Working Group on Application of Genetics in Fisheries and Aquaculture (WGAGFA)

2020/FT/ASG02 The **Working Group on the Application of Genetics in Fisheries and Aquaculture (WGAGFA)**, chaired by Naiara Rodriguez-Ezpeleta, Spain, will work on ToRs and generate deliverables as listed in the Table below.

	Meeting dates	Venue	Reporting details	Comments (change in Chair, etc.)
Year 2021	10–14 May	Olhao, PT	Interim report by 30 June to ASG, SCICOM and ACOM	
Year 2022	TBD May	Sukarrieta; ES	Interim report by 30 June to ASG, SCICOM and ACOM	
Year 2023	TBD May	Leuven; BE	Final report by 30 June to ASG, SCICOM and ACOM	

ToR descriptors

ToR	Description	Background	Science Plan codes	Duration	Expected Deliverables
a	Documentation: How the rapid advances in genomics and analytical methods are revolutionising population identification in marine fish and invertebrate species	Stock identification has always been a major aspect of fisheries genetics. In the genetic context, the term “stock” means population or discrete breeding stock, and has biological reality. For populations to be accepted as the fundamental units on which assessment is based, it is essential to accurately classify these units, and ideally describe how they originated and are maintained. Until recently, population identification has been limited by the availability of sufficiently powerful molecular markers and analytical methods. Now however complete genome sequences are available for several commercial species, it is quick and economical to compile WGS for other species, and exponentially-increasing computer power has led to a plethora of new analytical methods. The aim of this proposed TOR would be to list and describe these methods, and their actual or potential application in population identification. It would be presumed that details would be constantly updated during the next three year period, thus ultimately producing an up-to-date document for publication. Power analyses would be invoked to calculate suitable sample sizes and locus number, and relative implications of different approaches would be compared. How these population entities were formed during post glacial range expansion and are maintained, for example, by heterogeneous spawning habitat, oceanic barriers and other factors would also be investigated. Many marine species, while homing to discrete natal areas to spawn, mix at other life history stages. These stages, usually involving harvest, would be investigated using mixed stock analysis (MSA) methods, presuming that sufficiently large differences can be demonstrated between component populations. Adaptive loci, under directional selection, might be particularly useful in the latter context, but also in investigating population response to climate change.	2.7, 5.6, 6.1	3 years	Review paper and metrics for measures of indirect genetic impacts
b	To review and evaluate the	A growing body of evidence suggests marine species display local adaptation over moderate to fine	1.3, 1.5, 1.7, 2.2, 2.5, 5.2, 6.1, 6.3	3 years	Review paper and recomendations on the use genomic data to

	potential of adaptative variation for assessing fisheries.	spatial scales, and the genes and genomic regions contributing to adaptive diversity (e.g., temperature, pathogens, etc.) have been identified in a variety of marine species. Yet despite this knowledge and widespread biodiversity losses across the North Atlantic, we still lack an understanding of species responses to disturbance, such as future climate change, in many commercially, culturally, and ecologically important marine species. The overarching goal of this ToR is to evaluate the current capacity to quantify relevant adaptive diversity in marine species; and explore how this information may be utilized in predictions of future biodiversity response to change. Specifically, we will review the literature regarding the genomic basis of adaptation in marine species, and examine how genomic architecture (e.g., single loci, CNVs, and chromosomal rearrangements) influences phenotype associations and our ability to resolve relevant variation. Secondly, we will evaluate new methods that utilize genomic data to establish an evolutionary framework for understanding adaptive diversity and to predict future responses. These will include "genomic vulnerability", a metric that quantifies the shift in genomic variation required to adapt to future change and uses machine learning to incorporate genomic descriptions of adaptive diversity, climate projections, and ecological modelling. Such approaches have the potential to identify highly vulnerable marine populations and transform science advice regarding fisheries management and marine conservation. Thirdly, we will provide recommendations for how this information could be practically integrated with existing advisory and management frameworks in the Northern Atlantic. Ultimately, this ToR will directly inform the use of genomic approaches to both quantify adaptive diversity and to predict future responses to disturbance in marine species.			predict future population responses to environemtnal change and disturbance.
c	To evaluate available genetic-based solutions to better understand the mesopelagic ecosystem.	Recent estimates suggest that mesopelagic fish represent 90% of the fish biomass of the planet, which has raised interest in exploitation of this unknown ecosystem. Yet, the high estimated biomass also suggests that mesopelagic fish might play a key role in sustaining other commercially relevant species and carbon sequestration. Thus, there is an urgent need to understand this still pristine ecosystem before it becomes too late to take protecting actions. This ToR could be dedicated to explore and evaluate the different alternative genetic methods available that could be used for that aim such as environmental DNA samples for estimating biomass and species identification, stomach content DNA analysis for understanding trophic networks, population genomics for	1.4, 1.6	3 years	Review Paper and non-technical review topic sheet.

		species connectivity and diversity as proxies for resilience, etc.			
d	**WGAGFA & WGSEDA**: Explorative cost-benefit analysis of genetic methods with emphasis on SME and conservation program broodstocks dedicated to aquaculture or natural population enhancement.	Managing genetic relation-ships and diversity within broodstock enables a long-term basis for both selection of improved food fish material for aquaculture production and supportive augmentation of natural populations. The loss of genetic variability due to inbreeding is detrimental for the cost-effectivity of re-stocking and it may even be impossible to retrieve variability again from the wild. While the use of genetic tools is part of day-to-day routines in large breeding companies, the lack of logistically feasible and cost-effective tools has so far prevented proper broodstock genetic management in SME's and conservation programs. This ToR is planned as a shared ToR between WGAGFA and WGSEDA and has linking points to WGs with fish stock conservation focus (e.g. WGNAS) and contributes to the Science Plan topics "Emerging techniques and technologies", "Seafood production" and "Conservation and management science"	4.4, 5.5, 7.6	1 (initially. - Reserving the possibility to extend further)	Explorative study on market availability for genetic breeding consultation and genotyping services, evaluating the occuring costs and contrasting these to their benefits in report form.

Summary of the Work Plan

Year 1	**ToR a)** Review the literature, with special focus on the application of genomic data analysis to the study of population structure and connectivity in exploited (directly or indirectly) marine species (vertebrates and invertebrates). **ToR b)** Review the literature regarding the genomic basis of adaptation in marine species, and examine how genomic architecture influences phenotype associations and our ability to resolve relevant variation. We will identify approaches that build on this genomic understanding of adaptive diversity, to predict future responses of populations to disturbance. **ToR c)** Produce an overview of the mesopelagic ecosystem, identify key species and review the literature on different genetic methods available to study this ecosystem. In addition to this overview, focus will be on identifing where especially eDNA and stomach contant DNA analysis are being used or could be used in the mesopelagic ecosystem. Identify the key species in the mesopelagic ecosystm with respect to the trophic network – create a simple flowchart. **ToR d)** Report on explorative study on market available genetic advices and genotyping services, evaluating the occuring costs and contrasting these to their benefits in report form. Evaluation of outcome and value of further deepening of anlysis. Decision as to whether ToR will be carried on.
Year 2	**ToR a)** Identify analytical approaches used and evaluate their power and accuracy. Start drafting an "analytical framework" that will attempt at standardising the sampling/processing/ statistical approaches to be used when producing results that will feed into management measures. **ToR b)** Evaluate new methods which build on a genomic understanding of adaptive diversity, to predict future responses of marine populations to distburbance These will include but not be limited to an examine of genomic vulnerability. **ToR c)** Continue the evaluation and identification of genetic methods as well as key species for studies of the mesopelagic ecosystem, including any relevant studies describing the ecosystem. Evaluate any new genetic methods for utilisation in studies of the mesopelagic ecosystem. Start to formulate review paper manuscript. **ToR d)** To be determined. Pending decision of year 1.
Year 3	**ToR a)** Complete review paper for publication and develop recommendations. **ToR b)** Complete a review paper for publication and develop recommendations. **ToR c)** Finalise and update the evaluation: identify problematic areas requiring future research as well as identify areas where novel techniques show particular promise. Finish review paper and non-technical review topic sheet. **ToR d)** To be determined. Pending decision of year 1 and 2.

Supporting information

Priority	The WGAGFA Terms of Reference for the reporting period 2021 to 2023 will produce information, knowledge and advice in line with the ICES Science priorities. Particularly ecosystem science, impacts of human activities, observation and exploration, emerging techniques and technologies and seafood production, as well as conservation and management will be tackled and reported upon.
Resource requirements	The research programmes which provide the main input to this group are already underway, and resources have been committed.
Participants	The Group is normally attended by some 15-25 members and guests.
Secretariat facilities	None.
Financial	No financial implications.
Linkages to ACOM and groups under ACOM	Joint SCICOM/ACOM group.
Linkages to other committees or groups	There is a very close working relationship with EPDSG, EOSG and EPISG. Additionally, several EGs, particularly WGSEDA but also including WGITMO, WGBIODIV, WGBOSV.
Linkages to other organizations	European Commission; Scientific, Technical and Economic Commitee for Fisheries (STECF); European Fisheries Control Agency (EFCA); GFCM; FAO; IFREMER, NOAA, DFO Canada.