Sustainable management and improvement of genetic resources for aquaculture

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Acronyms

Acronym	Meaning
ABS	Access and Benefit Sharing
AqGR	Aquatic Genetic Resources for Food and Agriculture
CBD	Convention on Biological Diversity
CITES	Convention on International Trade in Endangered Species of Wild Fauna and Flora
DAD-IS	Domestic Animal Diversity Information System
FAO	Food and Agriculture Organization of the United Nations
GLIS	Global Information System on Plant Genetic Resources for Food and Agriculture
IUCN	International Union for the Conservation of Nature
MAT	Mutually Agreed Terms
NP	Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity
OIE	World Organisation for Animal Health
PIC	Prior informed consent
R&D	Research and Development
SNP	Single Nucleotide Polymorphism
SoW AqGR	The State of the World's Aquatic Genetic Resources for Food and Agriculture
TK	Traditional knowledge
UPOV	Union for the Protection of New Varieties of Plants
WIEWS	World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture

Summary

Effective genetic management of the ~700 aquatic species that are cultured globally is an important factor that must be addressed for global aquaculture to make a significant contribution towards meeting the Sustainable Development Goals of the United Nations. The aim of this paper is to identify the current status and challenges relating to management of farmed aquatic genetic resources (AqGR) and to make recommendations for future improvement of this management in four specific areas identified as needing increased attention.

The first section addresses sustainable use and conservation and covers farmed types and populations of their conspecific wild relatives. This section summarises the conservation status of key species and highlights some of the issues constraining the sustainable use of domesticated genetic resources used in aquaculture. This section highlights the importance of having information and monitoring systems to assess this status of genetic resources in the wild and throughout the seed supply chain. It notes the importance of identifying threated populations and setting up conservation programmes for these and of putting in place systems that can more effectively monitor of the status of domesticated resources and identify where interventions are necessary to ensure their effective genetic management. The second section is about risk management applied to manage genetic harm posed by distribution and production of introduced species, the use of which is already widespread in global aquaculture, and of developed farmed types which are becoming increasingly prevalent. It describes a step-by-step consideration of risk analysis for aquatic farmed types. The third section addresses the potential and technological development of breeding programmes as a tool to increase productivity and sustainability of global aquaculture production highlighting the urgency to accelerate the uptake of genetic improvement, especially of well managed selection programmes. The final section regards regulations addressing access to aquatic genetic resources and the fair and equitable sharing of benefit arising from their utilisation. This section highlights that national and globally applicable instruments and regulations are available, but are not always well suited to aquatic genetic resources and are generally little used.

In summary, there is great potential for utilising AqGR more effectively to enhance global food production, and the wild conspecific relatives of the farmed types make up a reservoir of genetic variation that can underpin the effective utilisation of these resources into the future. However, this utilization must be done responsibly both with regard to management of conspecific wild populations and domesticated resources under national jurisdictions. It is necessary to improve awareness of the importance of effective management and development of genetic resources and develop strategies and national and international regulatory instruments to support and transformation in the way in which vitally important resources are managed.

Key messages

Conservation and sustainable use

- The conservation status of wild relatives of farmed AqGR is threatened for some species, but there is an overall lack of information on the genetic status of most wild relative stocks. For most cultured aquatic species, there is a similar lack of information on genetic status, particularly below the level of species (i.e. farmed types). This lack of information constrains the implementation of effective conservation and genetic management for their long-term sustainable use.

- To enhance understanding of the genetic status of key farmed aquatic types and plan necessary interventions to conserve genetic variation for the future, there is a need to identify key threatened genetic resources with a focus on wild relatives, and to develop information systems that will enhance the monitoring of farmed types and the identification of threaten wild-relative genetic resources. Based on this identification, specific *in situ* and/or *ex situ* conservation programmes should be developed.

- Cost effective molecular tools to enable widespread monitoring of the genetic status of domesticated farmed types should be developed and applied within major seed supply systems, enabling targeted interventions to secure the future potential for development and conservation of these resources.

Risk assessment and management of non-native and developed farmed types

- Culture of non-native species and well-developed farmed types delivers economic benefit to aquaculture and underpins significant aquaculture production in many countries, but also can pose environmental/ecological risks to natural ecosystems and genetic risks to native AqGR including conspecifics.

- There is a need to apply existing frameworks to assess, communicate and manage risks of culture of non-native species and developed farmed types, and also to assess the possibilities of expanded culture of native species.

- Responsible stakeholders in member countries should develop and apply policies and provide training to promote utilization of the risk assessment framework to culture of non-native and developed native species to promote sustainability of their aquaculture sector.

Genetic improvement

- Selective breeding is a proven and powerful tool to increase production efficiency, product quality and disease resistance, among other traits. The principles of selective breeding are well established and transferrable with adaptation to the reproductive specificities and production systems of any species, with the potential to deliver large long-term benefits for the aquaculture industry. There is a low uptake of selective breeding, and it is evident that the potential of selective breeding is heavily underutilised in aquaculture.

- In order to increase the uptake of selective breeding in domesticated aquaculture farmed types, especially for incipient farming systems and aquaculture activities producing low-value species in both developing and developed countries, it is necessary to develop applicable business plans, breeding plans and long-term financial support instruments.

- Strategies for developing successful long-term selective breeding programmes must be implemented, including partnerships between public and private players, to execute the breeding programmes and to effectively disseminate the selectively bred material. These strategies should be supported by education and raised awareness of the costs and benefits of long-term selective breeding and related techniques among aquaculture producers and other stakeholders.

Access and benefit sharing

- There is a need to ensure access to AqGR for research and development (R&D) as well as to share the benefits arising from the utilisation of these resources. Countries that decide to adopt access and benefit-sharing (ABS) measures need to be aware of the distinctive features of AqGR.

- Many countries have adopted or are in the process of adopting ABS measures relevant to AqGR and associated traditional knowledge (TKAqGR). However, there is large variation in existing ABS measures, and there is a lack of knowledge on how ABS measures and patents affect AqGR R&D, including in selective breeding.

- The awareness and understanding of stakeholders of ABS and patents and their capacity to operate within this legal environment at national, regional and global levels need to be improved. A way forward includes building capacity among relevant stakeholders concerning how to accommodate the distinctive features of aquaculture AqGR/TKAqGR subject matter and activities, when developing, implementing and reviewing national ABS measures.

1. Genetic diversity in aquaculture: monitoring, characterization, conservation and sustainable use

Current status

Domestication in aquaculture is relatively recent, with a few exceptions, such as common carp (*Cyprinus carpio*), for which domestication may have occurred in China about 3000 years ago (Hu et al., 2018; Zhang et al., 2019) and in Europe during the early Roman Empire in the first and second centuries A.D. (Balon, 1995). Duarte et al. (2007) report that 97% of cultured aquatic species entered domestication in the 20th Century. In consequence, most present-day cultured farmed types still retain relatively high levels of genetic diversity compared to their wild relatives (Lind et al., 2012) in contrast to the situation with terrestrial livestock. This high genetic diversity of the aquaculture populations gives these population a high potential to deliver significant gains in commercially important traits through selective breeding, 13% per generation was reported for growth rate (Gjedrem and Rye, 2016). Such genetic gains are rarely seen in terrestrial animal breeding. As will be discussed later in this section, this presents the opportunity to retain genetic diversity for the future, ensuring the potential for long-term genetic gains, through effective management of genetic diversity in domesticated farmed types.

Wild stocks (i.e. wild relatives of farmed species) still exist for all reported aquaculture species, although some are threatened, including by habitat change, aquaculture activities and overfishing (FAO, 2019a). While we know that these wild relatives can be found in nature, we often do not know whether these wild relative genetic resources are impacted by anthropogenic activities, as we lack information on these stocks' genetic status. An initial analysis of the conservation status of cultured species (Lucente *et al.*, 2021) indicates that up to 5.4% of these species are listed in the CITES appendices of endangered species (www.cites.org), and 9.6% of cultured species referenced by the International Union for Conservation of Nature are listed with status as vulnerable or worse (www.iucn.org). Wild-relative genetic resources are essential reservoirs of genetic diversity for future genetic management of the species in the wild and for farmed types. We thus have the incentive to protect our wild relative resources and to try to ensure that none will become extinct, thereby retaining the opportunity to utilize this genetic resource now or in the future.

In the context of aquaculture, 'conservation' and 'sustainable use' of AqGR are not synonymous. Conservation relates mainly to wild relative genetic resources and a subset of important domesticated farmed types. As outlined in the second section of this paper, there are relatively few improved farmed types, certainly when compared to terrestrial agriculture. However, the number of farmed aquatic species (nearly 700 are reported - FAO, 2019a) is much higher than for terrestial animal species (38) (http://www.fao.org/dad-is/en/). Given that the aquaculture industry is in the relatively early stages of development of its genetic resources and breeding programmes have yet to establish differentiated farmed types for most species, there are relatively few developed farmed types (e.g. strains of aquatic animals and varieties of aquatic plants and seaweeds) that must be conserved, certainly when compared to the many breeds of livestock that are threatened.

The main exceptions where there are relatively large numbers of developed farmed types are common carp (*Cyprinus carpio)* and rainbow trout *(Oncorhynchus mykiss)*, which are aquatic species with relatively long histories of domestication and breeding. Bogeruk and Federatsii (2008) list 72 recognized breeds (farmed types) of common carp in Central and Eastern Europe alone.

Whilst there may not be a strong need for conservation of all these farmed types, especially where significant reservoirs of genetic diversity reside with wild relatives, it is nevertheless crucial that these developed farmed types are recorded and monitored to identify those that will need to be conserved. Thus, for AqGR, whilst it is important to conserve some developed farmed types, the current main priority for conservation is to preserve the wild relative genetic resources as the main reservoirs of genetic diversity for the future development of farmed types of aquatic species. These conservation efforts should focus on the important wild relative resources that are considered to be under threat. FAO (2019a) reports that most reporting countries recorded conservation efforts for AqGR, with the majority of these being *in vivo* conservation programmes such as aquatic protected areas, with only 260 *in vitro* collections being reported globally (mostly sperm cryopreservation). However, coverage of species was very limited in most countries.

Sustainable use relates narrowly to farmed aquatic species under domestication. For these it is vital that we recognize the opportunity to effectively manage and thus sustainably utilise these resources and conserve this genetic diversity before it is lost. There is a wide range of different approaches to managing genetic diversity during the domestication of species for aquaculture. Generally, the initial emphasis in early domestication addresses technical issues in artificial breeding and then scaling breeding systems to produce commercial quantities of seed. Often genetic diversity is not actively considered in these early stages when emphasis often is on meeting the demand for quantity of seed over quality. First, a common problem is that the genetic quality of base populations (the genetic resource on which the initial domestication process is developed) is often not adequately considered, and that base populations are often too small in both census and effective population sizes. Effective population size considers the ability of the population to maintain genetic variation based on the relationship among individuals in the population and is a function of the size of the population and the number of breeding individuals contributing to the next generation of broodstock. Second, often genetic variation is not managed well in the early stages, this being a clear problem if broodstock are large and expensive to rear such as for several marine finfish, which can lead to loss of genetic diversity (e.g., Hansen *et al*, 2006, Frost et al., 2007) and inbreeding. Also, given the relative ease of mating closely related aquatic species, hybridisation is often attempted. However, uncontrolled hybridisation can lead to species introgression, resulting in the loss of the discrete species e.g., in *Clarias* catfishes *Clarias macrocephalus* and *C. gariepinus* (Na-Nakorn et al., 2004) and in Chinese carp *Hypophthalmichthys molitrix* and *Aristichthys nobilis* (Mia et al., 2005). Poor genetic management practices amount to unsustainable utilisation of the genetic resource.

Typically, only when an aquaculture species sector reaches a certain scale and value, will thoughts turn to the genetic status of the domesticated farmed types and the potential for genetic improvement. There are many poorly managed aquaculture breeding populations suffering from inbreeding and genetic erosion (Evans et al., 2004; Li, Xu and Yu, 2007; Yue et al, 2009). The high fecundity of aquatic species and lack of managerial competencies in genetic management are major reasons for this. In these cases where genetic variation is lost through domestication fortunately, it is often possible to return to wild relative stocks to supplement genetic variation in farmed types. However, this approach can dilute the benefits of domestication selection for traits that enable farmed types to adapt and thrive in the artificial environment of aquaculture systems (Janssen, 2015). Sustainable use in the context of AqGR should thus apply to the effective genetic management of farmed types during and subsequent to the domestication process, irrespective of whether genetic improvement is prioritised. Unfortunately, the genetic status of most farmed types of species under domestication is unknown and is not monitored. This situation encourages speculation about the genetic status when adverse production events occur. The lack of information on the genetic status of cultured species below the level of species is a pervasive problem in modern aquaculture (FAO, 2019a).

There are very few countries that have developed information systems on AqGR at species level and even fewer that maintain records or monitor the status of farmed types. This often means that planners and policy makers are attempting to develop sustainable aquaculture in an information vacuum regarding AqGR.

Today's challenges and needs

With the majority of the world's aquaculture sectors lacking information about characteristics of its genetic resources there is a strong need to develop related information systems. The development of good information systems on these genetic resources and the targeted conservation and use of these genetic resources in the aquaculture sector would enable us to secure the future of our genetic resources more effectively, given our current level of understanding of genetic management issues (certainly relative to the levels of understanding prevalent at the time when most terrestrial species were being domesticated for agriculture). The fundamental basis of improved conservation and sustainable use of genetic resources in aquaculture must be the broader understanding and characterization of genetic resources and implementation of an information system or systems to make this information widely accessible. Several countries do have information systems at some level for their national resources (e.g., the German National Inventory on AqGR[1]), but each system records different information with different objectives in mind.

One issue that was noted in the development of *The State of the World's Aquatic Genetic Resources for Food and Agriculture (SoW AqGR)* (FAO 2019a) is the significant variation in the use and interpretation of terminology to describe AqGR, and the report identified a need to develop, harmonize and promote a standardized language for describing AqGR. FAO is developing a global information system for AqGR[1], utilizing a proposed standardized nomenclature around the concept of "farmed type" (Mair and Lucente, 2020). The adoption of more internationally standardized terminology and recording of information would greatly facilitate the organization and sharing of information on AqGR as DAD-IS[2] does for breeds of livestock and GLIS[3], WIEWS[4], Genesys[5], and UPOV[6] do for crops.

Whilst noting that some farmed types (particularly in the case of long-domesticated species) may require monitoring and a specific focus for conservation, this paper identifies wild genetic resources as the principal focus of efforts to conserve AqGR that represent the future potential to develop farmed types best suited to culture. It is essential to recognize which genetic resources are under threat, particularly concerning their relevance to food supply and human nutrition, and that appropriate efforts are made to conserve these resources. Some aquatic species are listed as under various levels of threat by IUCN and trade of some aquatic species is limited by CITES. However, Lucente *et al.* (2021) report that fully 50% of farmed species are classified by IUCN as data deficient or not assessed. The IUCN system is primarily focused on wild species and whilst it includes many aquatic species that are used as food (>8000), it does not have adequate focus on wild relatives of farmed species. Today there is no generic methodology or tools to classify the threat status of farmed types of AqGR and thus those that are deemed worthy of conservation are classified on an *ad hoc* basis by government technical advisers.

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[1] https://agrdeu.genres.de/?L=2
[2] http://www.fao.org/dad-is/en/
[3] http://www.fao.org/plant-treaty/areas-of-work/global-information-system/en/
[4] http://www.fao.org/wiews/en/
[5] https://www.genesys-pgr.org/
[6] https://www.upov.int

Furthermore, genetic resources of migratory species require coordinated transboundary approaches to their management and conservation.

Generally, in the conservation of wild relative genetic resources, where feasible, preference should be given to *in situ* conservation through habitat protection or rehabilitation, effective use of aquatic protected areas, and effective fisheries management for those species that are also fished. Often, the genetic implications of such conservation approaches are unknown, and the genetic status of species conserved *in situ* should be considered in addition to the size of fished populations. Where *in situ* conservation is not feasible or can be effectively complemented by *ex-situ* conservation, this should be considered and will become increasingly necessary as new farmed types are progressively developed. However, *in-situ, in-vivo* conservation requires monitoring and management of the genetic diversity within the conserved population and, to be effective, requires long-term resourcing, and thus widespread adoption is perhaps unlikely. One of the major challenges for conserving AqGR is the limited scope for *ex situ, in-vitro* conservation, given that, with a few exceptions, such as for bivalves and microalgae, the primary option for this is cryopreservation of male gametes, particularly fish sperm. To date, there has been little success in the cryopreservation of fish oocytes or embryos. It seems that, until such methods can be developed for multiple aquatic species, the role of *ex-situ in-vitro* conservation will remain limited.

The focus of sustainable use of AqGR is on applying existing understandings and methods to manage genetic variation and control inbreeding. There is considerable scope for improvement in awareness of the implications of how seed supply systems are established and managed, and particularly the mechanism for renewal of broodstock over generations. There is need to develop a changed mindset, in significant and emerging and in established aquaculture sectors, that seed quality (in the context of this paper, the genetic quality of the seed) is as important as the quantity of seed. In the development of an aquaculture sector for a species, genetic management (including the source base populations) should be considered as soon as significant seed supply systems are initiated. The principles of management of effective population size need to be applied in relation to the fecundity and generation time of the species in question. For most aquaculture species cultured around the world today, the basic principles of genetic management of broodstock have received little attention, with the resulting risk that the genetic status of the farmed types has already been compromised. There is a tremendous opportunity to put in place or adapt breeding and seed supply systems for aquaculture species, such that they focus on maintenance of genetic diversity as well as meeting the demand for quantity of seed.

There are also numerous examples of well managed and successful aquaculture breeding programmes (controlling inbreeding) using low tech equipment where identification of families and pedigree is managed by physical tagging and separate rearing of families until tagging (Gjedrem, 2010; Bentsen et al., 2017). These breeding programmes improve production performance, but they require careful management and infrastructure to implement effective management of families. This level of effective management of genetic diversity is far less common outside of organised breeding programmes. To realise the opportunity to enhance genetic management more fully across existing seed supply systems, it is highly desirable to have a cost-effective means of assessing the genetic status of farmed types, relative to that of wild relatives, especially the wild stocks from which the farmed types were derived. Whilst such genetic technology does exist, most cost-effectively through the application of appropriate single nucleotide polymorphism (SNP) panels or genotyping by sequencing, the access to and cost of such services could nevertheless be relatively high and prohibitive for low value farmed species in the developing world.

Therefore, such characterisation efforts remain mostly in the realm of R&D or commercial aquaculture in the developed world. There is thus a need for the development and dissemination of cost-effective genetic tools that can be applied across the seed supply chain for monitoring the genetic status of key genetic resources of major species/production systems enabling the maintenance of genetic diversity and avoidance of inbreeding. Possible options to enable this include the development of tailored marker systems and the strengthening of the necessary capacities and infrastructure, in developing countries and countries with economies in transition, for the implementation of more advanced genetic technologies. An example could be to develop national or regional mechanisms for quantitative assessment of genetic diversity within seed supply systems, possibly based on analysis of eDNA samples representing pooled DNA, using well designed marker systems. This might be best achieved with support of strong collaborative linkages between developed and developing countries.

The interaction between farmed types of cultured species and their wild relatives will be a prominent feature of the conservation, sustainable use, and development of AqGR. These interactions should be managed more effectively, including through appropriate management and conservation of wild resources, with a view to their current and potential future role in aquaculture in addition to their sustainability in the wild. Where cultured genetic resources, either derived from non-native species or farmed types of native AqGR, are potentially invasive, the harm they could pose to native wild genetic resources must be factored into any assessment of proposed introduction and use in aquaculture (refer to section 2). In line with a proposed target of the post-2020 Global Biodiversity Framework, which aims to reduce the number of introductions of potentially invasive alien species, introductions of non-native species should be based on low risk of environmental harm and high potential for economic benefit. The challenge in implementing such a strategy is the relative paucity of information on the impacts of non-native species introduced for aquaculture.

Lastly, the development of new species for aquaculture often competes for the same resources available for the development of farmed types of existing culture species. It is not easy to quantify the costs of developing aquaculture of new species, but unless a species is readily adapted to culture systems developed for other species, this requires significant effort in R & D and sometimes also in developing the value chain and the market for a product. Before investment in R&D for adapting these species in aquaculture, procedures to pre-evaluate new species should be established. Sometimes the objectives of developing a new species for aquaculture could be met, perhaps more cost-effectively, by adapting an existing cultured species through a suitably targeted breeding programme than by introducing/developing a new species. It is essential in the development of aquaculture production strategies, to set an appropriate balance between species diversification and the development and adaptation of existing cultured species. For example, rising temperatures due to climate change can challenge the tolerance ranges of existing cultured species. Such a challenge could be met by seeking a new species to farm in that environment or by developing or adapting a breeding programme designed to develop farmed types with greater tolerance to higher temperatures and/or greater temperature fluctuations. The cost and benefits of both approaches should be evaluated. There is thus a need for countries to take a strategic approach and strike a balance between introducing a new species to aquaculture and developing farmed types of existing species, based on specific target objectives, including the existing and projected market demand for associated products.

The way forward and key recommendations

There are several recommendations that address the needs and challenges in enhancing the conservation and sustainable use of aquatic genetic resources.

We must identify key genetic resources (mostly wild relative stocks, although some farmed types should be included) most under threat (globally, nationally and regionally) and develop appropriate responses using a combination of *in-situ* (preferred) and *ex-situ* conservation approaches. *In situ* conservation approaches could incorporate inclusion of conservation in fisheries management objectives habit restoration and restorative aquaculture. Genetic monitoring programmes of wild populations should also be considered, even if these populations are not under threat to better understand the genetic resource enabling reliable assessment the future risks of genetic introgression, selection of appropriate founder stock for domestication and to establish baselines for future monitoring (Vandeputte at al., 2002).

This may involve an analysis of the threat and conservation status of all major aquaculture species in all countries. Conservation efforts should be coordinated regionally for transboundary resources. Guidelines on conservation of AqGR should be developed. Given the limitations on the maintenance of *ex-situ and in-vivo* gene banks, it is further recommended to expand research efforts to develop methods for cryopreservation of oocytes and zygotes, embryos or diploid cells for threatened species recovery. Such techniques, where appropriate and cost effective, could greatly facilitate *ex situ* conservation programmes but may also enhance genetic improvement and dissemination for species with limiting reproductive characteristics.

Given the paucity of information on AqG, the future availability of a global information system for AqGR represents an opportunity to standardise the nomenclature and terminology with which AqGR are described, promote the appropriate characterisation and monitoring of these resources, facilitate the sharing of information on them, and facilitate access to them. We recommend the broad participation, by national focal points and investment of resources in the development of a global information system to populate this system with information on species and farmed types used in aquaculture. The availability of this information will provide a strong basis to inform the development of strategic management approaches for AqGR nationally and regionally and would be transformative in developing governance and policies aimed at improving this management.

There is a clear need to strengthen the role of genetic management in the development and implementation of seed supply systems for aquaculture to promote the sustainable use these important genetic resources. This recommendation is also valid for the management of gene banks, where currently proper management strategies and practices are often lacking. This can be achieved through effective capacity building and communication of the importance of genetic management and the consequences of poor management, including through education, training and extension and the promotion of simple guidelines. Furthermore, the development and wide availability of cost-effective genetic tools specific to cultured species (with initial prioritisation on lower-value species most important to food security) could be transformative in characterising genetic resources and preventing or identifying bottlenecks where intervention is necessary. For example, a species-specific SNP marker system could be applied to analyse the genetic status of farmed types at different points in the seed supply chain (e.g., breeding nucleus, multiplier hatchery, and growers) and compared to a benchmark, perhaps of wild relatives of the same species, to understand the implications of broodstock management through the chain, on the genetic diversity within the farmed type. Widespread use of such tools, combined with a broader understanding of the importance of genetic management in seed supply systems, could be a major step in securing the long-term future of our domesticated genetic resources for aquaculture.

2. Introduction of invasive species or farmed types (either native or non-native) – risk assessment and management, relevance

Current status

AqGR commonly farmed outside their natural range, such as common carp, salmonids, tilapias, shrimps and Pacific oysters, and developed farmed types that are differentiated from their conspecific wild types, comprise a large and growing component of global aquaculture production. Nine of the top 10 aquaculture species are farmed in more countries where they are non-native than where they are native (FAO 2019a). While the development and production of genetically improved farmed types may target increased aquaculture productivity, human well-being, and economic development, they also may pose ecological hazards to native ecosystems (Costa-Pierce 2003) and genetic hazards to native AqGR (Hallerman 2008).

Risk analysis is the formal process of identifying, assessing, and managing factors that may jeopardize achievement of a goal. In the context of aquaculture, the goal is to promote food security while protecting AqGR. Principles of risk analysis can be applied to manage genetic harms posed by distribution and production of introduced species and developed farmed types (Hallerman 2008). Risk analysis is a formal approach to estimate the likelihood of undesirable outcomes stemming from a given action. It seeks to identify risk pathways, estimate risk probabilities and consequences, develop procedures to manage risk, and communicate the results to stakeholders, thereby minimizing harm to aquatic and human populations. Principles of risk analysis have been applied to aquaculture (Bondad-Reantaso et al. 2006), including production of non-native species and developed farmed types. The scope of case studies regarding impacts of non-native aquaculture species and farmed types on AqGR is narrow, limiting our ability to predict and manage the likelihood of harms being realized from distribution and production of non-native species and developed farmed types. However, even with limited predictive ability, risk analysis provides approaches for managing risks to acceptable levels.

Risk analysis

Risk pathways. Aquaculture has been the justification for many introductions of species to regions where they are not native (FAO 2007). There is a large literature on harm posed by non-native species, including introductions pertinent to aquaculture. Environmental/ecological harms may be realized through competition, predation, habitat alteration, and transmission of exotic pathogens (including parasites in the term "pathogen") and pests (Table 1), that may add to and increase existing challenges from anthropogenic activities. While procedures exist for conducting risk analysis of non-native fishes (e.g., Zambrano et al. 2006), decisions on new introductions can be biased and often are based on incomplete data (Pullin et al. 1997). Hence, ecological impacts frequently are recognized only after introduction and establishment. The impacts of such introductions are not adequately studied, and associated risks of aquaculture-related introductions need to be more comprehensively assessed.

Table 1. Examples of ecological or environmental impacts of the introduction of non-native species for aquaculture.

Species or farmed type	Location and documented impact	Source
Golden apple snail (*Pomacea canaliculata)*	Introduced to several Asian countries from South America as a source of protein and supplementary farm income in the 1980s-1990s, the snail invaded rice fields, consuming rice seedlings. The economic cost in the Philippines alone was estimated at US$ 420,000-1,200,00 *per annum* (1990)	Halwart (1994), Naylor (1996)
Hybrid characiforms (*Colossoma macropomum*, *Piaractus mesopotamicus* and *Piaractus brachypomus*) and silurifomes (*Pseudoplatystoma corruscans*, *P. reticulatum*, and *Phractocephalus hemioliopterus*)	Produced in Colombia, Venezuela, Peru, Argentina, and chiefly in Brazil to yield genetically improved secondary farmed types, this process has resulted in fertile F_1 hybrids in aquaculture operations, which have been verified in the wild as farm escapees. In addition, assessments have reported the presence of post-F_1, introgressed individuals, confirming genetic contamination of wild populations, jeopardizing the gene pools of the parent species.	Vaini et al. (2014), Hashimoto et al. (2012, 2016)
African catfish *Clarias gariepinus*	*Clarias gariepinus* has been introduced to various countries worldwide for aquaculture. Its adaptations include the ability to withstand low dissolved oxygen, early maturity, and primarily its voracity, which qualify this species as highly invasive. Escapes from aquaculture and deliberate releases have resulted in the establishment of *C. gariepinus* in the wild in several countries, with the potential for habitat change and impacts on native species.	Rocha et al. (2008), Weyl et al. (2016)
Striped catfish *Pangasianodon hypophthalmus*	Striped catfish native to Asia have been introduced in many countries as an aquaculture candidate. Despite the large fish diversity present in Neotropical countries, with many species potentially suited to in aquaculture, striped catfish has been introduced to Brazil as an ornamental species and food fish. This introduction jeopardizes native fish species once escapees from aquaculture generate feral populations. The wisdom of this introduction for regional aquaculture is being questioned.	Garcia et al. (2018)
Oreochromis species	Tilapia species are moderately to highly invasive, with a 60%–90% probability of becoming established in new open waters of tropical and subtropical regions. Tilapia introductions have led to habitat alteration, including declines in aquatic plants and decreased availability of	Pullin et al. (1997), Moreau (1983), Canonico et al. (2005), D'Amato et al. (2007), Deines et

	breeding areas for native species. Africa is the center of tilapia diversity, with many species native to different countries. Since the 1950s, several waves of tilapia translocations were made to promote aquaculture and fisheries. Due to its superior culture qualities, Nile tilapia, native to northern Africa, has been introduced into many countries across the continent. Most *Oreochromis* species will readily hybridize, resulting in fertile progeny; thus, the introduction of non-native Nile tilapia jeopardizes the natural genetic diversity of native *Oreochromis* species, some of which are themselves candidates for regional aquaculture. Wild populations of Nile tilapia can be threatened by introduced farmed types, resulting in long-term erosion of genetic variation on which breeders may rely for future tilapia breeding programmes.	al. (2014), Shechonge et al. (2019)
Introduction of oyster *Saccostrea cucullata*	Native oysters along the Brazilian coast comprise two species, *Crassostrea rhizophorae* and *Crassostrea gasar.* Both species are essential fisheries resources for local communities. Moreover, due to its rapid growth rate, *C. gasar* is a candidate species for aquaculture. Since 2004, the presence of *Saccostrea cucullata,* native to the Indo-Pacific, has threatened populations of native oyster stocks, mostly due to competition for resources. Assessments have reported the fast establishment of this species in *Crassostrea* oyster banks, lead to declines of native *Crassostrea* populations.	Galvão et al, (2017); Amaral et al., (2020)
Introduction of common carp (*Cyprinus carpio*)	This is an example of a pathogen-related impact due to the introduction of common carp to various countries at the global level, both for aquaculture and ornamental purposes, which led to the introduction and spread of Koi Herpesvirus (KHV), which an OIE-listed disease, with devastating economic effects.	Motohiko et al. (2004)

Entry of farmed types into natural populations may pose genetic harm to receiving native populations. Such harm may be realized through loss of adaptation in natural populations, introgression of new genetic material into species' gene pools and in the extreme case, loss of locally adapted populations, (Box 1).

Box 1. – Genetic harm posed by farmed types.

Interbreeding of non-native or conspecific farmed types with natural populations poses risks of genetic harm. Natural selection operates upon fitness-related loci, mediating adaptation of populations to their environments. Spatial heterogeneity of natural selection results in adaptive genetic divergence of populations. Escape of widely cultured farmed types and their interbreeding with local populations of wild relatives can homogenize genetic variation. The best-demonstrated case studies involve salmonids (reviewed by Ferguson et al. 2007), although it should be noted that salmonids have a migratory life history that contributes to their susceptibility to genetic harm. Reviewing studies of the genetic effects of cultured fish on natural salmonid populations, Hindar et al. (1991) found a wide variety of effects, from no detectable effect, to complete introgression, and complete replacement of natural populations. Interbreeding of farmed with wild Atlantic salmon (*Salmo salar*) resulted in lowered fitness of the wild stocks, and repeated fish escapes resulted in cumulative fitness depression (McGinnity et al. 2003). Dramatic losses of fitness were observed after just two generations of captive breeding in anadromous rainbow trout (*Oncorhynchus mykiss*), as well as reduced fitness of their wild-born descendants (Araki et al. 2007, 2009). Conceptual models have been developed to predict the effects of introductions of maladapted individuals into locally adapted gene pools (Tufto 2001, 2010) and to predict the relative likelihoods of beneficial or negative impacts of gene flow on receiving gene pools (Garant et al. 2007). However, empirical studies of the effects of interbreeding of escaped farmed types upon populations of wild relatives are lacking for most cultured species. Hence, we lack the empirical data to parameterize models predicting the effects of introgression of farmed types into native gene pools.

Escape or release of interspecific hybrids, if fertile, pose the risk of harm due to introgressive hybridization. For example, hybrid catfish (*Clarias macrocephalus* x *C. gariepinus*) escaping from farms in Thailand interbred with native populations of *C. macrocephalus*, causing introgressive hybridization with both wild and cultured stocks (Senanan et al. 2004). Poor management of tilapia stocks led to unwanted hybridization of previously pure populations in the wild and in culture (McAndrew and Majumdar 1983, Macaranas et al. 1986). The genetic integrity of many Mozambique tilapia (*Oreochromis mossambicus)* populations is threatened by hybridization with Nile tilapia (*O. niloticus)* (Cambray and Swartz 2007, Weyl 2008). Mwanja and Kaufman (1995) showed hybridization in both directions among *O. niloticus* and *O. esculentus* in the satellite lakes of Lake Victoria, and no pure stocks of *O. esculentus* remain in these systems. In Bangladeshi hatcheries, 8.3 percent of farmed silver carp (*Hypophthalmichthys molotrix*) broodstock exhibited bighead carp (*Aristichthys nobilis*) alleles, and 23.3 percent of farmed bighead carp exhibited silver carp alleles (Sattar et al. 2005), compromising the integrity of the broodstock and their performance in aquaculture.

Overview of risk analysis framework. – Consideration of ecological and genetic harm posed by culture of non-native species or developed farmed types must be based on understanding of key concepts underlying the science and practice of risk analysis (Hallerman 2008).

A *harm* is a perturbation resulting in negative impacts to a population.

A *hazard* is an agent or process that has the potential to produce harm.

Risk is the likelihood of harm resulting from exposure to the hazard. Risk, *R*, is the product of the probability of exposure, P(*E*), and the conditional probability of harm given that exposure has occurred, P(*H*|*E*); i.e., *R* = P(*E*) x P(*H*|*E*). The steps in risk analysis, then, are to:

1) identify potential harms;
2) identify hazards that might lead to harms;
3) define and assess the likelihood of exposure, P(*E*);
4) quantify the likelihood of harm given that exposure has occurred, P(*H*|*E*); and
5) multiply the resulting probabilities to yield a quantitative estimate of risk.

Furthermore, risk (*R*) is the product of the likelihood (*p*) and consequences or damage measure (*x*) of undesirable happenings or scenario(s). A common definition of risk (e.g. Kaplan and Garrick 1981) includes a set of triplets (*R* = {<s_i, p_i, x_i>}, *i* = 1, 2 ,..*N*) and hazard is a set of duplets (*s* and *x*). Hence, it is important to consider a risk curve (or even a risk surface) rather than a single risk measure, because the risk of a low probability and big harm is not equal to a high probability and small harm. Furthermore, Arthur (2008) cites the definition of risk provided by the OIE where "Risk means the likelihood of the occurrence and the likely magnitude of the consequences of an adverse event to public, aquatic animal or terrestrial animal health in the importing country during a specified time period."

Exact probabilities of risk are difficult or impossible to determine for all types of possible harm. Indeed, it is unlikely that all possible harms would be known *a priori*, particularly regarding any indirect causal pathways. Hence, it may be necessary – based on current knowledge of population genetics, population dynamics, aquatic ecology, and empirical experience with farmed types – to classify levels of concern regarding likely ecological or genetic impacts posed by farmed types into qualitative categories ranging from "low" to "high".

Risk assessment might best be considered as embedded within an interactive framework involving a range of stakeholders (Figure 1). Involvement of the full range of stakeholders will bring all existing knowledge into the process, make the process transparent to stakeholders, and enhance the understanding and acceptance of the outcome of risk analysis. Stage I involves identifying the problem at hand, engaging stakeholders, identifying possible technical solutions to the problem at hand and identifying potential harms, risk pathways and assessment methods. Stage II is the risk assessment itself, leading to estimating the likelihood that harm could become realized should a proposed action be taken. Upon estimation of that risk, a decision is faced as to whether the risk is acceptable. If it is acceptable, the decision may be made to go forward. If the level of risk is unacceptably high, risk management measures would be identified, residual risk quantified, and the decision of whether to go forward would be reconsidered. Should the proposed action be implemented, genetic, environmental/ecological, and social outcomes should be monitored. Because all potential harms and associated pathways cannot be known and predicted *a priori*, it will be necessary to update the risk analysis as knowledge accumulates using an adaptive management approach (Kapuscinski et al. 1999).
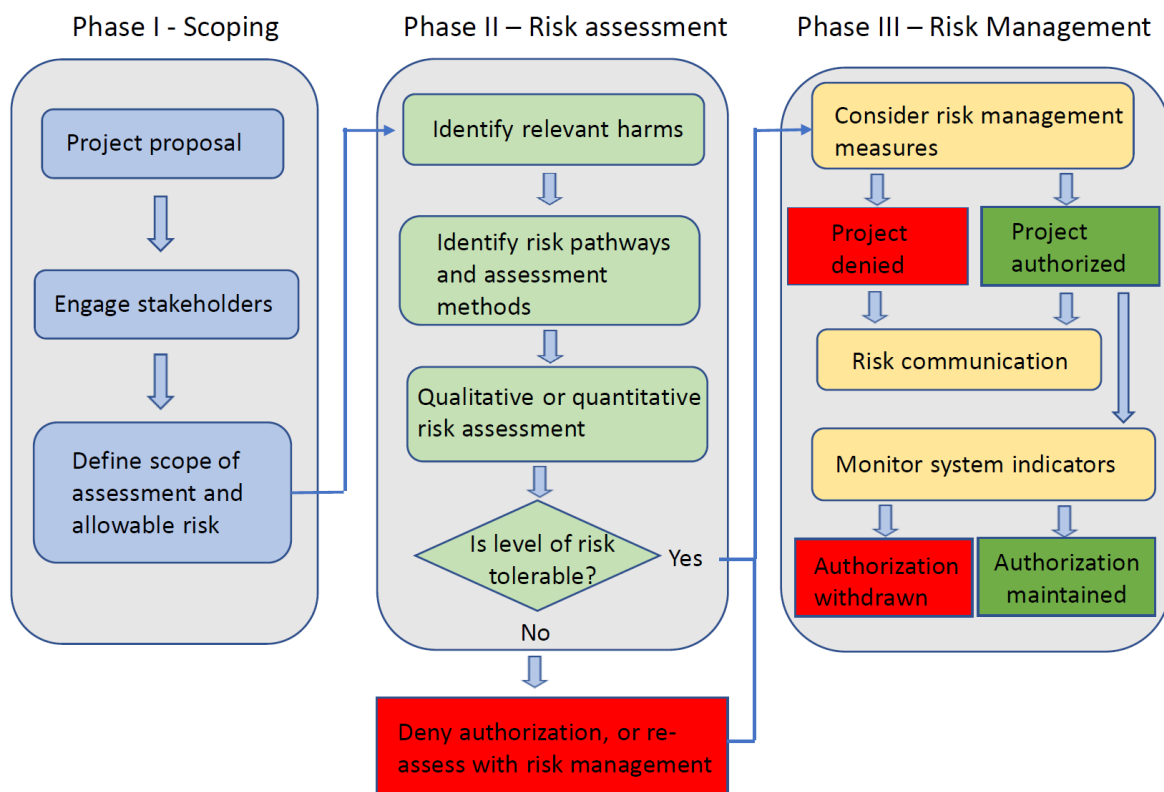
Figure 1. Overview of stages in the formal process of risk analysis and management.

Step-by-step consideration of risk analysis for aquatic farm types (either native or non-native)

Harm identification. Potential harms posed by culture of a farmed type relate to chains of events occurring after an escape or release from a culture system. Potential harm must be identified on a case-by-case basis and will depend on the phenotype of the organism, and not *per se* on the method used to produce the farmed type. Ecological harms posed by farmed types of tilapia are discussed in Box 1. Direct genetic harm would flow from the farmed type interbreeding or hybridization with reproductively compatible aquatic populations in the receiving ecosystem (Box 1). The degree of harm will be a function of the degree of differentiation among the two gene pools, the relative proportion of spawners from the respective groups and the natural selective pressure imposed by the receiving ecosystem. Escape or stocking of a non-native species or fertile hybrid poses the risk of interbreeding with reproductively compatible species in the receiving environment and the risk of introgressive hybridization.

Hazard identification. In this context, the hazardous agent is the farmed type because it is the entity that poses ecological or genetic harm to the receiving ecosystem or native populations.

Risk assessment. Realization of harm following exposure of a natural ecosystem or native population to a farmed type would require the occurrence of a chain of events. Aquaculture operations frequently lose small numbers of individuals to the natural environment, with occasional catastrophic losses of larger numbers due to equipment failure, storm, or flood. However, for a farmed type to prove a hazard, it must establish itself in the receiving ecosystem. The likelihood that the farmed type will become established in the receiving ecosystem, $P(E)$, is dependent on the species' invasiveness, the fitness of the farmed type, and characteristics of the receiving ecosystem (Hallerman 2008).

Evaluating ecological or genetic risk will have to be conducted on a case-by-case basis. The likelihood of harm being realized given exposure to a farmed type is difficult to quantify, especially given lack of empirical data for the many farmed types at issue, resulting in this being currently the weakest aspect of applying risk analysis. We often will be restricted to evaluating risk qualitatively based on: (1) the species, (2) the effect of genetic change on the fitness of the farmed type in the receiving ecosystem, and (3) the stability and resiliency of receiving community.

The outcome of such risk analysis is likely to be a prediction that likelihood of harm given exposure to a farmed type is "high", "medium", "low" or "negligible". That prediction might then be compared to the "acceptable" level of risk to determine whether to go ahead, whether to reconsider the action under conditions of risk management, or whether to reject the action at issue. As was mentioned above, the balance between possible risks and expected benefits of a certain introduction is key in decision-making. Therefore, within the risk assessment, the likelihood (introduction, survival and spread) and the consequences are assessed; the combination of the likelihood and consequences assessment will provide the final risk rating, which is necessary for the overall risk assessment and risk management.

To summarize, the risk assessment process is based on the following steps:

1. Assessment of the likelihood of introduction or release.
2. Assessment of the likelihood of spread or exposure.
3. Calculation of the likelihood rating, based on the release and exposure assessment.
4. Assessment of the consequences derived from the release and exposure of farmed stock to the pathogen.
5. Calculation of the final risk rating, based on the likelihood rating and the consequences assessment.

The following risk rating matrix is based on the ISO 31000:2018. risk management guidelines (ISO 2018).

Table 2. Risk rating matrix (ISO 2018)

Likelihood of hazard entry, establishment and spread	Consequences of hazard entry, establishment and spread					
	Negligible	Very low	Low	Moderate	High	Extreme/ Catastrophic
High	Negligible risk	Very low risk	Low risk	Moderate risk	High risk	Extreme risk
Moderate	Negligible risk	Very low risk	Low risk	Moderate risk	High risk	Extreme risk
Low	Negligible risk	Negligible risk	Very low risk	Low risk	Moderate risk	High risk
Very low	Negligible risk	Negligible risk	Negligible risk	Very low risk	Low risk	Moderate risk
Extremely low	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Very low risk	Low risk
Negligible	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Negligible risk	Very low risk

The term acceptable level of risk (ALOR) describes the likelihood of an event whose probability of occurrence is small, whose consequences are so slight, or whose benefits (perceived or real) are so great, that individuals or groups in society are willing to take or be subjected to the risk that the event might occur. Appropriate level of protection (ALOP) is the level of protection deemed appropriate by the member (country). ALOP can be regarded as an acceptable level of risk or tolerable risk.

Risk management. Should an oversight body determine that distribution and production of a farmed type poses harm to a receiving ecosystem or native population, the question turns to managing the associated risk. Risk management is the design, selection, and implementation of a programme of actions to minimize risk to an acceptable level. The best approach to minimize likelihood of harm being realized is to minimize exposure to the hazard. Four non-mutually exclusive approaches include: (1) geographic location, (2) physically confining the farmed type on aquaculture facilities, (3) reproductively confining farmed types and (4) operations management.

Risk communication. Risk communication transmits the ongoing process and results of risk analysis to key stakeholders, who would include international, regional and national agency/government officials (national, regional and international agencies, including FAO), aquaculturists, nongovernmental organizations, academic researchers, and the general public. Different groups of stakeholders will be reached most effectively by different means.

Today's challenges and needs
There is a need to raise the debate among fish farmers about the importance of AqGR to the sustainability of fish production in the long term.
Greater application of risk analysis is needed in the aquaculture, research, and government sectors, as introductions of either native or non-native species and farmed types that can become invasive is a common practice in many countries and these genetic resources continue to make large contributions to aquaculture production. Policy makers must have the necessary tools and scientific information derived from a well-developed risk analysis to balance benefits and risks associated with the introduction of native and non-native AqGR that can become invasive in a specific context. Concerns regarding genetic harm apply to non-native species and developed farmed types of native species.

Improving confinement of farmed types at aquaculture operations is necessary to promote the protection of native AqGR in adjacent aquatic ecosystems. There are existing related models for the development, implementation, and verification of best management practices for aquaculture operations (Tuckett et al. 2016).

Aquaculture risk assessment, risk management and risk communication (which are three pillars of the risk analysis process) are emerging areas in aquaculture science. While the risk pathways are reasonably well known, the associated risks are not well quantified. Much information potentially useful for risk analysis of farmed types is scattered across the scientific and grey literature. Understanding of some key issues – e.g., fitness of farmed types in the wild and likelihood of outbreeding depression following interbreeding of wild and farmed types – is still emerging. Furthermore, many wild populations are not well characterized genetically, plus wild populations previously thought to be undifferentiated have turned out to be differentiated when SNPs are used as opposed to microsatellites, uncovering evidence of local adaptation. In practice, it is more difficult to assess the risk of introducing a non-native species than that of a developed farmed type. Development of quantitative risk analysis, especially regarding estimation of likelihood of harm becoming realized given exposure to a farmed type, is incomplete.

18

While application of principles of risk analysis to issues pertaining to farmed types has been described conceptually, there are relatively few empirical case studies. Leading examples include assessment of risks posed by field testing of transgenic common carp at Auburn University (OAB 1990) and introduction of triploid Asian oysters into Chesapeake Bay (Dew et al. 2003, NRC 2004). Risk management, while widely applied in research facilities, is not widely applied in commercial aquaculture operations. We need risk assessments of farmed-type escapes and introgression with wild relatives and synthesis of findings from such studies. We do not yet have a body of case studies to exemplify effective communication of aquaculture risk management.

Operation-level practice of risk assessment and management will not become commonplace unless required. There is a need for incorporation and implementation of risk assessment and management in aquaculture development policy.

Considering the uncertainty surrounding the impacts of non-native species and farmed types on native ecosystems, a precautionary approach has been recommended by FAO and others (FAO 1995). The precautionary approach calls for establishment of target and limit reference points, pre-agreed actions when reference points are reached or breached, and a monitoring system. The precautionary approach allows development to continue in the face of uncertainty. The establishment of reference points and pre-agreed actions needs to involve key stakeholders and sectors, e.g., from private industry, government, academic, and conservation. Reference points generally have not been established for genetic parameters, but they can be formulated. In general, the approach has not been widely used in natural resources management and monitoring the ecological and genetic impacts from introductions is very uncommon (Bartley, and Funge-Smith 2018).

The way forward and key recommendations
There is a need for developing or strengthening national policies regulating the introduction of non-native species and protection of indigenous AqGR. Such policy frameworks should make provision for the decision on introductions of non-native species or specific farmed types of native species based on science-based evaluation and consideration of potential risks and benefits. The potential need for introducing non-native species and developed farmed types for aquaculture production must be balanced with concerns for conserving native AqGR. Alternatives to non-native species, i.e., development of genetically improved farmed types of native species (recognizing that these may in turn present their own risks), must be considered, perhaps based in part on the strategic appeal of introducing new products into the marketplace.

Because aquaculture risk assessment and risk management are emerging areas, we need further risk assessment studies of farmed-type escapes and introgression with wild relatives and synthesis of findings among such studies. We need further effort in communication of aquaculture risk management to governments and aquaculturists. As examples of international guidelines and standards related to the risks associated with the introduction of AqGR, The International Council for the Exploration of the Sea has established protocols for governments to follow when considering the introduction of non-native species and farmed types (ICES 2012) that can be used. Furthermore, the OIE has specific guidelines and standards on the introduction of non-native aquatic species and farmed types from the pathogen-related perspective (OIE, 2019), and FAO has FAO Fisheries and Aquaculture Technical Paper. No. 519 *Understanding and Applying Risk Analysis in Aquaculture* (Bondad-Reantaso, 2008).

In the context of risk management, while reliable confinement can be achieved for capital-intensive aquaculture systems, more effort must be directed to developing and demonstrating cost-effective confinement systems for reducing escapes from small aquaculture operations. Among measures for reducing wild spawning, the utility of triploid farmed types for aquaculture varies among species and should be more widely assessed. Gene editing could offer the potential for inducing reversible sterility (Wargelius et al. 2016), although it is still a technical possibility needing further development, especially for other species.

The principles of risk analysis are established, and governments and non-governmental organizations need to apply it routinely to oversight of aquaculture. FAO can play a leading role in capacity building by training responsible parties, especially in the public sector, to raise awareness of risk perception, assessment, management, and communication. FAO can present reports of case studies of successful implementation of policies promoting risk analysis in the aquaculture sector. FAO and regional bodies can also play role in developing harmonized policies on introduction of species, among the countries which share water flows.

3. Genetic improvement- the role of public and private sectors, dissemination, and seed supply

Current status
Selective breeding is an important contributor to advancing global aquaculture for addressing the Sustainable Development Goals of the UN, such as the SDG 14.7. For example, the WorldFish and partners created an improved strain of Nile tilapia, called the Genetically Improved Farmed Tilapia (GIFT), by pioneering a systematic breeding method. This was based on selective breeding programmes for salmon and trout established in Norway in the 1970s. By selecting broodstock that are superior for important traits, the performance of the entire population is improved. This process of selective breeding is a proven and powerful tool to improve traits such as production efficiency, product quality and disease resistance in domesticated farmed types of cultured species (Gjedrem et al., 2012). Selective breeding is also an important approach to adapt populations to a changing climate, e.g., through selection for temperature/hypoxia tolerance. Similarly, increased genetic gain for feed efficiency will reduce the required amount of feed for the same product output. Selective breeding is a cumulative process, where the genetic gains of the current generation build on the genetic gains of the previous generation, and where the natural additive genetic diversity in the population is utilised to attain genetic improvements. Genetic improvement thus has a very major role to play in the sustainable growth of aquaculture.

Selective breeding is a technology applied to virtually all terrestrial farmed animals and certain plant genetic resources. However, reproductive specificities, degree of technology development and industrial maturation impact the cost and benefits of breeding programmes. Properties specific to aquaculture breeding programmes include the potentially very large number of individuals that can be produced from each family given the high fecundity of many cultured species. Also, in most cases, individuals cannot be tagged with individual identifiers until later in life when they have reached a sufficiently large size. These specificities in aquaculture breeding programmes generates certain requirements for infrastructure, often in the form of multiple smaller holding units where families can be reared until tagging. It also results in unwanted structure in the data used for genetic analysis. An alternative system can be used, where large mixed sex groups of broodstock are spawned in a few large tanks or individuals in early life stages from several families are pooled. These systems have less precise control of the family contribution in a population and needs to be compensated by increasing the number of individuals that need to be tested for different traits and genotyped to track pedigree and calculate genomic breeding values.

There also exist low-cost options of mass selection programmes as presented by Gjedrem (2005) and Sonesson et al., (2005). In general, the large number of individuals results in very high rates of genetic improvement, due to the potentially high selection intensity and high levels of genetic variation often present in recently domesticated species.

Aquaculture breeding programmes can have large effects upon aquaculture production systems, with genetic gains of, on average, 13% per generation for growth rate (Gjedrem and Rye, 2016) for all aquaculture species. Genetic gains valued at 0.2€/kg have been reported after one round of selection of gilthead seabream (Janssen et al., 2018), and Atlantic salmon (Wu, 2021). However, selective breeding technologies are far from being fully utilised in the aquaculture industry. Zhou and Gui, 2015 reported that 156 strains had been developed in China using e.g. selective breeding and hybridisation, but in *The State of the World's Aquatic Genetic Resources for Food and Agriculture*, FAO (2019a) it is reported that over 40% of all aquaculture species were produced from unimproved wild types globally. Furthermore, 45% of reporting countries noted that genetic improvement is still not significantly impacting aquaculture production in their countries. In an older reference, Gjedrem and Robinson (2014) reported that less than 10% of the global aquaculture production was based on well-managed selective breeding programmes. Whilst it is likely that this proportion may have increased slightly, in general, the adoption of selective breeding to date is slow taking into consideration its proven cost-benefit and its potential to substantially enhance production efficiency in aquaculture. Table 3, which is adapted from FAO (2019a) and Hallerman et al. (2021) shows the top fifteen species or species groups (by production) and a subjective assessment of the status on their genetic improvement listed in order of their production in tonnes. These species account for 62.5% of global production (by volume).

Table 3. The top fifteen cultured species or species groups (by production volume) and the projected status of their genetic improvement at a global industry level.

Species/Species item	Genetic Improvement Status	Comment
Eucheuma seaweeds (Kappaphycus alvarezii, Eucheuma cottonii, Eucheuma denticulatum and Eucheuma spp)	Very low	Vegetative propagation predominates.
Japanese kelp (Laminaria japonica)	Low	Hybrids predominate; some genetically improved material is used.
Grass carp (Ctenopharyngodon idellus)	Very low	No selective improvement, but gynogenesis is used to some degree to induce disease resistance.
Silver carp (Hypophthalmichthys molitrix)	Low	Some selective breeding for growth, artificial gynogenesis is also used.
Cupped oysters (Crassostrea gigas)	Moderate - High	Selective breeding for e.g. disease resistance, growth, shell colour and glycogen content.

Common carp (Cyprinus carpio)	High	Many strains have been developed due to long history of domestication.
Manila clam/Japanese carpet shell (Ruditapes philippinarum)	Low	Some genetic improvement.
Nile tilapia (Oreochromis niloticus)	Moderate	Some commercial programmes. GIFT has been widely distributed, but many countries still culture unimproved farmed types
Whiteleg shrimp (Penaeus vannamei)	Very high	Several private, national, and multinational breeding programmes with global distribution.
Gracilaria seaweeds (Gracilaria spp)	High	Most production in China is from selective improvement programmes.
Bighead carp (Hypophthalmichthys nobilis)	Very low	No selective improvement.
Carassius spp.	High	Many strains have been developed due to long history of domestication. It has specific natural gynogenetic and sexual reproduction modes. Selective breeding and hybridization and cell engineering breeding are used techniques.
Labeo rohita	Moderate	The strain Jayanti rohu is developed through selective breeding and evaluated in farmer's field which revealed superiority of the strains over native variety. The dissemination through identified hatcheries, country-wide is put in place.
Catla (Catla catla)	Very low	Some selective improvement programmes initiated, but little progress to date and little or no impact on production

Freshwater fishes nei[7]	Very low	Few selective improvement programmes exist outside of salmonids and tilapias
Atlantic salmon (Salmo salar)	Very High	Close to 100% of production comes from GI programmes

The main components of a breeding programme are the three following tiers: i) a breeding nucleus that manages and develops the elite brood stock; ii) multipliers that propagate and disseminate improved seed to tier iii) consisting of farmers or growers. The multiplier tier is typical for lower-fecundity species such as salmonids and shrimps but are not prevalent for less-developed sectors and highly fecund marine species. Sometimes, the breeding programmes operate as specialised entities, but mostly the breeding activities are integrated within the farming enterprise among activities covering the value chain from reproduction to consumer product, thereby completing the value chain for that company.

Technological development differs greatly between breeding programmes, between species, and even within species, and reflects the degree of development of the breeding programme. Most aquaculture selective breeding programmes start with very simple breeding goals, including increased weight at a certain age. This is the development stage and most present-day breeding programmes are at this stage, for example programmes for shrimp, some tilapias, and carps. As the production systems mature, they tend to expand and intensify, and the breeding programmes expand correspondingly to include more traits, such as disease resistance; see also Figure 2. A large differentiating factor for the technological development of a breeding programme is whether the traits can be recorded on the individual selection candidates themselves, e.g., weight of the fish, versus on their siblings. In the case of the latter, sibling/family means are used for traits that are not easily measured on breeding candidates, e.g., disease resistance (because of infection risks) or carcass traits such as flesh quality or texture (requires slaughter). A breeding programme with the capacity to test for sib traits is more sustainable, because it can include a larger spectrum of traits, and therefore can take account of genetic correlations between important traits, but it also has higher operating costs. The largest modern aquaculture breeding programmes today record up to 20 traits, each with a different weighting within the overall breeding goal.

The use of genomic information in the breeding programme is another differentiating factor and is a means to enhance traditional selective breeding and add value and accuracy to the existing breeding programme. By including individual genomic information in the prediction of genetic values, the accuracy of selection of parents and genetic gain can be increased up to 100%, even for traits that cannot be measured on the breeding candidates themselves.

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[7]Nei – not elsewhere identified

There are two main ways to include genomic information in the prediction of breeding values:

- Marker-assisted selection, where genetic markers, that are closely linked to the quantitative trait loci (QTL), are used. Marker-assisted selection assumes that a thorough, sometimes time-consuming and expensive, gene mapping study identifies the genetic markers that should be included in the selection programme (Dekkers and Hospital, 2002). Once identified, only a small number of genetic markers may need to be assayed, which makes it very cost-efficient once the markers have been identified. However, many traits are polygenic and there are only a few examples of marker assisted selection in aquaculture, given the difficulty of identifying markers linked to the QTL for complex traits. The QTL for resistance to Infectious Pancreatic Necrosis in Atlantic salmon (Houston et al., 2008; Moen et al., 2009) is the most well-known example.

Genomic selection (Meuwissen et al., 2001) does not assume that the linkage between a marker and a single QTL is known. Instead, it utilises dense single nucleotide polymorphisms distributed across the whole genome (put on a SNP array or obtained using genotyping-by-sequencing) to predict genetic values of the selection candidates based on a prediction model developed in a training population. This typically consists of siblings or other relatives of the selection candidates. Genomic selection today is increasingly being applied in well-developed and well-resourced breeding programmes, see e.g., Zenger et al. (2019) for more details. The genomic selection designs of breeding programmes may differ (Nielsen et al., 2009; Sonesson et al, 2009).

Business plans, including cost-benefit analysis and financial instruments, are already established for mature commercial aquaculture sectors, but not in the less-mature or less commercialised sectors in both developing and developed countries. Many successful aquaculture breeding programmes receive public funding for their initial selective breeding activities (Hallerman et al., 2021). Often the selective breeding activity is integrated with the production activity in the company, although there are also many examples of breeding companies focused on management of broodstock and the commercialization of fertilized eggs or juveniles.

Whereas selective breeding is the basic technique to attain genetic gain over generations, there are related genetic and reproductive methods in use to achieve specific goals. Firstly, hybrid crossing between species, e.g., *Carassius auratus* × *Cyprinus carpio*, *C. auratus* × *Megalobrama amblycephala*, *Oreochromis niloticus* x *O. aureus* and *Clarias gariepinus* x *C. macrocephalus* is used to exploit heterosis, also called hybrid vigour and/or to combine specific and commercially important traits of both species. Whilst these breeding programmes are technically simple, they do require maintenance of two viable, well-managed and pure breeding populations of the respective species. Also, the genetic gains produced with hybrids are non-cumulative, and therefore need to be repeated at every crossing of parents. An advantage of hybrid crossing is the possibility to protect the intellectual property (IP) of the broodstock of the pure-breeding populations by controlling access to the parental farmed types. Secondly, monosex populations can be produced in some species, e.g., of Japanese flounders *Paralichthys* sp., yellow catfish and tilapias, because of benefits associated with sexual dimorphism, mainly in growth and sexual maturity. Thirdly, certain species e.g., blue mussels (*Mytilus edulis*), Pacific oysters (*Crassostrea gigas*) and salmonids, sterile individuals are produced through ploidy manipulation. Reasons for producing sterile individuals include investment of production into somatic tissues and not in reproduction, reduced risk of genetic interaction between wild and farmed populations, sometimes for improved product quality, and IP protection of the broodstock. Monosex and triploid production can be applied independently of selective breeding activities, and they do not result in cumulative genetic gains.

Selective breeding is a technology that utilises the natural genetic variation in each population to select the individuals that will become parents of the next generation, based on their own performance and on the performance of their siblings and other family members. The frequency changes of important gene variants are made relatively slowly over generations and cover the whole genome simultaneously. This approach should not be confused with production of genetically modified organisms (GMOs), where directed changes are made in the DNA of the fish, and the whole lineage could potentially be changed within one generation. Today, the AquaAdvantage® Atlantic salmon developed by AquaBounty (www.aquabounty.com) is a well-known example of a transgenic fish, where an additional copy of the growth hormone gene from Pacific Chinook salmon, under the control of a different expression-regulating promoter, was introduced. This fish is now on the market in the USA and Canada, the only example of a transgenic animal product available for human consumption.

Today's challenges and needs

Today's challenges and needs are to a large extent related to the low uptake of selective breeding by certain aquaculture industry sectors, especially for low-value species, small-scale farming systems and developing countries/countries in transition. This low rate of adoption of selective breeding in global aquaculture is a missed opportunity to increase production, efficiency, disease resistance and product qualitative and nutritional quality with the potential to significantly improve the sustainability of aquaculture and increase its contributions to the SDGs and, among other benefits, enhance mitigation of and adaption to climate change.

Financing of the selective breeding activity is pivotal, and (Olesen et al, 2015) identified development of appropriate business models for benefit sharing between the breeding, multiplier and grow-out operators as one out of three key factors for developing improved stocks. Especially for small sectors, the financial needs and risks can be too big, for an SME for example, to carry alone. For specialised breeding programmes, high initial investment costs can include building hatcheries and related facilities and forming a biologically sound base population for the breeding activities. For the breeding programmes that are integrated in the production of a company, expansion of facilities is usually needed, e.g., to handle broodstock from different age-classes. Long-term investments are also needed to manage a more complex infrastructure to support selective breeding activities. These short- and long-term financial commitments provide a challenge for (small) private aquaculture companies to include selective breeding activities in their portfolio. There are many examples of publicly and privately owned breeding programmes supported by public financing in the early phases, and which ceased when the initial public funding ended (Hallerman et al., 2021) because of poor transition plans.

The difficulty of intellectual property protection of the developed farmed types is a second pivotal constraint for adoption of selective breeding in aquaculture, which discourages initial investments in new programmes (Rosendal et al., 2006). There are currently few legal instruments to protect intellectual property in developed farmed types, as they exist for newly bred plant varieties (plant breeders' rights). The most common protection is a statement in the purchasing contract that the genetic material may not be propagated and used for other purposes than food, which, however, often proves difficult to enforce. However, with the genotyping of all parents in the nucleus with (high-density) genetic markers, it is possible to identify at least the population origin and even individual parent origin if desired using a tracing/tracking scheme through the production chain.[8] Whilst such traceability markers do exist, they are rarely applied for commercial intellectual property protection in the aquaculture sector.

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[8] e.g https://aquagen.no/en/products/salmon-eggs/product-documentation/dna-tracking-of-salmon/

A second option is to sell sterile fish to the market. At present, the main approach to generating sterility in aquaculture species is the production of triploids, and whilst this is feasible in many aquaculture species, it is not applied at a large scale, because of technological issues, biological challenges such as health and animal welfare issues and/or because of consumer acceptance issues.

Gene editing is a group of genomic techniques that are used to alter the genome of individuals. In many countries, there are discussions in relation to the classification of GMO on whether gene edited animals should be allowed for human consumption[9]. A global map of gene editing regulation can be seen here [10]. Issues under discussion include animal integrity (unknown risk for individual animals related to the technology itself or the effects of the genes that are edited) and environmental impact (e.g., what are the effects on the wild populations if the gene-edited individuals escape and mate with or compete with their wild counterparts and the possible negative impacts of diseased farmed fish on their wild counterparts when using gene-edited disease-resistant fish). Arguments in support of gene editing is that it is unethical to not use the powerful gene-editing technique to improve animal welfare traits or to make sterile fish that can reduce the potential environmental harms of escapes or releases from aquaculture (see section 2). Another issue is whether the technology itself or its effects should be regulated. For the aquaculture production industries, including breeding, gene-editing technology has a huge potential with the possibility of changing frequencies of important gene variants in a short time, although this is not that feasible for complex traits at the moment, with corresponding effects at the phenotypic level. In addition to legal regulations with which the breeding industry must comply, the acceptance of gene-edited products among consumers is an important prerequisite to consider before adopting this technology on a routine basis in breeding activities and production. Genetic modification is an emotive topic and often elicits strong sentiments which often translate to negative perspectives on other forms of genetic improvement. Given the low production of genetically modified fish and livestock, debate on this issue often detracts from the more urgent and important need to expand and accelerate the application of selective breeding.

Selective breeding is a technology which requires high understanding of quantitative genetics and know-how of management of genetic variation, i.e., for controlling inbreeding. In integrated companies, the selective breeding activities increase the logistical challenges of fish holding, because (groups of) individual fish must be traceable. Personnel must have the skills to manage and analyse large data sets with thousands of fish and records on many traits. Additional specific skills are needed when including genomics data, e.g., for genomic selection or gene mapping. Few companies have in-house competence in quantitative and genomics analysis, and hence hire consultants. Overall, there is a lack of these competencies at the industry level. For almost all species in aquaculture, there are also large knowledge gaps in fields related to selective breeding, such as genomics (gene mapping, available reference genomes and genetic marker arrays), as well as in reproductive techniques and sex determination. Although selective breeding techniques are known in general, different species and production systems require their specific adaptation, which is often unexplored.

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[9] See (https://sites.google.com/a/vt.edu/animalbiotechresources/2020-online-workshops) for an example of a discussion on gene editing in animals

[10] See https://crispr-gene-editing-regs-tracker.geneticliteracyproject.org/#jet-tabs-control-1403 for a global map of gene editing regulation

The way forward and key recommendations

Acknowledgement of selective breeding as a fundamental genetic improvement technology and a main driver for a sustainable and productive aquaculture sector and awareness of its benefits needs to be enhanced at global, regional and national levels. Producers need to be aware of the genetic qualities of the farmed types they buy, policy makers need to set up guidelines that are relevant and accurate for each sector. A major role of private and public funding bodies should be to initiate breeding programmes for currently unimproved stocks, being aware of the potential and risks of selective breeding programmes and to secure long-term financing (Olesen et al., 2015; Hallerman et al., 2021). Targeted communication is needed to disseminate the benefits of genetically improved farmed types to these stakeholder groups.

Improved business and innovation plans and financial support are needed. These plans should acknowledge different phases of the development of breeding companies, and transitions from one phase to the next. Some are still at a phase where they are being surveyed on their effectiveness, some are at an expanding phase, and some are at an optimization phase. Short- and long-term financing instruments are needed, sometimes in a structure of a public-private partnership (PPP). PPP programmes should target effective engagement with the private sector from the beginning with a view to long-term (20-year) sustainability and effective uptake of improved farmed types. Technical support needs to be given to resource managers and policy makers to plan appropriately and facilitate private-sector investments. Intellectual property protection plans and devoted regulatory frameworks with appropriate enforcement for AqGR are needed (see also section 4).

Greater focus needs to be on capacity-building. Personnel educated on quantitative genetics and selective breeding are needed at all levels, e.g., farmers, hatchery managers, bioinformatics and data analysts, and policy makers. Although the fundamentals of selective breeding are known for the aquaculture sectors, there is a need to increase the knowledge on how to run long-term breeding programmes, using experience from successful existing examples and developing new systems and concepts. The examples should cover, e.g., the developed and developing parts of the world, different (groups of) species and both specialised and integrated breeding programmes and including complex and more basic programmes.

Technology transfer from established breeding programmes can be facilitated. From established breeding programmes, we can foresee developmental stages. Such evolution of applied genetic technology should comply with and reflect the needs resulting from other developments in the sector. Infrastructure needs to be built for breeding programmes, which usually differs among aquatic species.

Along the development of selective breeding programmes, R&D activities should follow on using and optimising selective breeding as well as related technologies and methodologies. The R&D plans should be part of the business and innovation plans for each species. Some of this R&D is more fundamental, e.g., specific biological knowledge of each species, gene mapping and gene editing. Some is more applied, e.g., defining breeding objectives (that should be aligned with the market demand and farmers' needs) and breeding strategies and uptake of genomics techniques in traditional selective breeding activities.

1 The number of species and sectors with selective breeding programmes needs to increase to utilise the
2 full potential of the genetic diversity in aquaculture species. Obviously, not all of the approximately 700
3 species used in aquaculture can and should be developed simultaneously, and not all of them have a
4 future as a farmed species and thus many do not warrant investment in selective breeding programmes.
5 Important criteria for prioritisation of species are: (1) market (current and future size and accessibility);
6 (2) price (product, production cost); (3) biological constraints (poor survival, disease susceptibility, stress
7 tolerance) and; (4) reproductive traits (control, generation interval, sex ratios). A balance needs to be
8 found among efforts on existing and emerging species. Whilst breeding designs with combined selection
9 with large number of families are ideal there are options for lower cost breeding programme designs,
10 acknowledging that these will deliver lower genetic gains. The latter can be integrated into production
11 systems when based on good genetic management with some selection pressure applied. Such breeding
12 programmes can be advanced over time to deliver larger genetic gains or to increase number of traits
13 such as disease resistance and product quality.

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16 **4. Access and Benefit Sharing of Aquaculture Genetic Resources and Associated Traditional**
17 **Knowledge**

18 **Current status**
19 Many countries have adopted or are in the process of adopting access and benefit sharing (ABS) measures
20 relevant to AqGR and associated traditional knowledge (TK). But there is a large variation in existing ABS
21 measures, and there is a lack of knowledge on how ABS measures and patents affect aquaculture genetic
22 resources R&D, including selective breeding.

23

24 There are several international ABS frameworks that are relevant to aquatic resources. The *Convention*
25 *on Biological Diversity* (CBD) and the *Nagoya Protocol on Access to Genetic Resources and the Fair and*
26 *Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity* (NP)
27 apply to genetic resources, including AqGR and TK.[11] These international access and benefit sharing (ABS)
28 frameworks target biological resources used for their genetic material potential in R&D, rather than for
29 other attributes, such as using them for consumption as food.

30 The above-mentioned agreements explicitly recognise the sovereign rights of states over their natural
31 resources and the authority of national governments to determine access to and benefit-sharing from use
32 of genetic resources within their jurisdiction. Parties to the CBD must endeavour to create conditions to
33 facilitate access to genetic resources for environmentally sound uses by other Parties and not impose
34 restrictions that run counter to the objectives of the CBD.[12]

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[11] As a special agreement, the International Treaty on Plant Genetic Resources for Food and Agriculture applies to plant, including aquatic plant, genetic resources for food and agriculture.

[12] The objectives of the CBD, to be pursued in accordance with its relevant provisions, are the conservation of biological diversity, the sustainable use of its components and the fair and equitable sharing of the benefits arising out of the utilization of genetic resources, including by appropriate access to genetic resources and by appropriate transfer of relevant technologies, taking into account all rights over those resources and to technologies, and by appropriate funding.

37 Similarly, Parties to the NP shall take measures "as appropriate" and "in accordance with domestic law",
38 with the aim of ensuring that TK is accessed with the prior and informed consent (PIC) or approval and
39 involvement of the communities holding the TK. However, access to genetic resources and TK, where
40 granted, must be on mutually agreed terms (MAT), and benefits arising from R&D on genetic resources as
41 well as subsequent applications and commercialization must be fairly and equitably shared with the Party
42 providing such resources and/or the TK holders (CBD articles 1 & 15; NP articles 5,6 &7).

43 The NP provides that in developing and implementing ABS measures, Parties shall consider the
44 importance of genetic resources for food and agriculture and their special role for food security" (Article
45 8(c)). While this does not specifically require special measures or simplified arrangements for aquaculture
46 activities, it does suggest that countries consider ways to accommodate the "special nature of agricultural
47 biodiversity, its distinctive features and problems needing distinctive solutions" (NP, Preamble) in their
48 ABS regimes and tailor ABS measures accordingly. The NP also acknowledges "the potential role of access
49 and benefit sharing to contribute to the conservation and sustainable use of biological diversity, poverty
50 eradication and environmental sustainability" (NP, Preamble).

51 ABS obligations are increasingly relevant for users and providers of AqGR that are globally exchanged for
52 R&D, including selective breeding and other genetic improvement technologies. As it has been mentioned
53 above, currently there is a low uptake of selective breeding in aquaculture production. However, the
54 situation is expected to change with the growing importance of aquaculture production and the
55 increasingly important role of genetic improvement in this sector (see section 3). The need for access to
56 AqGR to breed new farmed types and to promote genetic diversity is particularly acute for aquaculture as
57 a relatively new production sector with increasing relevance for global trade.

58 A key rationale for introducing international access and benefit-sharing frameworks was to address
59 conflicts arising from the exploitation of genetic resources originating from "mega-diverse" countries
60 (predominantly from the South) by technology-rich countries (predominantly from the North) by
61 providing a system for the fair and equitable sharing of benefits derived from the utilization of the genetic
62 resources. The idea was that benefit-sharing may compensate biodiverse countries for the costs of the
63 conservation of the resources *in situ* and create an incentive for them to continue with these conservation
64 efforts (Lawson 2012). While the current gene flow (meaning the exchange of AqGR between different
65 regions or zones) for aquaculture purposes is primarily North-North (e.g. salmonids, marine finfish
66 temperate species such as seabass and seabream), North-South (e.g. common carp, salmonids) and South-
67 South (e.g. tilapia, shrimp), similar conflicts (as seen in the case of plant genetic resources - Pistorius, 1998;
68 Wallbott, 2014) may arise as R&D and global exchange of AqGR increase along with an increasing
69 commercial interest from the private sector in accessing AqGR from all regions of the world, including
70 South to North (Olesen et al., 2007; FAO, 2009).

71 Notwithstanding the global ABS regime, there is a diversity of national ABS measures and there is little
72 information or guidance available about how these measures apply in practice to AqGR and TK of AqGR.
73 While several countries have opted not to restrict access to genetic resources within their jurisdiction, nor
74 enacted ABS measures to regulate access and benefit-sharing abroad (and therefore do not require that
75 benefits derived from their or other countries' resources be shared), many other countries have
76 established ABS measures, most of which include in their scope AqGR and associated TK of AqGR.

77

78 With the entry into force of the NP only in 2014, experience with the implementation of ABS laws is still
79 limited and there is little empirical evidence of the positive or negative effects of ABS measures (or their
80 absence) on aquaculture R&D, or on the conservation and sustainable use of AqGR or the aquaculture
81 sector in general (Humphries et al., 2018). There is also little awareness of ABS issues among the great
82 variety of AqGR stakeholders, which include small- to large-scale farms, public and private facilities, and
83 subsistence to commercial production facilities (FAO, 2019).

84 There is a wide variation in the scope of subject matter in national ABS laws, according to domestic and
85 various stakeholder needs:[13] wild and/or domesticated resources; native and/or non-native species;
86 resources *in situ*, *ex situ* and/or *in silico* (e.g., digital sequence information) conditions; and resources from
87 private, public and/or communal lands and facilities. Relatively few laws (e.g., Australia's Northern
88 Territory) exclude resources collected for aquaculture under certain circumstances. The scope of TK falling
89 under ABS obligations is also varied under national laws, and the level of TK in aquaculture is much smaller
90 than in terrestrial agriculture (FAO, 2009: 33). Many national laws do not define the scope of TK, others
91 confine it to knowledge concerning genetic material uses or biological resources, while others extend
92 obligations to knowledge concerning the aquatic environment and ecosystems more generally.

93 The activities triggering the requirement for PIC under the NP is access for their "utilization", meaning "to
94 conduct R&D on the genetic and/or biochemical composition of genetic resources, including through the
95 application of biotechnology" (NP, article 2). However, ABS measures vary as to what "access",
96 "utilization" and "research and development" mean in practice.[14] ABS measures are ultimately meant to
97 capture and share monetary and non-monetary benefits derived from the commercialization of products.
98 Some ABS laws therefore distinguish between commercial and non-commercial R&D. It is, however, often
99 difficult in practice to distinguish between commercial and non-commercial R&D activities, which may
100 partly explain the variety of ABS measures: Some ABS obligations apply to the "collection" of AqGR, others
101 apply to their "transfer" and/or export. Some ABS measures require PIC for access to R&D and
102 commercialization relating to genetic resources (e.g., breeding and biotechnology), while fewer measures
103 (perhaps unintentionally) appear to apply more broadly to grow out and/or conservation and taxonomic
104 research. Some laws require PIC only for activities, such as R&D, as of a specific date or the date of
105 collection, while others require PIC for new and continuing uses of previously accessed materials
106 (Humphries, 2021).

107 The fair and equitable sharing of benefits arising from the utilization of genetic resources, as well as
108 subsequent applications and commercialization, is most and foremost a matter for the provider and user
109 to agree upon. The NP includes in its Annex a non-exhaustive list of monetary and non-monetary benefits
110 that may inform benefit-sharing negotiations. Benefits users and providers may agree to share include
111 capacity building, technology/information transfer, payments of royalties, and license fees from
112 intellectual property rights.

113 Whereas for many years, living material was excluded from patentability, patent authorities and the
114 courts began in the 1980s to increasingly accept patents relating to biotechnological innovations, using
115 DNA sequences, micro-organisms, plants, and animals.

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[13] See Humphries 2021 expanding on the examples below.
[14] See Humphries 2021 expanding on the examples below.

116 Although most such patents are still granted to patent holders situated in the Northern hemisphere, the
117 material often has its origin in the Southern hemisphere. ABS aims to strike a balance between the
118 interests of providers/holders and users of genetic resources and associated TK (Esquinas-Alcazar, 2005;
119 Pavoni, 2013). Striking the right balance between users and providers of genetic resources may become
120 increasingly relevant with the consolidation of the aquaculture industry, including for AqGR originating in
121 the South, such as growing external interest in tilapia genetic resources (Rosendal et al., 2012; Joshi et al,
122 2020). With the increasing interest of the private sector in aquaculture, including aquaculture R&D,
123 patents might play an increasingly important role in this sector.

124 ABS-patent linkages may nowadays be found in patent laws as well as ABS measures of some countries.
125 Few developed and several developing countries require patent applicants to disclose in their patent
126 applications the country of origin of any material they used while developing their innovation (WIPO
127 2020). Such disclosure in patent applications may assist in monitoring the utilization of genetic resources
128 and therefore function as a 'checkpoint' for ABS. ABS administrators may then use the information
129 disclosed in patent applications to check compliance of patent applicants with relevant ABS measures.
130 While this potential is there, there are very few countries that have made the relevant changes to their
131 patent legislation, and hence the check-point effect is still small.

132
133 **Today's challenges and needs**

134 There is an urgent need to raise the awareness among all relevant stakeholders of ABS and its potential
135 implications for the future use and exchange of AqGR, including seed supply, breeding and R&D. Capacity
136 building is needed also due to the rapidly changing context of actors and their responsibilities in the
137 aquaculture sector (Ponzoni et al., 2010; Ramanna Pathak, 2012). While ABS has generated less conflict
138 between users and providers of AqGR in the past when compared with terrestrial genetic resources, this
139 may be changing with altered structures in the aquaculture sector (Greer and Harvey, 2005, Olesen et al.
140 2007; Rosendal and Olesen, submitted). The corporate structure in aquaculture is rapidly changing, as
141 evidenced by the privatization of the Norwegian public breeding programme for salmon (Rosendal et al.,
142 2013).

143 There is a need to develop ABS measures that accommodate the distinctive features of AqGR. In 2013,
144 the Commission on Genetic Resources for Food and Agriculture developed *Elements to Facilitate Domestic*
145 *Implementation of Access and Benefit-Sharing for Different Subsectors of Genetic Resources for Food and*
146 *Agriculture* (ABS Elements), including AqGR. The ABS Elements aim to assist governments considering
147 developing, adapting, or implementing ABS measures to consider the importance of genetic resources for
148 food and agriculture, including AqGR, their special role for food security, as well as the distinctive features
149 of the different subsectors of genetic resources, while complying, as applicable, with international
150 instruments (FAO, 2019a). The next phase of the work is to explore the effects and impact of ABS
151 implementation on the use and exchange of AqGR (Humphries, 2021). Distinctive features of AqGR and
152 TK of AqGR policy- and decision-makers may wish to consider when developing and implementing ABS
153 measures include: the degree of incremental improvement of AqGR; the dependency on multiple sources;
154 the interdependence among users and providers (Schloen et al., 2011; Chiarolla, 2011; Medaglia et al.,
155 2013); international gene flow and the traceability of AqGR (FAO, 2019a).

156

157　There is a need to understand the effects of ABS measures and patents on aquaculture sectors. There is a
158　need to systematically collect information on the real or potential positive and negative effects of
159　compliance with national ABS measures and patents on the collection, use, movement, open access
160　(where relevant) and the equitable sharing of benefits from use of AqGR, associated information (e.g.
161　digital sequence information) and TK of AqGR. The collection of this information can start with key
162　aquaculture producing countries. There is a need to forecast future global movements of aquaculture
163　farmed types for R&D, including those that incorporate genetic materials from several countries of origin
164　(for which PIC and MAT may then be required from several countries). There is also a need for systematic
165　studies that determine the origin of the materials in patented genetic resource inventions relevant to
166　aquaculture and to determine their effect on the conservation and sustainable use of AqGR.

167

168　**The way forward and key recommendations**

169　For aquaculture actors, including farmers, businesses and bioprospectors, building understanding of and
170　capacity for carrying out ABS concerning AqGR and TK of AqGR are key steps for promoting certainty for
171　the use and exchange of materials, information and knowledge in aquaculture sectors, and equitable
172　benefit-sharing from use of AqGR. Sources of information include the ABS Clearinghouse [15] as well as
173　National Focal Points, which Parties of the Nagoya Protocol must establish, as well as patent offices as far
174　as patent law is concerned. Various capacity-building initiatives aim to inform stakeholders as well as
175　policymakers on ABS and patent issues (CBD, 2019; WIPO 2018).

176　Policymakers, need to take account of the distinctive characteristics of AqGR and TK of AqGR when
177　developing, adapting, or implementing ABS and other measures (including biocultural protocols). A
178　central normative objective is maintaining affordable access to breeding material given that such access
179　is essential for progress in R&D for food security. Another objective is to share lessons learned from
180　aquaculture-specific benefit-sharing examples. A common concern among all actors involved should
181　therefore be to maintain affordable access to breeding material and promote the sharing of benefits
182　arising from the utilization of AqGR if ABS measures are in place.

183　Policymakers may wish to take account of the actual gene flows of AqGR and the fact that many AqGR are
184　currently primarily exchanged amongst countries of the same region or the same hemisphere. For such
185　cases, ABS policy makers could consider regional or special ABS arrangements, that facilitate exchange of
186　AqGR for R&D within a specific region or group of countries under pre-agreed terms of reference,
187　including those concerning benefit-sharing.

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[15] (https://absch.cbd.int/)

194 While facilitating access and exchange may be important in regional cases, the facilitation of equitable
195 benefit sharing may be more important in circumstances of access by external corporate users. As the
196 effects and impact of ABS measures on sustainable aquaculture development are still poorly understood,
197 national or local case studies could help to better understand whether and how ABS measures may
198 contribute to: (a) the conservation and sustainable use of AqGR and TK of AqGR for use in aquaculture;
199 (b) the fair and equitable sharing of benefits from their use with provider countries/communities (e.g.,
200 evidence of successful benefit-sharing agreements in aquaculture); (c) poverty eradication (e.g.,
201 contribution to aquaculture livelihoods); and (d) food security. Case studies on the impact of patents on
202 the use and exchange of AqGR and TK of AqGR are also essential for the development of aquaculture
203 sectors. However, it should be noted that the effects or impacts on the use, exchange and R&D of AqGRs
204 are usually caused by a multiplicity of factors, and it will often be difficult to identify with any degree of
205 accuracy the proportional impact of an ABS measure as opposed to other factors, including availability of
206 research funds, adequate infrastructure, qualified workforce, and incentives.

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229   **References**

230   Section 1.
231   Balon, E.K., 1995. Origin and domestication of the wild carp, Cyprinus carpio: from Roman gourmets to
232   the swimming flowers. *Aquaculture*, *129*(1-4), pp.3-48.
233   Bentsen, H.B., Gjerde, B., Eknath, A.E., Palada de Vera, M.S., Velasco, R.R., Danting, J.C., Dionisio, E.E.,
234   Longalong, Reyes, R.A., Abella, T.A., Tayamen, M.M., Ponzoni, R.W. 2017. Genetic improvement of
235   farmed tilapias: Response to five generations of selection for increased body weight at harvest in
236   *Oreochromis niloticus* and the further impact of the project. Aquaculture, 468, 206–217.
237   https://doi.org/10.1016/j.aquaculture.2012.01.027
238   Bogeruk, A.K. and Federatsii, M.S.S.K.R., 2008. Catalogue of carp breeds (*Cyprinus carpio* L.) of the
239   countries of Central and Eastern Europe.
240   Duarte, C.M., Marbá, N. and Holmer, M., 2007. Rapid domestication of marine species. *SCIENCE-NEW
241   YORK THEN WASHINGTON-*, *316*(5823), p.382.
242   Evans, B., Bartlett, J., Sweijd, N., Cook, P. and Elliott, N.G., 2004. Loss of genetic variation at microsatellite
243   loci in hatchery produced abalone in Australia (*Haliotis rubra*) and South Africa (*Haliotis midae*).
244   *Aquaculture*,*233* (1-4), pp.109-127.
245   FAO. 2019a. The State of the World's Aquatic Genetic Resources for Food and Agriculture. FAO
246   Commission on Genetic Resources for Food and Agriculture assessments. Rome.
247   FAO 2019b. Status and trends of animal genetic resources. Item 11.2 of the Provisional Agenda of the
248   Seventeenth Regular Session of the Commission of Genetic Resources for Food and Agriculture.
249   Rome. Italy. http://www.fao.org/3/my867en/my867en.pdf.
250   FAO. 2020. The State of World Fisheries and Aquaculture 2020. Sustainability in action. Rome.
251   https://doi.org/10.4060/ca9229en
252   Frost, L.A., Evans, B.S. and Jerry, D.R., 2006. Loss of genetic diversity due to hatchery culture practices in
253   barramundi (Lates calcarifer). *Aquaculture*, *261*(3), pp.1056-1064.
254   Gjerde, B., Mengistu, S.B., Ødegård, J., Johansen, H. & Altamirano, D.S. 2012. Quantitative genetics of
255   body weight, fillet weight and fillet yield in Nile tilapia (Oreochromis niloticus). Aquaculture, 242–
256   243: 117–124. Gjedrem, T., 2012. Genetic improvement for the development of efficient global
257   aquaculture: a personal opinion review. *Aquaculture*, *344*, pp.12-22.
258   Gjedrem, T.; Rye M. (2016). Selection response in fish and shellfish: a review. *Reviews in Aquaculture,*
259   10(1): 168-179.
260   Hansen, M.M., Simonsen, V., Mensberg, K.L., Sarder, M.R. and Alam, M.S., 2006. Loss of genetic variation
261   in hatchery-reared Indian major carp, *Catla catla*. *Journal of fish biology*, *69*, pp.229-241.
262   Hu X S, Ge Y L, Li C T, Jia Z Y, Shang M, Wang S H, Shi L Y. Developments in Common Carp Culture
263   and Selective Breeding of New Varieties. In Gui JF, Tang QS, Li ZJ, Liu JS, De Silver SS, Aquaculture in
264   China: Success Stories and Modern Trends Oxford: John Wiley & Sons Ltd, 2018, 125.
265   Janssen, K.P.E.; Berentsen, P.B.M.; Komen, J. 2015. Current status of selective breeding in European
266   aquaculture. ISGA XII, Santiago de Compostella, Spain, 2015-06-21/2015-06-27.Lind, C.E., Ponzoni,
267   R.W., Nguyen, N.H. and Khaw, H.L., 2012. Selective breeding in fish and conservation of genetic
268   resources for aquaculture. *Reproduction in domestic animals*, *47*, pp.255-263.
269   Li, Q., Xu, K. and Yu, R., 2007. Genetic variation in Chinese hatchery populations of the Japanese scallop
270   (*Patinopecten yessoensis*) inferred from microsatellite data. *Aquaculture*, *269*(1-4), pp.211-219.
271   Lind et al., 2012. Exploitation and conservation of fish genetic resources in Africa: Issues and priorities for
272   aquaculture development and research September 2012. Reviews in Aquaculture 4(3):125-141.
273   DOI:10.1111/j.1753-5131.2012.01068.xLucente, D., Sims, S., Lei, G. & Mair, G. (2021). Conservation

274 of Farmed Aquatic Species: an Opportunity We Must Not Miss! FAO Aquaculture News, No. 63, pp.
275 51-53. (also available at http://www.fao.org/3/cb4850en/cb4850en.pdf#page=51)

276 Mair, G. and Lucente, D., 2020. What are" Farmed Types" in Aquaculture and why do they Matter? *FAO*
277 *Aquaculture Newsletter*, (61), pp.40-42.

278 Mia, M.Y., Taggart, J.B., Gilmour, A.E., Gheyas, A.A., Das, T.K., Kohinoor, A.H.M., Rahman, M.A., Sattar,
279 M.A., Hussain, M.G., Mazid, M.A. and Penman, D.J., 2005. Detection of hybridization between
280 Chinese carp species (*Hypophthalmichthys molitrix* and *Aristichthys nobilis*) in hatchery broodstock
281 in Bangladesh, using DNA microsatellite loci. *Aquaculture*, 247(1-4), pp.267-273.

282 Na-Nakorn, U., Kamonrat, W. and Ngamsiri, T., 2004. Genetic diversity of walking catfish, *Clarias*
283 *macrocephalus*, in Thailand and evidence of genetic introgression from introduced farmed *C.*
284 *gariepinus*. *Aquaculture*, 240(1-4), pp.145-163.

285 Vandeputte M, Quillet E, Chevassus B (2002) Early development and survival in brown trout (Salmo trutta
286 fario L.): indirect effects of selection for growth rate and estimation of genetic parameters.
287 Aquaculture 204:435–445.

288 Yue, G.H., Zhu, Z.Y., Lo, L.C., Wang, C.M., Lin, G., Feng, F., Pang, H.Y., Li, J., Gong, P., Liu, H.M. and Tan, J.,
289 2009. Genetic variation and population structure of Asian seabass (*Lates calcarifer*) in the Asia-
290 Pacific region. Aquaculture, 293(1-2), pp.22-28.

291 Zhang X J, Zhou L, Gui J F. Biotechnological innovation in genetic breeding and sustainable green
292 development in Chinese aquaculture (in Chinese). Sci Sin Vitae, 2019, 49: 1409–1429

293

294

295 Section 2.

296 Araki, H., Cooper, B., and Blouin, M.S. 2007. Genetic effects of captive breeding cause a rapid, cumulative
297 fitness decline in the wild. *Science,* 318:100–103.

298 Araki, H., Cooper, B., and Blouin, M.S. 2009. Carry-over effect of captive breeding reduces reproductive
299 fitness of wild-born descendants in the wild. *Biology Letters*, 5:621–624.

300 Bartley, D.M. and S.J. Funge-Smith. 2018. Pp 284-307 In Funge-Smith, S.J. 2018. *Review of the state of*
301 *world fishery resources: inland fisheries.* FAO Fisheries and Aquaculture Circular No. C942 Rev.3,
302 Rome. 397 pp.

303 Bentsen, H.B., Gjerde, B., Eknath, A.E., de Vera, M.S.P., Velasco, R.R., Danting, J.C., et al. (2017) Genetic
304 improvement of farmed tilapias: Response to five generations of selection for increased body
305 weight at harvest in *Oreochromis niloticus* and the further impact of the project. *Aquaculture*,
306 468:206–217.

307 Cambray, J., and Swartz, E. 2007. *Oreochromis mossambicus*. IUCN Red List of Threatened Species. Version
308 2013.1. www.iucnredlist.org.

309 Canonico, G.C., Arthington, A., McCrary, J.K., and Thieme, M.L. 2005. The effects of introduced tilapias on
310 native biodiversity. *Aquatic Conservation: Marine and Freshwater Ecosystems*, 15:463–483.

311 Costa-Pierce, B. 2003. *Ecological Aquaculture*. Ames, IA, Iowa State University Press.

312 D'Amato, M.E., Esterhuyse, M.M., Van Der Waal, B.C., Brink, D. and Volckaert, F.A. 2007. Hybridization
313 and phylogeography of the Mozambique tilapia *Oreochromis mossambicus* in southern Africa
314 evidenced by mitochondrial and microsatellite DNA genotyping. *Conservation Genetics,* 8(2):475-
315 488.

316 Da Silva, S.S., Subasinghe, R.P., Bartley, D.M., and Lowther, A. 2004. Tilapias as alien aquatics in Asia and
317 the Pacific: A Review. Food and Agriculture Organization, Rome. Volume 453.

318   Deines, A.M., Bbole, I., Katongo, C., Feder, J.L. and Lodge, D.M., 2014. Hybridisation between native
319   *Oreochromis* species and introduced Nile tilapia *O. niloticus* in the Kafue River, Zambia. *African
320   Journal of Aquatic Science,* 39(1):23-34.
321   Dew, J., Berkson, J., and Hallerman, E. 2003. A model for assessing the likelihood of self-sustaining
322   populations resulting from commercial production of triploid Suminoe oysters (*Crassostrea
323   ariakensis*) in Chesapeake Bay. *Fisheries Bulletin*, 101: 758–768.
324   FAO. 1995. Precautionary approach to fisheries. Part 1: Guidelines on the precautionary approach to
325   capture fisheries and species introductions. Elaborated by the Technical Consultation on the
326   Precautionary Approach to Capture Fisheries (Including Species Introductions). Lysekil, Sweden, 6–
327   13 June 1995. FAO Fish. Tech. Pap. No. 350, Part 1. Rome, FAO, 52 pp.
328   FAO. 2007. Database of introductions of aquatic species.
329   (http://www.fao.org/waicent/faoinfo/fishery/statist/fisoft/dias/index.htm).
330   FAO. 2019. The State of the World's Aquatic Genetic Resources for Food and Agriculture. FAO Commission
331   on Genetic Resources for Food and Agriculture assessments. Rome.
332   Ferguson, A., Fleming, I.A., Hindar, K., Skaala, O., McGinnity, P., Cross, T., and Prodohl, P. 2007. Farm
333   escapes. In: Verspoor, E., Stradmeyer, L., Nielsen, J.L., Eds. *The Atlantic Salmon: Genetic
334   Conservation and Management*. Blackwell Publishing: Oxford, UK. pp. 357–398.
335   Garant, D., Forde, S.E., and Hendry, A.P. 2007. The multifarious effects of dispersal and gene flow on
336   contemporary adaptation. *Functional Ecology,* 21:434–443.
337   Garcia, D.A.Z., Magalhães, A.L.B., Vitule, J.R.S., Casimiro, A.C.R., Lima-Junior, D.P. Cunico, D.P., Brito,
338   M.F.G., Petrere-Junior, M., Agostinho, A.A. and Orsi., M.L. 2018. The same old mistakes in
339   aquaculture: the newly available striped catfish *Pangasianodon hypophthalmus* is on its way to
340   putting Brazilian freshwater ecosystems at risk. *Biodiversity and Conservation*, 27:3545-3558.
341   Hallerman, E. 2008. Application of risk analysis to genetic issues in aquaculture. In: M.G. Bondad-
342   Reantaso, J.R. Arthur, and R.P. Subasinghe (eds). Understanding and Applying Risk Analysis in
343   Aquaculture. FAO Fisheries and Aquaculture Technical Paper No. 519. Rome, FAO. pp. 47-66.
344   Halwart, M. 1994. The golden apple snail *Pomacea canaliculata* in Asian rice farming systems: present
345   impact and future threat. *International Journal of Pest Management*, 40:199-206.
346   Hashimoto, D.T., Prado, F.D., Foresti, F. and Porto-Foresti, F., 2016. Molecular identification of intergenus
347   crosses involving catfish hybrids: risks for aquaculture production. *Neotropical Ichthyology*, 14(2).
348   Hashimoto, D.T., Senhorini, J.A., Foresti, F., Martinez, P. and Porto-Foresti, F., 2014. Genetic identification
349   of F_1 and post-F_1 Serrasalmid juvenile hybrids in Brazilian aquaculture. *PLoS One*, 9(3), p. e89902.
350   Hashimoto, D. T., J. A. Senhorini, F. Foresti & F. Porto-Foresti. 2012. Interspecific fish hybrids in Brazil:
351   Management of genetic resources for sustainable use. *Reviews in Aquaculture,* 4: 108-118.
352   Hindar, K., Ryman, N., and Utter, F. 1991. Genetic effects of cultured fish on natural fish populations.
353   *Canadian Journal of Fisheries and Aquatic Sciences,* 48:945–957.
354   ICES (International Council for the Exploration of the Seas). 2012. Report of the ICES Working Group on
355   Introduction and Transfers of Marine Organisms. ICES CM 2012/ACOM: 31:1-301
356   ISO (International Organization for Standardization). 2018. the ISO 31000:2018.
357   https://www.iso.org/standard/65694.html. Accessed 29 July 2021.
358   Kaplan, E.L., Meier, P. 1958. Nonparametric estimation from incomplete observations. *Journal of the
359   American Statistical Association*, 53:457–481.
360   Kapuscinski, A.R., Nega, T., and Hallerman, E.M. 1999. Adaptive biosafety assessment and management
361   regimes for aquatic genetically modified organisms in the environment. In R.S.V. Pullin, D.M. Bartley
362   & J. Kooiman, eds. Towards policies for conservation and sustainable use of aquatic genetic
363   resources. *ICLARM Conference Proceedings*, 59, pp. 225–251.

Macaranas, J.M., Taniguchi, N., Pante, M.J.R., Capili, J.B., and Pullin, R.S.V. 1986. Electrophoretic evidence for extensive hybrid gene introgression into commercial *Oreochromis niloticus* (Linn.). stocks in the Philippines. *Aquaculture and Fisheries Management,* 17:249–258.

McAndrew, B.J., and Majumdar, K.C. 1983. Tilapia stock identification using electrophoretic markers. *Aquaculture*, 30: 249–261.

McGinnity, P., Prodöhl, P., Ferguson, A., Hynes, R., ó Maoiléidigh, N., Baker, N., Cotter, D., O'Hea, B., Cooke, D., and Rogan, G. 2003. Fitness reduction and potential extinction of wild populations of Atlantic salmon, *Salmo salar*, as a result of interactions with escaped farm salmon. *Proceedings of the Royal Society of London Series B: Biological Sciences*, 270:2443–2450.

Moreau, J. A review of introductions of tilapia in open waters of Africa, their influence on ecology and fisheries. In Fishelson, L., and Yaron, Z., Eds., Proceedings of the International Symposium on Tilapia in Aquaculture; Nazareth, Israel, 1983. Tel Aviv University Press, Ramat Aviv, Israel. pp. 77–85.

Motohiko, S., Takafumi, I., Jun, K., and Yanai T. 2004. First detection of koi herpesvirus in cultured common carp *Cyprinus carpio* in Japan. *Fish Pathology*. 39:165-167.

Mwanja, W., and Kaufman, L. 1995. A note on recent advances in the genetic characterization of tilapia stocks in Lake Victoria region. *African Journal of Tropical Fisheries*, 6:51-53.

Naylor, R. 1996. Invasions in agriculture: assessing the cost of the golden apple snail in Asia. *Ambio,* 25:443-448.

NRC (National Research Council). 2004. Non-native oysters in the Chesapeake Bay. Washington, DC, National Academy Press (www.nap.edu).

OIE (Office International des Epizooties). 2018. Aquatic Animal Health Code. https://www.oie.int/en/what-we-do/standards/codes-and-manuals/aquatic-code-online-access/. Accessed 29 July 2021.

OAB (Office of Agricultural Biotechnology). 1990. Environmental assessment of research on transgenic carp in confined outdoor ponds. Washington, DC, Office of the Secretary, U.S. Department of Agriculture.

Pullin, R.S.V., Palomares, M., Casal, C., Dey, M., and Pauly, D. 1997. Environmental impacts of tilapia. In Fitzsimmons, K., Ed. Fourth International Symposium on Tilapia in Aquaculture. Northeast Regional Aquacultural Engineering Services, Ithaca, NY, USA. pp. 554–570.

Rocha, G.R.A. 2008. The introduction of the African catfish *Clarias gariepinus* (Burchell, 1822) into Brazilian inland waters: a growing threat. *Neotropical Ichthyology,* 6(4):693-696.

Sattar, M.A., Das, T.K., Rahman, M.A., Penman, D.J., McAndrew, B.J., Mazid, M.A., Taggart, J.B., Hussain, M.G., Mia, M.Y., Gilmour, A.E., Gheyas, A.A. & Kohinoor, A.H.M. 2005. Detection of hybridization between Chinese carp species (*Hypophthalmichthys molotrix* and *Aristichthys nobilis*) in hatchery broodstock in Bangladesh using DNA microsatellite loci. *Aquaculture,* 247: 267–273.

Senanan, W., Kapuscinski, A.R., Na-Nakorn, U., and Miller, L.M. 2004. Genetic impacts of hybrid catfish farming (*Clarias macrocephalus* x *C. gariepinus*) on native catfish populations in central Thailand. *Aquaculture,* 235:167–184.

Shechonge, A., Ngatunga, B.P., Bradbeer, S.J., Day, J.J., Freer, J.J., Ford, A.G., Kihedu, J., Richmond, T., Mzighani, S., Smith, A.M. and Sweke, E.A., 2019. Widespread colonisation of Tanzanian catchments by introduced *Oreochromis* tilapia fishes: the legacy from decades of deliberate introduction. *Hydrobiologia*, 832(1):235-253.

Tuckett, Q.M., Ritch, J.L., Lawson, K.M., and Hill, J.E. 2016.Implementation and enforcement of best management practices for Florida ornamental aquaculture with an emphasis on nonnative species. *North American Journal of Aquaculture,* 78:113-224.

Tufto, J. 2001. Effects of releasing maladapted individuals: A demographic-evolutionary model. *American Naturalist*, 158:331–340.

Tufto, J. 2010. Gene flow from domesticated species to wild relatives: Migration load in a model of multivariate selection. *Evolution,* 64:180–192.

Vaini, J.O., Grisolia, A.B., Prado, F.D.D. and Porto-Foresti, F., 2014. Genetic identification of interspecific hybrid of Neotropical catfish species (*Pseudoplatystoma corruscans* vs. *Pseudoplatystoma reticulatum*) in rivers of Mato Grosso do Sul State, Brazil. *Neotropical Ichthyology*, 12(3):635-641.

Wargelius, A., Leininger, S., Skaftnesmo, K.O., Kleppe, L., Andersson, E., Taranger, G.L., Schulz, R.W., and Edvardsen, R.B. 2016. *Dnd* knockout ablates germ cells and demonstrates germ cell independent sex differentiation in Atlantic salmon. *Scientific Reports*, 6(1):1-8.

Weyl, O.L.F. 2008. Rapid invasion of a subtropical lake fishery in central Mozambique by Nile tilapia, *Oreochromis niloticus* (Pisces: Cichlidae). *Aquatic Conservation*, 18:839-851.

Weyl, O.L.F., Daga, V.S., Ellender, B.R. and Vitule, J.R.S. 2016. A review of *Clarias gariepinus* invasions in Brazil and South Africa. *Journal of Fish Biology*, 89:386-402.

Zambrano, L., Martínez-Meyer, E., Menezes, N., and Peterson, A.T. 2006. Invasive potential of common carp (*Cyprinus carpio*) and Nile tilapia (*Oreochromis niloticus*) in American freshwater systems. *Canadian Journal of Fisheries and Aquatic Sciences,* 63:1903–1910.

Section 3.

FAO. 2019a. The State of the World's Aquatic Genetic Resources for Food and Agriculture. FAO Commission on Genetic Resources for Food and Agriculture assessments. Rome.

Dekkers, J.C.M; Hospital, F. (2002) The use of molecular genetics in the improvement of agricultural populations. *Nature Reviews Genetics* **3:**22–32.

Gjedrem, T. & Olesen, I. 2005. Basic statistical parameters. In: Gjedrem, T. (Ed.), Selection and Breeding Programs in Aquaculture. Springer, pp. 45–72.

Gjedrem, T., Robinson, N., Rye, M. (2012) The importance of selective breeding in aquaculture to meet future demands for animal protein; a review. *Aquaculture,* 350-353: 117-129.

Gjedrem, T., Robinson, N. (2014) Advances by Selective Breeding for Aquatic Species: A Review. *Agricultural Sciences*, 5, 1152-1158. doi: 10.4236/as.2014.512125.

Gjedrem, T. and Rye, M. (2016) Selection Response in Fish and Shellfish: A Review. 10:1. doi:10.1111/raq.12154

García-Ruiz, A. Cole, J.B., VanRaden, P.M., Wiggans, G.R., Ruiz-López, F.J., Van Tassell, C.P. (2016) Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection. *PNAS, July* 12, 2016 113 (28) E3995-E4004, https://doi.org/10.1073/pnas.1519061113

Hallerman, E., Hilsdorf, A.W.S., Bartley, D.M., and Mair, G.C. 2021. Towards increasing production of genetically improved farmed types in aquaculture. *Reviews in Aquaculture.* https://doi.org/10.1111/raq.12561.

Houston RD, Haley CS, Hamilton A, Guy DR, Tinch AE, Taggart JB et al. (2008). Major quantitative trait loci affect resistance to infectious pancreatic necrosis s in Atlantic salmon (*Salmo salar*). *Genetics,* 178: 1109–1115.

451 Janssen, K.P.E., Saatkamp, H.W., Komen J. (2018) Cost-benefit analysis of aquaculture breeding programs.
452   *Genetics Selection Evolution* 50:2
453 Meuwissen T. H.E, Hayes B. J., Goddard M. E. (2001) Prediction of total genetic value using genome-wide
454   dense marker maps. Genetics **157**: 1819–1829.
455 Moen, T., Baranski, M., Sonesson, A.K., Kjøglum, S. (2009) Confirmation and fine-mapping of a major QTL
456   for resistance to infectious pancreatic necrosis in Atlantic salmon (*Salmo salar*): population-level
457   associations between markers and trait. *BMC Genomics* 10: 368.
458 Nielsen, H-M, Sonesson, A.K., Meuwissen, T.H.E. (2010) Optimum contribution selection for traditional
459   BLUP and genome-wide breeding values in aquaculture. J. Anim. Sci. 89: 630-638.
460 Olesen I, Bentsen HB, Phillips M, Ponzoni RW (2015) Can the global adoption of genetically improved
461   farmed fish increase beyond 10%, and how? *Journal of Marine Science and Engineering,* 3:240-
462   266.
463 Sonesson, A.K. (2005) A combination of walk-back and optimum contribution selection for fish. Genetics
464   Selection Evolution. 37: 587-599
465 Sonesson, A.K., Goddard, M.E. and Meuwissen, T.H.E. The use of communal rearing of families and DNA
466   pooling in aquaculture genomic selection schemes (2010) Genet. Sel. Evol. 42: 41
467 Wu, L (2020) Derivation of economic values for important production traits in Atlantic salmon. Master's
468   Thesis, Department of Animal Breeding and Genetics, Norwegian University of Life Sciences.
469 Zenger, K.R.; Khatkar, M.S. Jones, D.B.; Khalilisamani, N.; Jerry, D.R.; Raadsma, H.W. (2019) Genomic
470   selection in aquaculture: Application, limitations and opportunities with special reference to
471   marine shrimp and pearl oyster. *Frontiers in. Genetics* https://doi.org/10.3389/fgene.2018.00693
472 Zhou L and Gui J F. Applications of Genetic Breeding Biotechnologies in Chinese Aquaculture. In Gui JF,
473   Tang QS, Li ZJ, Liu JS, De Silver SS, Aquaculture in China: Success Stories and Modern Trends
474   Oxford: John Wiley & Sons Ltd, 2018, 465-481

475
476
477 Section 4.
478 CBD. 2019. *Update on existing capacity-building and development initiatives and resources supporting the*
479   *implementation of the Nagoya Protocol on Access and Benefit-sharing* (CBD/NP/CB-
480   IAC/2019/1/2)
481 Chiarolla, C. 2011. *Intellectual property, agriculture and global food security: The privatization of crop*
482   *diversity*. Cheltenham: Edward Elgar.
483 Gjedrem, T., Robinson, N. and Rye,M. 2012. The importance of selective breeding in aquaculture to meet
484   future demands for animal protein: A review. *Aquaculture*, Volumes 350–353, pp. 117-129.
485 Gjedrem, T. 2005. Selection and Breeding Programs in Aquaculture. ISBN 978-1-4020-3342-1.
486 Greer, D. and Harvey. B. 2004. *Blue Genes. Sharing and Conserving the World's Aquatic Genetic Resources*.
487   Earthscan: London.
488 Esquinas-Alcazar, J. 2005. Protecting crop genetic diversity for food security: Political, ethical, and
489   technological challenges. *Nature*, 6(12), 946–953.
490 FAO. 2009. The Use and Exchange of Aquatic Genetic Resources for Food and Agriculture. BACKGROUND
491   STUDY PAPER. Rome, FAO. 44 pp. (also available at http://www.fao.org/3/aak527e.pdf).FAO.
492   2019. *ABS Elements: Elements to facilitate domestic implementation of access and benefit-sharing*
493   *for different subsectors of genetic resources for food and agriculture – with explanatory notes*.
494   FAO, Rome.

Houston, R.D., Bean, T.P., Macqueen, D.J. *et al.* Harnessing genomics to fast-track genetic improvement in aquaculture. *Nature Review Genetics,* **21,** 389–409 (2020). https://doi.org/10.1038/s41576-020-0227-y

Humphries, F., Benzie, J.A.H and Morrison, C. 2018. A Systematic Quantitative Literature Review of Aquaculture Genetic Resource Access and Benefit Sharing. *Reviews in Aquaculture* 11(4) 1133-1147 doi: 10.1111/raq.12283.

Humphries, F. 2021. *Survey of ABS Country Measures Accommodating the Distinctive Features of Genetic Resources for Food and Agriculture (GRFA) and Traditional Knowledge Associated with GRFA*, FAO Draft survey for comment.

Joshi, R., A. Skaarud, M.de Vera, A.T. Alvarez, J. Ødegård. 2020. Genomic prediction for commercial traits using univariate and multivariate approaches in Nile tilapia (*Oreochromis niloticus*). *Aquaculture.* 516, 734641

Lawson, C. 2012. *Regulating genetic resources: Access and benefit sharing in international law*. Cheltenham: Edward Elgar Publishing.

Medaglia, J.C., Tvedt, M.W., Perron-Welch, F., Jørem, A. and Phillips, F.-K. 2013. *The Interface between the Nagoya Protocol on ABS and the ITPGRFA at the International Level: Potential Issues for Consideration in Supporting Mutually Supportive Implementation at the National Level,* FNI Report, 1/2013, Lysaker, Norway: Fridtjof Nansen Institute.

Olesen, I., Rosendal, G.K., Bentsen, H.B., Tvedt, M.W., and Bryde, M. 2007. 'Access to and protection of aquaculture genetic resources - Strategies and regulations'. *Aquaculture,* 272, Supplement 1, S47-S61.

Ponzoni, R.W., Khaw, H.L. and Yee, H.Y. 2010. GIFT: *The Story Since Leaving ICLARM (now known as The WorldFish Center) Socioeconomic, Access and Benefit Sharing and Dissemination Aspects*. FNI report, 14/2010. ISBN 978-82-7613-602-9-print version, 978-82-7613-603-6-online version

Pavoni, R. 2013. The Nagoya protocol and WTO law. In E. Morgera, M. Buck, & E. Tsioumani (Eds.), The 2010 Nagoya protocol on access and benefit sharing in perspective (pp. 185–213). Leiden: Martinus Nijhoff.

Pistorius, R. 1998. Scientists, plants, and politics: a history of the plant genetic resources movement. SERBIULA (sistema Librum 2.0).

Rosendal, G. K., Olesen, I. and Tvedt, M.W. 2013. 'Evolving Legal Regimes, Market Structures and Biology Affecting Access to and Protection of Aquaculture Genetic Resources'. *Aquaculture*, DOI: 10.1016/j.aquaculture.2013.03.026.

Rosendal, G. K and Olesen, I (forthcoming 2021) 'Breeding for lice resistance in Norwegian farmed Atlantic salmon: an ignored path for sustainable innovation?' *Aquaculture*, submitted.

Rosendal, G. K, Olesen, I and Tvedt, M.W. 2012. *Access to, Equity and Protection of Genetic Resources in Ghana: The Case of Tilapia* (*O. niloticus*). FNI Report 15/2012. Lysaker, FNI, 2012.

Ramanna Pathak, A. 2012. *Access to Genetic Resources and 'Rings of Protection' in Indian Shrimp Aquaculture*. FNI report 5/2012

Schloen, M., Louafi, S. and Dedeurwaerdere, T. 2011. *Access and benefit sharing for genetic resources for food and agriculture. Current use and exchange practices. Commonalities, differences and user community needs. Report from a multi-stakeholder expert dialogue*. Rome: CGRFA Background study paper no. 59.

Wallbott, L. 2014. 'Goals, strategies, and success of the African Group in the negotiations of the Nagoya Protocol'. In Oberthür and Rosendal (eds) *Global governance of genetic resources*. Routledge.

WIPO (World Intellectual Property Organisation). 2020. *Key questions on patent disclosure requirements for genetic resources and traditional knowledge,* 2nd edition. WIPO: Geneva, Switzerland.

WIPO (World Intellectual Property Organisation). 2018. *A Guide to Intellectual Property Issues in Access and Benefit-sharing Agreements.* WIPO: Geneva, Switzerland.