating some degree of homing to natal breeding grounds (Rogers 2003). Nor is it known whether they return to the same spawning ground each time they spawn, or simply go to the nearest suitable location. If the latter occurs, then given the longevity of this species and potential number of spawning events within a lifetime, there is considerable potential for genetic mixing, due adult migration. However, It cannot be assumed that species with an extended pelagic larval duration will show panmictic populations, as species such as the bluemouth *Helicolenus dactylopterus* and the black spot sea bream *Pagellus bogaraveo* exhibit significant genetic structure over relatively small scales: although this population structure may be influenced by historical demographic effects, such as changes in climate (Aboim *et al* 2005; Stockley *et al* 2005). While Roques *et al* (2002) found very little population structure in *Sebastes mentella* (which again has a long larval stage) across the North Atlantic, later work by Stefansson *et al* (2009) found that although the geographical distribution of the population clusters they identified appeared to overlap, the populations showed clear depth segregation.

Many deep sea fishes have immense geographical ranges, but most display more or less species-specific depth ranges (e.g. Haedrich and Merrett, 1988). This means that the geographical distribution of a depth-limited species may be split up to varying degrees by bathymetric features. Over time this mosaic of habitable subareas of varying quality may facilitate population structuring. In essence, a shallow ridge may constitute a barrier to dispersal for a very deep-living species, and deep troughs or deep ocean basins could have the same restrictive effect on a shallower-living species. Many species also appear to be limited in their migrations and dispersal due to certain oceanographical features, such as specific water masses or circulation features including persistent regional and mesoscale gyres (Koslow, 1993), for example Knutsen *et al* (2009a) found genetic subdivision among tusk (*Brosme brosme*) samples drawn from across the North Atlantic, in both cases were attributed to bathymetric barriers. Shaw *et al* (2004) and Rodgers *et al* (2006) investigating the Patagonian toothfish (*Dissostichus eleginoides*), and Kuhn *et al* (2008) for the Antarctic toothfish (*D. massoni*) also found support for population structure due to bathymetric barriers and oceanographical features. In such situations the assumption of panmixia could have detrimental effects on stock structure and population persistence.

However, it must be noted that that while all of the species discussed above are covered by the ICES definition of a deep sea species, few of them inhabit the lower reaches of the deep sea. Recently there have been a number of genetic resources published for deep sea fish species, including grenadiers (Knutsen *et al.,* 2008; Helyar *et al.*, 2009; White *et al.*, 2009b, Schneider *et al.*, 2009), scabbardfish (Knutsen *et al.,* 2008; Stefanni *et al* 2009), and also some deep-sea shark species (Helyar *et al* in press) indicating that there are more population scale studies currently being carried out on species with lower depth ranges. The ESF funded DEECON project (http://www.imr.no/deecon/) is also due to finish this year, and more results on the species studied in that project (*Coryphaenoides rupestris, Macrourus berglax, Aphanopus carbo, Molva molva, Centroselachus crepidator*) are expected.

2.5.3 Priorities and needs in relation to recent and future trends in deep sea fisheries.

As is demonstrated by the brevity of the above review, there are many gaps in our knowledge of deep sea organisms and in particular their taxonomy and population structure- vital elements if species are to be well managed rather than overexploited, and fundamental for implementing an ecosystem based approach to management. Although projects such as the Census of Marine Life (CoML; http://www.coml.org/) have made a huge impact on our understanding of marine diversity, resources are still needed to catalogue the biodiversity (of both species and populations) of the deep-sea to mitigate our still limited knowledge. In addition, there are a number of research and monitoring bodies (both national and international), and commercial interests, such as oil and mineral extraction companies that are working in deep-sea habitats or in areas on the fringe of deep-sea. Efforts to collate all the available data and to increase the collaboration between scientific research and commercial bodies should be encouraged. The use of new molecular tools, such as metagenomic approaches (for examples see Woyke *et al.*, 2009; Creer *et al.*, 2010), should be adopted to gain a deeper insight into those taxa that are difficult to sample using traditional methods.

To prevent further anthropomorphic impacts on the most vulnerable deep sea ecosystems, bottom trawling, especially in areas with deep-sea corals, should be limited as the activity has great destructive potential on corals which represent important nursery grounds. This non-selective fishing technique has the potential to have serious negative effects on both the target species and a range of non-targeted species. Key habitats utilized as spawning, nursery, feeding areas should be identified and Marine Protected Areas (MPAs) should be established for a range of these habitats. This will not only ensure protection of economically important fish, but also in effect indirectly improve conservation of non-targeted fish and other species. Additionally other existing fisheries on deep-sea species should be reviewed to establish if they are sustainable. Expansion of deep-sea fisheries above current levels and development of new deep-sea fisheries should not commence unless it can be demonstrated that such activity is sustainable. These are necessary precautions as the biological knowledge of many deep-sea fishes is not present and would prevent wiping out entire subpopulations that have not yet been assessed. For other aspects of deep sea exploitation, such as oil or mineral extraction, waste disposal etc environmental impact assessment should be carried out.

2.5.4 Conclusions

Future management decisions should be based on strong science and the precautionary principle. The burden of proof should be reversed to prevent fisheries from being developed without first understanding the basic biology of the target species and those that will be caught as by-catch. Scientific investigation lags behind the collapse of deep-sea fisheries (Haedrich *et al.*, 2001, Moore *et al.*, 1999). Conservation measures are necessary and ignorance should not be used as an excuse for causing long lasting, even irreversible, degradation of the deep-sea ecosystem. Prior to any deep sea resource exploitation or dumping of waste (including CO_2 sequestration) rigorous environmental and genetic impact studies should be undertaken. As any conservation measures established for the deep-sea ecosystem could be slow to demonstrate significant results, appropriate initiatives, including the establishment of large no-take marine protected areas (to protect both habitat, target species, and non-targeted species) must not be delayed, and any lack of instant results should not be justification

for discontinuing conservation initiatives. Additionally as most of the deep-sea is in international waters and not under national regulations it will be complex to establish regulatory frameworks that can be enforced. This lack of regulatory frameworks is a significant impediment to successful management and conservation of deep-sea resources. However, it is paramount that efforts are made to establish such frameworks.

2.5.5 References

Aboim, M. A., Menezes, G. M., Schlitt, T., and Rogers, A. D. 2005. Genetic structure and history of populations of the deep-sea fish *Helicolenus dactylopterus* (Delaroche, 1809) inferred from mtDNA sequence analysis. Molecular Ecology, 14, 1343–1354.

Akimoto, S., Itoi S., Sezaki K., Borsa P., and Watabe, S. 2006. Identification of alfonsino, Beryx mollis and *B. splendens* collected in Japan, based on the mitochondrial cytochrome b gene, and their comparison with those collected in New Caledonia. Fisheries Science, 72: 202–207.

Baker, K. D., Devine, J. A., and Haedrich, R. L. 2009. Deep-sea fishes in Canada's Atlantic: population declines and predicted recovery times. Environmental Biology of Fishes, 85(1): 79–88.

Clark, M. R., Anderson, O. F., Francis, R. I. C., and Tracey, D. M. 2000. The effects of commercial exploitation on orange roughy (*Hoplostethus atlanticus*) from the continental slope of the Chatham Rise, New Zealand, from 1979 to 1997. Fisheries Research, 45: 217–238.

Conference of the Parties to the Convention on Biological Diversity. 2004. COP 7 Decision VII/5: Marine and coastal biological diversity. Kuala Lumpur; United Nations Environment Programme (UNEP).

Conference of the Parties to the Convention on Biological Diversity (2006) COP 8 Decision VIII/21 Marine and coastal biological diversity: conservation and sustainable use of deep seabed genetic resources beyond the limits of national jurisdiction. Curitiba, Brazil; United Nations Environment Programme (UNEP).

Creer, S., Fonseca, V. G., Porazinska, D. L., Giblin-Davis, R. M., Sung, W., Power, D. M., *et al*. 2010. Ultrasequencing of the meiofaunal biosphere: practice, pitfalls and promises. Molecular Ecology, 19 (1): 4–20.

Cullis-Suzuki S, and Pauly, D. 2010. Failing the high seas: A global evaluation of regional fisheries management organizations. Marine Policy, 34: 1036–1042.

CPD. 2009. Convention on Biological Diversity. http://www.cbd.int/ convention/convention.shtml, last accessed 28 April 2010.

Danıelsdottir, A. K., Gıslason, D., Kristinsson, K., Stefansson, M. O., Johansen, T., and Pampoulie, C. 2008. Population structure of deep-sea and oceanic *Sebastes mentella* in the Irminger Sea and the continental slope in Icelandic waters based on allozymes markers: are they cryptic species? Transactions of the American Fisheries Society, 137: 1723–1740.

Devine, J. A., Baker, K. D., and Haedrich, R. L. 2006. Fisheries: deep-sea fishes qualify as endangered. Nature, 439(7072), 29.

Elliot, N. G., Ward, R. D. 1992. Enzyme variation in orange roughy (*Hoplostethus atlanticus*) samples from southern Australian and New Zealand waters. Australian Journal of Marine and Freshwater Research, 45: 51–67.

European Commission. 2007. Proposal for a COUNCIL REGULATION on the protection of vulnerable marine ecosystems in the high seas from the adverse impacts of bottom fishing gears. COM(2007) 605 final.

European Council. 2008. COUNCIL REGULATION (EC) No 734/2008 of 15 July 2008 on the protection of vulnerable marine ecosystems in the high seas from the adverse impacts of

bottom fishing gears. (EC) No 734/2008. Official Journal of the European Union L 201/8 (30.07.2008): pp. 6.

FAO. 1995. Code of Conduct for Responsible Fisheries. Rome.

FAO. 1996. The precautionary approach to marine capture fisheries and species introductions. *FAO Technical Guidelines for Responsible Fisheries* **2**: 73.

FAO. 2003. Fisheries management – 2. The Ecosystem Approach to Fisheries. *FAO Technical Guidelines for Responsible Fisheries.* **4** (2).

FAO. Fisheries and Aquaculture Department [online]. Rome. Updated 20 October 2008. [Cited 28 June 2010]. http://www.fao.org/fishery/rfb/en.

Garcia, S. M., Zerbi, A., Aliaume, C., Do Chi, T., and Lasserre, G. 2003. The ecosystem approach to fisheries. Issues, terminology, principles, institutional foundations, implementation and outlook. FAO Fisheries Technical Paper, 443.

Gordon, J. D. M., Merrett, N. R., and Haedrich, R. L. 1995. Environmental and biological aspects of slope-dwelling fishes. In: Hopper AG (ed) Deep water fisheries of the north Atlantic oceanic slope. Kluwer Academic, Dordrecht.

Griffiths, A. M., Sims, D. W., Cotterell, S. P., El Nagar, A., Ellis, J. R., Lynghammar, A., McHugh, M., Neat, F. C., Pade, N. G., Queiroz, N., Serra-Pereira, B., Rapp, T., Wearmouth, V. J., and Genner, M. J. 2010. Molecular markers reveal spatially segregated cryptic species in a critically endangered fish, the common skate (*Dipturus batis*). Proceedings of the Royal Society B-Biological Sciences, 277(1687): 1497–1503.

Haedrich, R. L., and Merrett N. R. 1988. Summary atlas of deep-living fishes in the North Atlantic. Journal of Natural History, 22: 1325–1362.

Haedrich, R. L., Merrett, N. R., and O'Dea, N. R. 2001. Can ecological knowledge catch up with deep-water fishing? a North Atlantic perspective. Fisheries Research, 51:113–122.

Helyar, S., Sacchi, C., Coughlan, J., and Mariani, S. 2009. Novel microsatellite loci for a deep sea fish (*Macrourus berglax*) and their amplification in other grenadiers (Gadiformes: Macrouridae). *Conservation Genetics Resources*, 1(1): 3–6.

Helyar Coscia I., Sala-Bozano M. and Mariani, S. (in press) New microsatellite loci for the longnose velvet dogfish *Centroselachus crepidater* (Squaliformes: Somniosidae) and other deep sea sharks. Conservation Genetics Resources.

Hoarau G, and Borsa, P. 2000. Extensive gene flow within sibling species in the deep-sea fish *Beryx splendens*. Compte Rendus Academie Des Sciences de la Vie/Life Science, 323, 315–325.

ICES. 2001. Report of the Study Group on Further Developments of the Precautionary Approach to Fishery Management. ICES Document CM 2001 / ACFM: 11.

Iglésias, S. P., Toulhoat, L., and Sellos, D. Y. 2010. Taxonomic confusion and market mislabelling of threatened skates: important consequences for their conservation status. Aquatic Conservation: Marine and Freshwater Ecosystems, 20(3): 319–333.

Johnson, G. D., Paxton, J. R., Sutton, T. T., Satoh, T. P., Sado, T., Nishida, M., *et al*. 2009. Deep-sea mystery solved: astonishing larval transformations and extreme sexual dimorphism unite three fish families. Biology Letters, 5(2): 235–239.

Knutsen, H., Le Goff-Vitry, M., Fiani, D., and Hoelzel, A. 2008. Isolation and characterization of microsatellite loci in the deep-sea marine fish, the roundnose grenadier (*Coryphaenoides rupestris*). Molecular Ecology Resources 8(5): 993–995.

Knutsen, H., Jorde, P. E., Sannaes, H., Rus Hoelzel, a., Bergstad, O. A., Stefanni, S., *et al*. 2009a. Bathymetric barriers promoting genetic structure in the deepwater demersal fish tusk (Brosme brosme). Molecular Ecology, 18(15): 3151–62.

Knutsen, H., Catarino, D., Sannæs, H., and Stefanni, S. 2009b. Development of eleven microsa-tellite loci in the deep-sea black scabbardfish (Aphanopus carbo). Conservation Genetics Resources, 1(1), 89-92.

Koslow, A. 1993. Community structure in North Atlantic deep sea fishes. Progress in Oceanog-raphy, 31: 321–338.

Koslow, J. A., Boehlert, G. W., Gordon, J. D. M., Haedrich, R. L., Lorance, P., and Parin, N. 2000. Continental slope and deep-sea fisheries: implications for a fragile ecosystem. ICES Journal of Marine Science, 57: 548–557.

Kuhn, K. L., and Gaffney, P. M. 2008. Population subdivision in the Antarctic toothfish (*Dissos-tichus mawsoni*) revealed by mitochondrial and nuclear single nucleotide polymorphisms (SNPs). Antarctic Science, 20(4):327-338.

Lugten, G 2010. The Role of International Fishery Organizations and Other Bodies in the Con-servation and Management of Living Aquatic Resources. In: Department FaA, editor. Rome: FAO. pp. 136.

Martin, A. P., Humphreys, R., and Palumbi, S. R. 1992. Population genetic structure of the armorhead, *Pseudopentaceros wheeleri,* in the north Pacific ocean — application of the poly-merase chain- reaction to fisheries problems. Canadian Journal of Fisheries and Aquatic Sciences, 49**:** 2386–2391.

Miya, M., Holcroft, N. I., Satoh, T. P., Yamaguchi, M., Nishida, M., Wiley, E. O., *et al*. 2007. Mitochondrial genome and a nuclear gene indicate a novel phylogenetic position of deep-sea tube-eye fish (Stylephoridae). Ichthyological Research, 54**:** 323–332.

Miya, M., Pietsch, T. W., Orr, J. W., Arnold, R. J., Satoh, T. P., Shedlock, A. M., Ho, H.C., Shi-mazaki, M., Yabe, M., and Nishida, M. 2010. Evolutionary history of anglerfishes (Teleo-stei: Lophiiformes): a mitogenomic perspective. BMC Evolutionary Biology, 10: 58.

Moore, J. A., and Mace, P. M. 1999. Challenges and prospects for deep-sea finfish fisheries. Fisheries, 24**:** 22–23.

Morato, T., Watson, R., Pitcher, T. J., and Pauly, D. 2006. Fishing down the deep. Fish and Fisheries, 7**:** 24–34.

Moura, T., Silva, M. C., Figueiredo, I., Neves, A., Muñoz, P. D., Coelho, M. M., *et al*. 2008. Mo-lecular barcoding of north-east Atlantic deep-water sharks: species identification and ap-plication to fisheries management and conservation. Marine and Freshwater Research 59(3): 214–223.

Pineiro ,C. G, and Banon, M. C. R. 2001. The deep-water fisheries exploited by Spanish fleets in the Northeast Atlantic: a review of the current status. Fisheries Research, 51: 311–320.

Roberts, C. M. 2002. Deep impact: the rising toll of fishing in the deep sea. Trends in Ecology & Evolution, 17: 242–245.

Rogers, A. D. 2003. Molecular ecology and evolution of slope species. *In* Ocean Margin Systems. Ed. By G. Wefer, D. Billett, D. Hebbeln, B. Jørgensen, M. Schlüter, and T. Van Weering. Pp. 323–337. Springer- Verlag, Berlin, Germany.

Rogers, A. D., Morley, S., Fitzcharles, E., Jarvis, K., and Belchier, M. 2006. Genetic structure of Patagonian toothfish (*Dissostichus eleginoides*) populations on the Patagonian Shelf and At-lantic and western Indian Ocean Sectors of the Southern Ocean. Marine Biology, 149(4): 915–924.

Roques, S., Sévigny, J., and Bernatchez, L. 2002. Genetic structure of deep-water redfish, Se-bastes mentella , populations across the North Atlantic. Marine Biology, 140(2), 297-307.

Schneider M., Sannæs, H., Jorde, P. E. J., and Knutsen, H. 2009, Isolation and characterisation of 11 microsatellite loci in the abbysal carapine grenadier *Coryphanoides carapipnus* (Actinop-erygii, Macrouridae) and cross amplification in two other deep-sea macrourid species. *Conservation Genetics*, DOI 10.1007/s10592-009-9838-8

Shaw, P. W., Arkhipkin, A. I., and Al-Khairulla, H. 2004. Genetic structuring of Patagonian toothfish populations in the Southwest Atlantic Ocean: the effect of the Antarctic polar front and deep- water troughs as barriers to genetic exchange. Molecular Ecology, 13(11): 3293–3304.

Smith, P. J., and Benson, P. G. 1997. Genetic diversity in orange roughy from the east of New Zealand. Fisheries Research, 31: 197–213.

Smith, P. J., Benson, P. G., and McVeagh, S. M. 1997. A comparison of three genetic methods used for stock discrimination of orange roughy, *Hoplostethus altanticus*: allozymes, mito-chondrial DNA and random amplified polymorphic DNA. Fisheries Bulletin, 95: 800–811.

Stefanni, S., and Knutsen, H. 2007. Phylogeography and demographic history of the deep-sea fish *Aphanopus carbo* (Lowe, 1839) in the NE Atlantic: Vicariance followed by secondary contact or speciation? Molecular Phylogenetics and Evolution, 42: 38–46.

Stefanni, S., Bettencourt, R., Knutsen, H., and Menezes, G. 2009. Rapid polymerase chain reaction–restriction fragment length polymorphism method for discrimination of the two Atlantic cryptic deep-sea species of scabbardfish. Molecular Ecology, 9: 528–530.

Stefansson, M. O., Reinert, J., Sigurosson, P., Kristinsson, K., Nedreaas, K., and Pampoulie, C. 2009. Depth as a potential driver of genetic structure of *Sebastes mentella* across the North Atlantic Ocean. ICES Journal of Marine Science, 66: 680–690.

Stockley B, Menezes G, Pinho MR, Rogers AD (2005) Genetic population structure in the black-spot sea bream (*Pagellus bogaraveo* Brunnich, 1768) from the NE Atlantic. Marine Biology, 146: 793–804.

Thiel, H. 2003. Anthropogenic Impacts on the Deep Sea. *In* Ecosystems of the Deep Oceans. Ed. by P. A. Tyler. Elsevier, pp. 427.

United Nations Division for Ocean Affairs and the Law of the Sea - Office of Legal Affairs (1997) Official Texts of the United Nations Convention on the Law of the Sea of 10 December 1982 and of the Agreement relating to the Implementation of Part XI of the United Nations Convention on the Law of the Sea of 10 December 1982. In: Nations U, editor. New York: United Nations. pp. 236.

United Nations General Assembly. 2005. Resolution 59/25. Sustainable fisheries, including through the 1995 Agreement for the Implementation of the Provisions of the United Nations Convention on the Law of the Sea of 10 December 1982 relating to the Conservation and Management of Straddling Fish Stocks and Highly Migratory Fish Stocks, and related instruments. United Nations A/RES/59/25.

United Nations General Assembly. 2007. Resolution 61/105. Sustainable fisheries, including through the 1995 Agreement for the Implementation of the Provisions of the United Nations Convention on the Law of the Sea of 10 December 1982 relating to the Conservation and Management of Straddling Fish Stocks and Highly Migratory Fish Stocks, and related instruments. United Nations A/RES/61/105.

White, T. A., Stefanni, S., Stamford, J., and Hoelzel, A. R. 2009a. Unexpected panmixia in a long-lived, deep-sea fish with well-defined spawning habitat and relatively low fecundity. Molecular Ecology, 18: 2563–2573.

White, T. A., Stamford, J., and Hoelzel, A. R. 2009b. Nine new microsatellite loci for the round-nose grenadier (*Coryphaenoides rupestris*) with four showing cross-amplification in the shortbeard grenadier (*C. brevibarbis*). Conservation Genetics, 10(5): 1421–1424.

White, T. A., Stamford, J., and Hoelzel, A. R. 2010. Local selection and population structure in a deep-sea fish, the roundnose grenadier (*Coryphaenoides rupestris*). Molecular Ecology, 19(2): 216–26.

Woyke, T., Xie, G., Copeland, A., González, J. M., and Han C., *et al*. 2009 Assembling the Marine Metagenome, One Cell at a Time. PLoS ONE 4(4): e5299.

2.5.6   Recommendations

We recommend:

1) that the biodiversity, of both species and populations of the deep sea be catalogued as broadly as possibly including the use of genetic tools (eg Barcode of Life, mitogenomic, metagenomic, and population genetic approaches) and modelling.

2) that an inventory of collections and information of deep sea species be collated (including from commercial sources).

3) that rigorous environmental and genetic impact studies are undertaken prior to any deep sea resource exploitation (e.g. fish, and minerals) or waste dumping.

4) that work on a regulatory framework for deep sea resources is initiated.

5) invoking the precautionary principle, the establishment of deep-sea Marine Protected Areas should be established for a range of habitat types.

2.6   ToR f) Current state of knowledge on the interaction of marine escaped farmed finfish on wild fish populations at a local and regional scale, and specific aspects for reducing uncertainty in risk assessment.

Geir Dahle.

2.6.1   Introduction

Genetic subdivision of a species indicates potential for local adaptation, and the genetic differences observed among populations are a key component of genetic diversity. Local environment can be different at different scales: geographically (across the natural range of a species) or spatially (related to human activity, e.g., mariculture). Many marine species show relatively low levels of structuring even over large distances.

Potential risks associated with translocation of marine finfish arise from introduction of pathogens and parasites new to an area, and genetic shift in natural populations through hybridization with reared individuals. With increasing threats to natural populations, more focus is put on the possible importance of genetic differences among populations, especially differentiation between reared and wild populations. However, presently we have little data and the models are not robust enough to be able to evaluate the vulnerability and eventual limits for such anthropogenic changes.

Today, most mariculture production is still based on stocks that have not been subject to selection over a long time period, and for some broodstock is regularly wild-caught. However, due to domestication genetic consequences of escapes must be considered. Selection and management of broodstock is an important component for the outcome of this activity. For example, in cod it has been shown that larval and juvenile growth differs between north east Arctic cod and Norwegian coastal cod, when reared under similar environmental and feeding conditions (van der Meeren and Jørstad, 2001).

One other possible impact of maricultured species is the genetic shifts in natural populations through inter-population hybridisation. When this results in a loss of genetic diversity, it is referred to as genetic erosion. More specifically, genetic erosion could be defined as loss of genetic diversity between and within populations of the

same species over time; or reduction of genetic variability of a species due to human intervention, environmental changes, etc. Genetic erosion in a population may result in a permanent reduction in richness or evenness of common localized alleles or the loss of combination of alleles over time in a defined area.

Wild populations are generally at risk from possible interbreeding with farmed fish that has been subject to selection and domestication in a farm environment. Inter-breeding between farmed escaped fish and its wild conspecific can result in genetic changes in the wild population, hence reducing the overall fitness and productivity (Utter, 1998). The experimental evidence of any such effects is limited, although knowledge about harmful effects has been acquired for Atlantic salmon (Flemming *et al.*, 2000, McGinnity *et al.*, 2003). In Atlantic salmon several attempts at quantifying interactions between farmed and wild conspecifics have been published (Crozier 1993; Clifford *et al.*, 1998a, 1998b; Crozier, 2000; Skaala *et al.*, 2006). These range from quantification of gene-flow from single escapement events affecting specific wild populations, to investigations quantifying genetic changes in historical and contemporary samples of wild populations that have been subject to differing numbers of farmed escapees. Both approaches have demonstrated genetic changes in wild populations, although the full extent of introgression and the long-term implications for conservation remains a subject of debate.

If the marine farmed individuals originate from a variety of different farms and strains, some even highly differentiated from each other, it is possible that highly variably allele frequencies among these sources may complicate the signal of gene flow to wild populations, and in the most extreme cases, potentially cancel each other out.

The possible effect from an interaction between farmed and wild individuals are dependent on a number of different parameters, such as **genetic diversity**, **local adaptation**, and the **relationship between the number of farmed escapees and the wild conspecifics**. Farmed marine individuals based on locally caught broodstock will not have the same potential genetic effect on the wild local population as offspring from broodstock collected from a population genetically different from the wild local individuals, since they are less divergent then individuals based on broodstock from distant populations (e.g. Arctic cod vs coastal cod). Another important factor in this equation is the behaviour of the species in question: does it migrate over long distances, or is it staying within a limited range.

If farmed individuals do not survive, or if they for some reason are not breeding either with their "peers", or their wild conspecifics, they will not have a direct genetic impact on the wild population. Therefore, sterile individuals in fish farming will be a beneficiary method to reduce any genetic interaction from escapees. From studies of Atlantic salmon the methods that are available seem to have negative effects, both on the welfare of the fish as well as the production. At present sterile fish can either be produced by crossing different species (hybrids) or by producing triploids. Some of the hybrids have been shown to mature and be fertile, and triploids are therefore the chosen solution. Triploid (all female) sterile rainbow trout is produced high pressure on newly fertilized egg, and triploid Atlantic cod has been produced at the Institute of Marine Research, and although it seems to be growing slower than its diploid brothers and sisters, it is still too early to tell what will happen when the "normal" cod starts the maturation process e.g. the growth rate is halted. Production of all-female individuals, would remove the potential problem of spawners in the net-pens.

Most of the species in culture today can be made triploid with temperature shock, but for some species the amount of triploids after heat treatment varies and the heat shock can also create a high mortality. Production of portion-sized triploid trout and rainbow trout is popular, and in pacific oyster farming, about 50% are triploids.

Despite the effort to keep farmed animals inside the cages and produce sterile individuals there exists the possibility for indirect genetic effects through diseases and infections. Difference in susceptibility for any diseases or infections between the farmed and the wild individuals would ultimately affect the genetic composition in the wild. If the farmed individuals are made resistant to these types of incidents they can still be carriers and transfer the disease or infection to its wild conspecific.

One strategy for reducing the possible genetic effect from farmed individuals on its wild conspecifics could be to make sure that the wild population is big and healthy. There is less chance for a small number of successful spawners from a farm to pose a threat to a large and healthy wild population.

2.6.2   State of knowledge

2.6.2.1 Cod (*Gadus morhua*)

The best studied fish species in European marine aquaculture apart from Atlantic salmon. Cod in netpens have a different behavior form Atlantic salmon and will more easily find holes in the net pen and escape, thus present specific technological challenges. As for all marine finfish all life stages of cod are bound to the marine environment, and this includes spawning in the netpens, if the cod reaches maturity before they are harvested. It has been shown that farmed cod in net-pens produce fertilized and viable egg, which drifts out in the system around the netpen, and that these egg hatch and produce viable larvae (Jørstad *et al.*, 2008). There has also been found egg and larvae at greater distance from the netpen caused by passive movement of the egg/larvae by currents.

Survival of larvae produced from farmed marine fish in netpens found in the wild population, indicate a potential of genetic spread to the wild stock through interbreeding with wild individuals, and in intensive culture the cod mature within 2 years from hatching, which is earlier than their wild counterparts. A considerable fraction of the total number of larvae (20–25%) in the close vicinity, originated from the net pen (Jørstad *et al.*, 2008)

The situation for coastal cod in Norway is severe, and for several years ICES has recommended no fishing on this stock (Anon., 2008). The effects of a potential large aquaculture production might increase the possible negative effects on the wild stocks.

The broodstock for farming was initially based on wild mature fish from different geographical regions. Today some breeding programs have been initiated, and these have carried out selection primarily on growth rate, but also on disease resistance and early maturation, possibly increasing the distance between the farmed and the wild individuals.

2.6.2.2 Halibut (*Hippoglossus hippoglossus*)

At present there are no available data on number of escaped farmed halibut, nor is there any knowledge about genetic differences between farmed and wild halibut. Most of the farm production today is land-based and any impact from farmed halibut on its wild conspecific should be minimal. However, due to the low abundance of the

wild halibut in parts of it distribution range, even a low number of farmed individuals could have an effect in the wild stocks.

2.6.2.3 Gilthead sea bream (*Sparus auratus*)

Population genetic data suggests a low, but still significant, differentiation between sea bream populations. The intentional restocking with fish of unknown origin or accidental escape of fish from farms has most certainly contributed to a mix of all sea bream stocks. Since there is no legislation or regulation requiring mandatory reports of escape incidents, little is known about the potential impact from farmed individuals on the wild stocks.

The geneflow across the Azores/Mediterranean scale appears to be extensive and population structure is not detected. It has been demonstrated that despite the lack of genetic variability in some makers, some (AFLP, and microsatellites) allow the identification of hatchery escapees of both Atlantic and Mediterranean origin among wild fish. Genetic tagging of seam bream broodstock in commercial hatcheries might be a suitable tool for monitoring genetic impact from farmed escapees

2.6.2.4 European sea bass (*Dicentrarchus labrax*)

The sea bass is one of the most important species in marine aquaculture in the Mediterranean, and relies in many cases on the production of fingerlings from wild breeders, and as for all marine fish escape events can occur at all stages of the farming process. Genetic studies of sea bass reveal that it consists of well defined stocks through the distribution range. The practice of crossing different strains, and movement of broodstock, eggs and larvae over long distances could involve a high risk of causing artificial geneflow from escapees to local populations, inducing possible biodiversity decline. There is little knowledge about the distribution, abundance, migration, reproductive behavior, and any genetic impact of escapees is not known at all. Natural populations might be at risk from genetic interaction with escaped aquaculture conspecifics. Sterile fish can be produced through manipulation of the chromosomes, i.e. triploid induction. Although triploidisation is mastered in sea bass, it is not used as it induces some growth retardation.

Based on our current knowledge on marine finfish, and data from Atlantic salmon farming and interbreeding, there is a need to strengthen the knowledge base required to assess the genetic impact of aquaculture on the environment. Such work has been initiated through the EU-project GENIMPACT.

2.6.2.5 Northern bluefin tuna (*Thunnus thynnus*)

Tuna farming started in the 1990s. Bluefin tunas are the main species used in farming. The countries involved include Australia, Japan, Mexico and several Mediterranean countries (particularly Croatia, Italy, Malta, Morocco, Spain and Turkey). Tuna farming is a fattening and farming activity introducing a possibility of getting higher prices for small fish that otherwise would not be suitable for sashimi.

Although the Atlantic bluefin tuna population is managed as two stocks, separated by the 45°W meridian, its population structure remains poorly understood and needs to be further investigated. Recent genetic and microchemistry studies as well as work based on historical fisheries tend to indicate that the bluefin tuna population structure is complex.

It is very well known that introduction of fattening and farming activities into the Mediterranean in 1997 and good market conditions resulted in rapid changes in the Mediterranean fisheries for bluefin tuna mainly due to increasing purse seine catches.

2.6.2.6 Meagre (*Argyrosomus regius*)

The history of meagre in aquaculture is quite recent. First trials with wild broodstock were conducted in the south of France. Starting from 1996, fry production has been very limited, with a single hatchery operating in France. The first commercial production (in France) was recorded in 1997. Since then production has expanded slowly in nearby regions.

Farmed meagre come from intensive production, conducted both in land-based tanks and cages. Production facilities are few and mainly distributed in southern France and Italy. Nowadays meagre is mainly farmed in the sea, using circular or square surface cages. More recently, submerged cages have also successfully been used.

Like the farming of other marine species, meagre culture might have some negative impacts on the environment (such as potential pollution and disease transfer), due to the intensity of its production. However, fish escapes from cages are not considered a major problem because meagre is endemic in the Mediterranean basin. There is a report on a few hundred meagre escaping from a cage in Tuscany but all were collected nearby within a few days by the local trawling fleet, indicating that this species does not move very fast and is easily recaptured; this reduces the risk of altering the existing fish community structure.

2.6.2.7 Cobia (*Rachycentron canadum*)

The cobia is abundant in warm waters off the coast of the US from the Chesapeake Bay south and throughout the Gulf of Mexico. There is a national initiative for aquaculture development and fishery enhancement of cobia in the US, looking at potential for both farming and restocking. Since its popularity as a 'game' fish, genetic tools to identify or distinguish products harvested in cobia aquaculture from 'wild' stocks are produced and tested on wild populations (Pruett *et al.*, 2005, Salaria Aliabadi *et al.*, 2008), and genetic differentiation is found between populations. In Asia cobia farming is done in netpens, which might result in some negative impact on the environment, while in the US, cobia is farmed inland with closed recirculation systems, which takes care of the potential for disease transfer and escapees. There is however a project looking at sea cages and a new invention called Aquapod for cobia farming

2.6.3   Risk analysis

Risk analysis includes the **likelihood** and the **consequence**s of any undesirable event. Risk analysis is presently being used in connection with the mariculture industry for evaluation of environmental factors and management of the health of aquatic animals.

There are several risk assessment models, but one that has been used in animal health risk analysis also seem to fit well with the requirements for risk analysis of possible genetic interaction between farmed and wild conspecifics. In this model, the CM model (Corvello and Merkhofer, 1993), risk analysis is divided into four different parts; **hazard identification**, **risk assessment**, **risk management** and **risk communication**. Risk assessment includes release, exposure, consequence and estimation of the risk.

Risk analysis is also described as either qualitative or quantitative. When the relevant factors are systematically discussed and magnitudes are expressed using non-numerical terms, we are looking at **qualitative risk analysis**. Given the resources and the appropriate data we would be in a position to do a **quantitative risk analysis**, where likelihood and exposures are expressed numerically. Risk analysis in connection with genetic interaction between farmed and wild fish is not a straight forward exercise, mainly due to the nature of the genetic interaction.

Many factors have to be considered for each species and each case:

1) Domestication/selection effect: How much has the farmed situation altered the genetic makeup of the farmed individuals?

2) Genetic differentiation: Is there enough difference between the farmed and the wild individuals for any identification of the two components?

3) The biology of the species in question: Will the farmed individuals stay in the vicinity of the farm (possibility for local interaction) or are they moving out of the area?

4) The quantity of possible interaction incidence: The number of farmed individuals compared to any wild individuals will determine the possible speed and direction of any genetic interaction between the farmed and the wild individuals.

5) The frequency of possible escape events.

It is obvious that at least three of the four factors mentioned above are species specific factors, making it virtually impossible to standardize a risk assessment tool for possible genetic interaction between farmed and wild fish. Therefore the recommendations made are general and should be carried out for any marine finfish put in farms in the marine environment. For the risk assessment each species must be treated separately but the issues are the same for each species.

Reproductive sterility (all-female or triploids) is recommended as a future key to eliminating the genetic potential of escaped fish. This might be the only way to reduce the genetic impact from escapees to its wild conspecific. However, we do not know if and how sterile fish escaping from the farm interact with the spawning wild fish, and thus have an indirectly impact on the wild population.

The maintenance of robust populations of wild fish is recommended as a key to minimizing the effects of escaped fish on wild populations.

2.6.4   References

Anon. Report of the ICES Advisory Committee, 2008. ICES Advice, 2008. Books 1–10.

Clifford, S. L., McGinnity, P., Ferguson, A. 1998a. Genetic changes in an Atlantic salmon population resulting from escaped juvenile farm salmon. Journal of Fish Biology, 52: 118-127

Clifford, S. L., McGinnity, P., Ferguson, A. 1998b. Genetic changes in Atlantic salmon (*Salmo salar*) populations of northwest Irish rivers resulting from escapes of adult farm salmon. Canadian Journal of Fisheries and Aquatic Sciences, 55: 358–363.

Corvello, V. T., and Merkhof, M. W. 1993. Risk assessment methods: Approaches for assessing health and environmental risks. Plenum Publishing, New York.

Crozier, W. W. 1993. Evidence of genetic interaction between escaped farmed salmon and wild Atlantic samon (*Salmo salar* L.) in a northern Irish river. Aquaculture 113: 19-29.

Crozier, W. W. 2000. Escaped farmed salmon, *Salmo salar* L., in the Glenarm River, Northern Ireland: genetic status of the wild population 7 years on. Fisheries Manag Ecol, 7: 437–446.

Flemming, I. A., Hindar, K., Mjølnerød, I. B, Jonsson, B., Dalstad, T., and Lamberg, A, 2000. Lifetime success and interaction of farm salmon invading a native population. Proc. R. Soc. Lond. B., 267: 1516–1523.

Jørstad, K. E., van der Meeren, T., Paulsen, O. I., Thomsen, T., Thorsen, A., and Svåsand T. 2008. "Escapes" of eggs from farmed cod spawning in net pens: recruitment to wild stocks. Rev. Fish. Sci., 16: 285–295.

McGinnity, P., Prodöhl, P., Ferguson, A., Hynes, R., Ó Maoiléidigh, N., Baker, N., Cotter, D., O'Hea, B., Cook, D., Rogan, G., Taggart, J., and Cross, T. 2003. Fitness reduction and potential extinction of wild populations of Atlantic salmon, *Salmo salar*, as a result of interaction with escaped farm salmon. Proc. R. Soc. Lond. B., 270: 2443–2450.

Pruett, C. L., Saillant, E., Renshaw, M. A., Patton, J. C., Rexroad, C. E., and Gold, J. R. 2005. Microsatellite DNA markers for population genetic studies and parentage assignment in cobia, *Rachycentron canadum.* Molecular Ecology Notes (5), 84–86.

Salari Aliabadi, M. A., Rezvani Gilkolaei, S., Savari, A., Zolgharnein, H., and Nabavi, S. M. B., 2008. Microsatellite polymorphism in Iranian populations of cobia (*Rachycentron canadum* G.). Biotechnology, 7: 775–780.

Skaala, O., Wennevik, V., and Glover, K. A. 2006. Evidence of temporal genetic change in wild Atlantic salmon, *Salmo salar* L., populations affected by farm escapees. ICES Journal of Marine Science, 1224-1233

Utter, F. 1998. Genetic problems of hatchery-reared progeny released into the wild, and how to deal with them. Bulletin of Marine Science, 62: 623–640.

van der Meeren T, and Jørstad, K. E. 2001. Growth and survival of Arcto-Norwegian and Norwegian coastal cod larvae (*Gadus morhua* L.) reared together in mesocosms under different light regimes. Aquaculture Research, 32(7): 549–563.

Youngson, A. F., Dosat, A., Saroglia, M., and Jordan, W. C. 2001. Genetic interactions between marine finfish species in European aquaculture and wild conspecifics. J. Appl. Ichthyology, 17: 153–162.

2.6.5 Recommendations

For any risk assessment of the genetic effect of escaped marine finfish on wild populations we recommend:

1) the collection of basic biology knowledge about new candidate and establish species in aquaculture; behaviour and reproduction;

2) that research be supported to provide information related to risk assessment to the following production technologies; sterile fish, local broodstock, cage technology;

3) that a review on "lessons learned" from other more established farmed species (agriculture and aquaculture) is carried out;

4) that a genetic inventory of wild populations of target species is undertaken.

2.7 The WGAGFM propose a theme session at the ICES ASC 2011, Gdansk, Poland

Advances in the traceability of fish and fish products: from species to populations

Conveners: Gary R. Carvalho (UK) and Jann Th. Martinsohn (IT)

Effective conservation and control of wild fisheries demands a focus on identification and monitoring of species as well as populations. This is also crucial to enable traceability of products, both for consumer protection and for regulatory enforcement, in particular with respect to illegal, unreported and unregulated (IUU) fishing and the identification of aquaculture escapees. Although in many countries a combination of monitoring, control and surveillance (MSC) procedures and legislation exists to support traceability from trawler to plate, there remains an urgent need to underpin such activity with a reliable and tractable framework of independent testing. Recent advances in technology, especially those related to molecular methods and their forensic validation, and in our understanding of the distribution and dynamics of fish populations, provide new opportunities for developing an integrated global framework for traceability. Here we invite contributions that examine the current status of technical advances, their application to fisheries, and key obstacles that remain in their implementation. We welcome consideration at both the species and population levels from across a broad spectrum, including origin assignment of individuals to populations/regions, the identification and monitoring of marine and anadromous escapees, confirmation of identity throughout the food supply chain, and the bourgeoning field of fisheries forensics.

Supporting Information

Priority:	Illegal fishing and fraud along the supply chain pose an imminent threat to fish stocks worldwide and greatly impede sustainable fisheries management While it is acknowledged by all stakeholders worldwide that efficient traceability schemes are urgently needed for control and enforcement purposes, uncertainties remain about most suitable technologies and how to transfer those effectively into applications for authorities. The ICES ASC provides an ideal platform to expose challenges and issues linked to traceability to a wide range of stakeholders in support of an open-minded ar result-oriented discussion.
Scientific justification:	Currently the field of molecular biology and genetics, also in the fisheries realm, advances at an unprecedented pace. This provides unique opportunities for fisheries management, including MCS, but also poses particular challenges, which should be addressed involving all stakeholders.
Participants:	Currently the field of molecular biology and genetics, also in the fisheries realm, advances at an unprecedented pace. This provides unique opportunities for fisheries management, including MCS, but also poses particular challenges, which should be addressed involving all stakeholders.
Linkages to advisory committees:	Within ICES there is a direct link to the WGAGFM, but the subject is relevant also for other expert groups, including: SGIMT (Study Group on Integrated Morphology and Molecular Taxonomy); SGMAS (Study Group on Management Strategies); SIMWG (Stock Identification Methods Working Group); and WGMAFC (Working Group on Marine Fish Culture). Topics are also of interest to Expert/Study Groups that address questions related to the stock status of specific fish species.
Linkages to other committees or groups:	SSGHIE (Parent Committee of WGAGFM)

| Linkages to other organizations: | FAO; European Commission, NOAA. |

Annex 1: List of participants

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Annex 2: Agenda

Wednesday 5st:

9.00	Welcome by local hosts
9.15	Welcome and updates from WG chair
9.30 - 10.30	Discussion on the procedures for the three ToR that will not be discussed (ToR a-c) at this year's meeting, and the one that has delivered a report (ToR d)
10.30 – 12.30	Presentation and discussion on ToR f: Current state of knowledge on the interaction of marine escaped farmed finfish on wild fish populations at a local and regional scale, and specific aspects for reducing uncertainty in risk assessment
12.30 - 14.00	Lunch
14.00 - 17.00	Further discussion and finalisation TOR f
17.00 - 18.00	Open session. (Present results, projects, management problems) Discussion of implications on potential and current contributions of the WG to the Strategic Initiative on Coastal and Marine Spatial Planning (SICMSP) that will be reported to the SSGHIE at a later stage

Thursday 6th:

09.00 - 12.30	Discussions on TOR a) and c)
12.30 - 14.00	Lunch
14.00 - 16.30	Presentation of revised TOR reports
17.00 - 18.00	Open session. (Present results, projects)
19.00 -.	

Friday 7th:

09.00 - 11.00	Final adjustments of TOR reports - Recommendations
11.00 - 12.15	Suggestions for new TOR's for 2010 and future meeting venue
12.15 - 12.30	Evaluation and closing of meeting.

Annex 3: WGAGFM terms of reference for the next meeting

2010/2/SSGHIE00   The **Working Group on the Application of Genetics in Fisheries and Mariculture (WGAGFM),** chaired by Geir Dahle, Norway, will meet in Bangor, Wales, 4–6 May 2011 to:

a) Oceanographic-genetic coupling in elucidating population genetic structure in exploited marine fishes

b) Coastal and Marine Spatial Planning

c) Review the issues and challenges associated with the utilization of SNPs as markers in population genetic studies with special attention to data handling and statistical tools

d) Define genetic data needs and explore opportunities and requirements for the integration of genetic data resulting from the implementation of the EU data collection regulation (DCR 199/2008)

e) Report on how to utilise genomic approaches to the study of adaptation of marine organisms in changing environments: what can populations tell us about genes underlying phenotypic and demographic changes and what can genes tell us about adaptive evolution of populations

WGAGFM will report by 31 May (via SSGHIE) for the attention of SCICOM.

Supporting Information

Priority	The current activities of this Group will lead ICES into issues related to the ecosystem affects of fisheries, especially with regard to the application of the Precautionary Approach. Consequently, these activities are considered to have a very high priority.
Scientific justification	**Term of Reference a)** A major impediment to sustainable management of fish resources is the identification and prediction of processes that determine the distribution and dynamics of population units or stocks, which in part may be identified genetically. Among the plethora of factors shaping the patterns and extent of population genetic structuring are oceanographic processes associated with water circulation. Uncertainty remains, however, in both the physical mechanisms responsible, and the relative roles of fine-scale and regional dynamics in shaping larval and adult fish distribution. Here, we will explore recent conceptual and technical advances that allow more effective assessment and prediction of how oceanographic variability might affect genetic structuring. We place particular emphasis on the role of coupled oceanographic-genetic models, and how such approaches can be effectively utilised to yield meaningful estimates of population connectivity. (Leads: Gary Carvalho, Dorthe Bekkevold) **Term of Reference b)** The human uses of ocean resources are accelerating faster than our ability to manage them. The coastal and marine spatial planning (CMSP) process strives to sustain economic, ecological, and cultural resources for future generations by identifying areas best suited for various types of human use. Effective management has three essential attributes: • Multi-objective. Coastal and marine spatial planning balances ecological, social, economic, and governance objectives. • Spatially focused. The ocean area to be managed must be clearly defined and large enough to incorporate relevant ecosystem processes. • Integrated. The planning process should address the

interrelationships and interdependence of each component within the defined management area, including natural processes, activities, and authorities.

Ecosystem-based management is increasingly accepted as a basis for compliance with the ecological objectives. But there are considerable gaps in our ecological knowledge. For example, an important ecological determinant to delineate zones of interest for fisheries, aquaculture and conservation connectivity and dispersal of organisms in time and space. Population genetics, in combination with other disciplines, has much to contribute to this issue. Here a synthesis on the potential and available information as well as the information needed in support of CMSP as related to dispersal and connectivity of larval and adult stages of shellfish and finfish will be prepared. Recommendations for ecological CMSP will be made.

Term of Reference c)

Over the past two decades, exceptional advances in molecular analytical methodologies have resulted in a myriad of new types of genetic markers. Single Nucleotide Polymorphisms (SNPs) have been one of the latest additions to the molecular toolbox. SNPs have greatly benefited from the recent development of high-throughput and relatively cost-effective genotyping platforms (e.g. Affymetrix, SNPstream, TaqMan, Sequenom, Illumina). The unprecedented amount of genetic information provided by SNPs, make them the marker of choice for studies ranging from individual, family and population identification, to the discovery of genes and genomic regions affecting adaptive phenotypic variation. While the potential usefulness of SNPs is unquestionable, they are not without problems. For instance, to deal with the often abundant SNP genotype data (varying from a few hundred to several thousand loci at the time), generated from distinct screening platforms, quality control to ensure accuracy of allele call is a critical issue. Where data are available, there is evidence of considerable amount of genotyping error. These have been shown to potentially bias the estimation of population demographic parameters, as well as, to affect linkage analysis, measures of linkage disequilibrium, and subsequent genomic wide association studies. In addition to genotyping error, missing calls also appear to be a common feature of high-throughput genotyping. While a number of independent investigations have elaborated on these and other related relevant issues, comparatively few published studies addressing the potential caveats of SNP screening and subsequent data analysis. Given the increasing number of research groups working on fish genetics considering embracing this new molecular methodology, a review of the current state-of-the-art focusing on technical challenges, good laboratory practices, data handling and analysis would be extremely useful as a guide to users.

(Lead: Paulo Prodöhl and Phil McGinnity)

Term of Reference d)

The WGAGFM has repeatedly emphasized the need to base the management of fish stocks on population units. Unfortunately the distribution and potential migration routes of populations rarely correspond to ICES or NAFO designated management areas. Hence management units can potentially cover the distribution range of more than one population. Information on the genetic diversity, structure and stability of exploited fish stocks is essential to a sustainable exploitation and the traceability of catches and fish products. To be prepared to answer questions on the response of marine genetic diversity in times of global climate change and heavy fishing pressure, genetic sampling on a regular and systematic basis is required. Therefore ICES should propose that the European Commission integrate genetic monitoring of marine (fish) stocks into the data collection regulation (DCR). This will provide a broad and reliable baseline for management, conservation and traceability purposes. A priority list of species and recommendations for sampling, storage and molecular markers to be applied should be suggested by ICES (WGAGFM and other Expert groups.) taking

into account the current genetic knowledge for the species and the availabilit
of marker systems.

To do:

Priority list of species

- Definition of sampling and storage protocols
- Select a certain set of markers for each species
- Calibration of methods between laboratories

(Lead: Jochen Trautner)

Terms of Reference e)

Genomics of aquatic organisms can contribute to reduce reduction of impact
of fish and shellfish diseases in several ways. Firstly, Genetically-based
differences between wild or culture populations have been demonstrated in
many cases. Genome scans, using microarray-based SNP genotyping
technology or alternative approaches, aims at identifying regions of the
genome associated with these differences in resistance/susceptibility.
Secondly, genomes and transcriptome sequencing contribute to the
characterization of genes involved in immune and defence systems that will
help to identify genetic bases of innate and acquired resistance to pathogens.
At the transcriptome level, differential gene expression of fish or shellfish
exposed to pathogens, or is genetically resistant/susceptible to pathogens, ca
also be used to identify genes involved in response to disease. Candidate
genes can then be validated using functional genomics (i.e. reverse genetics,
mutagenesis, RNAi.) and/or used for marker assisted selection. Such
approaches can be combined with QTL through the mapping of eQTLs,
providing further links between variation for disease resistance and its
molecular bases.

(Lead: Pierre Bodry)

Resource requirements	None required other than those provided by the host institute.
Participants	The Group is normally attended by some 15–25 members and guests.
Secretariat facilities	None.
Financial	No financial implications.
Linkages to advisory committees	SCICOM
Linkages to other committees or groups	SIMWG , WGECO, WGMAFC, WGMASC
Linkages to other organizations	Linkage with the EC Joint Research Centre at Ispra, Italy

Annex 4: Recommendations

RECOMMENDATION	FOR FOLLOW UP BY:
1. for any risk assessment of the genetic effect of escaped marine finfish on wild populations we recommend: the collection of basic biology knowledge about new candidate and establish species in aquaculture; behaviour and reproduction	OSPAR, WGAGFM
2. that research be supported to provide information related to risk assessment to the following production technologies; sterile fish, local broodstock, cage technology.	OSPAR, WGAGFM
3. that a review on "lessons learned" from other more established farmed species (agriculture and aquaculture) is carried out	OSPAR, WGAGFM
4. that a genetic inventory of wild populations of target species is undertaken	OSPAR, WGAGFM
5.that the biodiversity, of both species and populations of the deep sea be catalogued as broadly as possibly including the use of genetic tools (eg Barcode of Life, mitogenomic, metagenomic, and population genetic approaches) and modelling	SSGEF, WGAGFM
6.that work on a regulatory framework for deep sea resources is initiated.	SSGSUE, WGAGFM
7.invoking the precautionary principle, the establishment of deep-sea Marine Protected Areas should be established for a range of habitat types.	SSGSUE, WGAGFM
8.that an inventory of collections and information of deep sea species be collated (including from commercial sources).	SSGEF, WGAGFM
9.that rigorous environmental and genetic impact studies are undertaken prior to any deep sea resource exploitation (e.g. fish, and minerals) or waste dumping.	SSGSUE, WGAGFM
10.a working demonstration meta-database of molecular population genetic information be developed for the Atlantic salmon, building on the EU SALSEA Merge project, to assess the benefits, feasibility and practical operational issues of developing a full, multi-species meta-database	WGAGFM
11.an attempt, led by the EU SALSEA-Merge consortium and JRC, be made in 2010 to exploit the opportunities available in the EU Marie Currie Fellowship and Training programmes to acquire the human resources required to achieve a).	JRC, WGAGFM
12.an attempt be made by JRC to achieve further development and extension of the project crawler tool for populating the fish genetics meta-data base	JRC
13.a further report on progress in relation to the recommended actions 10, 11 and 12, be presented at the 2011 meeting of the WGAGFM.	WGAGFM

Annex 5: Technical Minutes of RGMAR

Request 2010_3 by OSPAR

While there is general agreement on the range of potential forms of interaction between farmed and wild stocks, there is much less agreement on the current and future significance of these interactions for wild stocks.

OSPAR ask ICES:

To provide advice on the current state of knowledge on the interaction of finfish mariculture on the condition and wild fish populations (both salmonid and non-salmonid) both at a local and regional scale, including from parasites, escaped fish and the use of fish feed in mariculture. Advice is requested on how the interactions will change as a result of an expansion of mariculture activities.

OSPAR suggest that this should be addressed through a risk analysis approach, making best use of both quantitative and qualitative methodologies, and that an important aspect of the outcome will be clear identification of the specific aspects of the risk analysis where additional research effort may best be targeted to reduce the uncertainty in the risk analysis.

Four expert groups (WGPDMO, WGEIM, WGAGFM and WGEIM) were asked to work on the OSPAR request during their meetings in 2010. The expert groups have considered:

1) Impacts due to disease transfer, especially with respect to sea lice (covered by WGPDMO);

2) Impacts on wild fish stocks due to their being used as raw material to provide fish oil and protein for fish feed (covered by WGEIM);

3) Impacts due to interbreeding of escapees and escaped gametes and wild fish and gametes; and (covered by WGAGFM);

4) Impacts due to interactions between wild and farmed fish due to competition, and other ecological processes (covered in part by WGNAS, WGEIM).

The reviewers were given very limited time to carry out their review. As a result not all EG reports were reviewed by all reviewers.

Summary of review

IMPACT:	1. DISEASE TRANSFER	2. DEPLETION OF STOCK FOR FEED PRODUCTION	3. INTERBREEDING	4. INTERACTIONS
Technically correct	Yes, for sea lice transfer to wild salmon and sea trout. Does not cover other species or other diseases.	Yes	Yes, but voluntarily skips salmonids literature. The genetic implications are not reviewed.	Yes

Scope and depth	Not much detail reported, rather general overviews.	Very good	Good, considering the paucity of specific information on interbreeding of non-salmonids.	Combining both WGNAS and WGEIM, very good. The material in WGNAS is particularly well presented and up to date and so where there is overlap the WGNAS material may be preferred. WGNAS review on means of identifying escaped salmon is very good.
Prediction of change vs mariculture expansion	Yes, for transfer of sea lice vs increased mariculture.	Briefly touched, in the sense that sustainability will be the main factor for those fisheries.	Were not made, although they are obvious and similar to the other impacts.	Yes, greater impact expected
Risk analysis approach	Not done in a useful way	Excellent work, focus was on this approach	Not done	Partial, only discussed, not done systematically
Identification of additional research needed to reduce uncertainty	Yes, but missing some	Missing, but the knowledge review seem to indicate that the uncertainty level regarding this question is low.	Yes – basic research on popn diversity needed to evaluate the potential impact of interbreeding.	Yes, research need identified but not in link to reduction of uncertainty.
Additional research recommended by reviewers	Other diseases and fish species. More information needed on the impact of the sea lice transfer on wild populations. More on sea lice treatment alternatives.		More research on low cost tagging methodologies to trace escaped fish (and origin)	More research to evaluate impact for a river under its reproductive baseline. Development of cage technologies (reducing escape potential)

Detailed Review of report and the responses

> 3) Impacts due to interbreeding of escapees and escaped gametes and wild fish and gametes;
> **(covered by WGAGFM)**

1) The knowledge is well covered in general, except that almost no specifics are given for salmons were most of the knowledge resides. Some of the perceived risks are well explained. Factors that modulate the risk are discussed, like the degree of selection and breeding of farm stocks, their divergence from the wild populations, the potential loss of adaptative traits in populations at risk, etc.

The impacts due to interbreeding are mostly speculative unfortunately. As mariculture continues to develop and wild populations' decline, the impact of interbreeding of escapees will become more important, this is a rather obvious conclusion but not stated (or I missed it).

It is stated that genetic changes in wild populations due to escapes and introgression is occurring, at least for salmon, and that the long-term implications for conservation remains a subject of debate. Personally, I think that this debate needs to take place for a risk evaluation to be made. What if the impact of introgression was not negative after all in some situations? Maybe some alleles and diversity can be lost, but for declining wild populations, it might be beneficial that escape fish colonize those environments where native fish do not thrive anymore – after all, several restocking projects are also in place.

A recommendation the group overlooked in order to reduce the risk of interbreeding would be to improve the biocontainment by developing better cages, adding extra barriers, developing land based culture, etc. But fundamentally, there is a need to be able to identify escaped fish, and distinguish them from wild stock, so that the assessment of interbreeding can be made. This is not easy, and the WGNAS report covered the difficulty of identifying escaped fish from wild fish.

It is commendable that the author(s) made an effort to cover as many farmed species as possible, although the literature for those species relates to the population diversity, but does not exist on the interbreeding of escaped fish with wild populations.

2) I found it clear and well structured and easy to appreciate. However, I was expecting that the first and longest species section in the review under "State of Knowledge" would be on Atlantic Salmon, given that that is by far the best known example and by far the most important. So I'm not sure why salmon was left out of this review. The genetic implications are not reviewed in WGNAS and that WG seems to assume that salmon would be included in the WGAGFM report. Is this something that needs to be added at this stage? It seems to be a rather important part that has been missed.

Overall conclusion

1) Overall, there is a tendency to remain cautious and on the safe side when providing advices and recommendations, hence the risk assessment approach should be used everywhere when possible, and I favour the approach of the WGEIM format for this purpose.

In both the impacts of escaped fish on interbreeding, ecology and competion, etc, a fundamental point is the ability to identify escaped fish and distinguish them from wild stocks, either using tags or other external signs. This is well covered by WGNAS, but not mentioned by WGEIM or WGAGFM.

2) I don´t know if our mandate makes it possible to give any suggestions how to proceed. Because of the insufficiency of knowledge on disease interactions between mariculture and wild populations of fish, it might, however, be beneficial to include risk analysis professional(s) in the work. They might have conception of the ways to proceed in a situation, where there is quite a limited data basis for risk analysis work.

Annex 1

A few sections where noted where the conclusions and recommendations made are questionable:

Risk analysis:

- Part of the risk lies in cage structure and resistance to storms – this risk can be decreased, so it should be a recommendation.

- *Without opportunities for interception, even the best marking or tagging program will be ineffective at facilitating the identification and removal of aquaculture escapees from the wild. Aquaculture escapees have unimpeded access to the majority of salmon producing rivers across the North Atlantic* – I disagree, better marking/tagging should facilitate identification of aquaculture escapees. Management practices can be improved to avoid release of marked fish, or to trace fish entering rivers to the farm of origin and audit the farm security. Microtags should be considered as a mean of tracking escapes. The percentage of fish to tag on a farm is to determine based on cost, escape rates, etc (e.g. 10% in Ireland was mentioned, smaller % may be sufficient depending on the farm situation). This technique appears promising, especially for long term escapes which may lose physical characteristics allowing their identification. Programs to encourage and report the capture by anglers (without release) of escaped fish could be favoured.

- *The potential impacts of aquaculture escaped salmon would be highest for rivers where salmon populations consist of low numbers of individuals. Many rivers in NEAC are of small population size (based on river-specific egg requirements, less than 1000 fish) and therefore more at risk from aquaculture escapee incursions.* – Indeed, impact is possible but judgment on this impact (positive, negative) is debatable. The WGEIM provided a good discussion on the impact e.g. competition for resources, for mates, genetic inbreeding etc. How to measure the impact for a river under its reproductive baseline is not easy, some literature and reports are providing contradictory information. A recommendation should be to promote more research to evaluate this impact.