

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

2017/MA2/ASG01 The Working Group on the Application of Genetics in Fisheries and Mariculture (WGAGFM) will be renamed the Working Group on the Application of Genetics in Fisheries and Aquaculture (WGAGFA), chaired by Jann Martinsohn, Italy/ European Commission, will work on ToRs and generate deliverables as listed in the Table below.

	Meeting dates	Venue	Reporting details	Comments (change in Chair, etc.)
Year 2018	15–17 May	Brest, France	Interim report by 30 June	
Year 2019	13–17 May	Ispra, Italy	Interim report by 30 June	
Year 2020	11-15 May	By correspondence	Final report by 12 June to ACOM and SCICOM	

ToR descriptors

ToR	DESCRIPTION	BACKGROUND	Science Plan codes	DURAT ION	EXPECTED DELIVERABLES
a	Review and report on genetic and genomic approaches for quantifying indirect genetics of salmon aquaculture on wild salmon populations	There is substantial existing evidence that interbreeding between wild Atlantic salmon and escaped domestic individuals occurs, and alters the nature and reduces the viability of wild populations. However, indirect genetic interactions may also occur. Caged or escaped farm fish can change the environment, so as to alter selective pressures and long-term fitness in wild populations even in the absence of direct interbreeding. This can lead to changes in the life history traits of wild populations, decreased survival, and reductions in population size. The production of all-female sterile triploids is seen as an approach to reduce the likelihood of effects on wild fish populations. In North America a large expansion has been approved involving the production of 7 million triploid Norwegian salmon annually. The use of triploid all female salmon is expected to reduce direct genetic interactions though the actual magnitude of direct and indirect genetic interactions remains unknown). This ToR will review the literature and explore the potential for genetic and genomic tools to quantify indirect interactions with wild salmon populations. This will involve the assessment of genomic tools to allow quantification of changes in wild populations due to changes in the selective landscape (i.e. disease, parasite, competition); as well as the estimation of effective population size of wild populations to allow declines in wild population size due to indirect effects to be quantified.	2.7, 5.6, 6.1	3 years	Review paper and metrics for measures of indirect genetic impacts
b	Review and report on principles of and prospects for genomic selection applied to aquaculture species	Genomic selection is a genome-wide marker-assisted selection method that caused a revolution in terrestrial animal and plant breeding in the last decade. Expected gains, such as acceleration of breeding cycle, increase of accuracy of prediction of multi-trait performance, are particularly high for long-lived species. The development of high-throughput SNP arrays for an increasing number of species now allows the potential implementation of genomic selection in aquaculture. However, biological characteristics of most aquaculture species request specific optimization of genomic selection studied prior to their application for these species,	4.1, 4.5, 5.5	2-3 years*	(a) Review Paper (b) seafood production brief (c) Publication

as clearly demonstrated by simulation studies. Results are promising as recent genome-wide association studies in different salmonid species have concluded that genomic selection could efficiently contribute to improve disease resistance. The present ToR will introduce basic principles of genomic selection and the key steps of its implementation in breeding programs. It will focus on current progresses and prospects for aquaculture species and propose recommendations to facilitate its future developments in these species.

c	Assess and report on the value of genetic and genomic tools for identifying species in mixed landings, fish products and by-products.	<p>Mixed-species landings and the use of a mix of species in fish products continues to pose a formidable challenge to fisheries control and enforcement as well as traceability along the supply chain.</p> <p>In light of the difficulties in monitoring mixed species landings and identifying species in fish products and by-products we aim to elaborate whether genetic and genomic tools can provide robust and cost-efficient support to determine species composition, also quantitatively, and directly supporting fisheries management and policy needs. A timely and relevant example is the global attempt to develop and implement rules that lead to the reduction of discards. Discarding is the rather common practice of returning unwanted catches to the sea, either dead or alive, because they are undersized, due to market demand, the fisherman has no quota or because catch composition rules impose this. In Europe, the reform of the Common Fisheries Policy (CFP) of 2013 aims at gradually eliminating this wasteful practice and seeks to phase in the implementation of the landing obligation (“the discard ban”) from 2015 through to 2019 for all commercial fisheries (species under TACs, or under minimum sizes) in European waters and for European vessels fishing in the high seas.</p> <p>The landing obligation requires all catches of regulated commercial species on-board to be landed and counted against quota. These are species under TAC (Total Allowance Catch, and so-called quotas) or, in the Mediterranean, species which have a minimum landing size (MLS – under the Landing Obligation: minimum conservation reference sizes (MCRS)). Undersized fish cannot be marketed for direct human consumption purposes whilst prohibited species cannot be retained on board and must be returned to the sea. The discarding of prohibited species should be recorded in the logbook and forms an important part of the science base for the monitoring of these species.</p> <p>https://ec.europa.eu/fisheries/cfp/fishing_rules.</p> <p>It is generally acknowledged that the implementation of the landing obligation is a highly challenging and complex endeavour. For example, how can it be assured that no prohibited species have been landed and that undersized fish are in fact from the officially reported species, given that in both cases the landed biomass tends to be immediately processed for products that are not for direct human consumption? These potentially mixed species samples are very difficult to identify once they have been processed, especially when considering products like fish oil and gelatine. Genetic and genomic methods might help with the challenge of ensuring that these “by-products” only contain the undersized catches (or potentially non- commercial</p>	1.6, 2.7, 6.3	3 years	a) Review Paper; b) ICES Viewpoint.
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bycatch species) but no other, illegal-to-land, species which might have been processed as “undersized, animal-by-products”.

If undersized commercial species need to be processed separated from bycatch species, genetics tools might further help to test if this is in fact the case in a given situation or if for example commercial species are being processed as “bycatch” to avoid overstepping a quota. If both do not need to be processed separately, the relative proportion of them within a product should be roughly according to their reported catch proportions. Focussing on, but not dealing with exclusively, we will elaborate whether genetic methods might efficiently support the implementation of rules designed to reduce discards and related control, monitoring and enforcement measures.

d	eDNA in Fisheries Management and Ecosystem Monitoring	<p>Developments in the field of genetics have transformed our understanding of the natural world. In a fisheries context among other things it has helped us identify species, define population structures, begin to understand the genetic basis of adaptive traits and monitor adaptive population changes. Typically such insights have been gained from analysis of DNA obtained from tissue samples collected directly from individuals across a study area. Additionally, the analysis of DNA through metabarcoding from a bulk sample composed of a mixture of individuals of different zooplankton and/or macroinvertebrate species has enabled more cost-effective biodiversity assessments. Recently however, a new source of DNA has begun to be used for analysis of macro species, so-called “environmental DNA” (eDNA), which relies on collection of DNA sloughed off from tissue (e.g. skin, blood, faeces, mucous, eggs) into the natural environment. This eDNA promises to revolutionise the examination of biodiversity in the wild by allowing the detection larger organisms without needing to sample them and may be of particular usefulness in the marine environment where traditional sampling is difficult to carry out.</p> <p>A number of approaches using eDNA have been utilised already and/or are under development. These include species identification (especially useful for rare/cryptic/small individuals), community composition, ecosystem monitoring, relative species abundance and even attempts at absolute species abundance. In the aquatic environment such techniques have often been developed in freshwater ecosystems but are now beginning to be utilised in the marine environment. As such there is a growing recognition that the use of eDNA in the marine sphere may in the near future bring powerful new tools to the arsenal of the fishery manager and also allow new approaches to ecosystem monitoring. However, there are also numerous caveats associated with eDNA approaches linked to sampling strategies, DNA stability in different environments, analytical approaches etc. that require expert attention to enable proper interpretation of study data. This ToR will summarise the research to date, identify areas where tools are already available for use and examine future developments whilst crucially seeking to also identify areas where the use of the new approaches should be undertaken with care if at all. The ToR will also try to produce a non-technical summary of the state of the field for direct</p>	1.6, 4.1, 4.4	3 years	(a) Review paper (b) Non-technical review topic sheet.
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dissemination to fishery managers with little or no genetic background.

Summary of the Work Plan

Year 1	<p>ToR a) Review the literature on indirect genetic interactions among aquaculture salmon and wild populations.</p> <p>ToR b) Review of the basic principles of genomic selection and the key steps of its implementation in breeding programs, focus on current progresses and prospects for aquaculture species and propose recommendations to facilitate its future developments in these species.</p> <p>ToR c) Review the legal framework and supporting information, such as reports on the Landing Obligation by the Scientific, Technical and Economic Committee for Fisheries (STECF); identify the stakeholders; develop a work flow chart to work up mixed species samples, with decision points; develop theoretical scenarios/cases where genetic testing would be helpful and how the implications would be for a given outcome.</p> <p>ToR d) Review of the literature on the use of eDNA in the aquatic environment. Together with an overview of the field, particular focus will be to identify where eDNA techniques have/are being used at present in the marine environment and on other techniques used in freshwater that may be utilised in the marine sphere. Produce a glossary or commonly used terms in the field.</p>
Year 2	<p>ToR a) Identify approaches to quantify indirect genetic impacts and explore their sensitivity and power.</p> <p>ToR b) Develop cases where genomic selection would be helpful and how its implementation would benefit selective breeding programs.</p> <p>ToR c) Real-life scenario test based on developed work flow chart (from year 1) using real product samples; report results and discuss; report on feasibility and cost issues; recommendations to adjust methods/work flow developed in year 1 if needed.</p> <p>ToR d) Continuation of the literature review and identification of key studies describing the use of eDNA in the marine environment where the techniques used have significant potential for novel species and/or situations. Produce a flowchart of the critical steps needed from sampling to biodiversity assessment. Start to formulate review paper manuscript.</p>
Year 3	<p>ToR a) Complete review paper, and develop recommendations.</p> <p>ToR b) Develop a knowledge transfer plan; industry briefs; publication; implications, advice and final recommendations.</p> <p>ToR c) Develop a knowledge transfer plan; topic summaries; publication; implications and recommendations.</p> <p>ToR d) Finalise and update review: detail key studies, identify areas where novel techniques show particular promise, and identify problematic areas requiring future research. Finish review paper and non-technical review topic sheet.</p>

Supporting information

Priority	The current activities of this Group will lead ICES into issues related to the sustainable management of fisheries and aquaculture practices, monitoring of marine biodiversity and ecosystem function, and assessing the species composition of fish products and by-products. Consequently, these activities are considered to have a very high priority.
Resource requirements	The research programmes which provide the main input to this group are already underway, and resources are already committed. The additional resource required to undertake additional activities in the framework of this group is negligible.
Participants	The Group is normally attended by some 15-20 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, including WGITMO, WGBIODIV, WGBOSV.
Linkages to other organizations	European Commission, IFREMER, NOAA, DFO
