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The role of genetics in fisheries management under the E.U. common fisheries policy[a]

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Exploitation of fish and shellfish stocks by the European Union fishing fleet is managed under the Common Fisheries Policy (CFP), which aims to ensure that fishing and aquaculture are environmentally, economically and socially sustainable and that they provide a source of healthy food for E.U. citizens. A notable feature of the CFP is its legally enshrined requirement for sound scientific advice to underpin its objectives. The CFP was first conceived in 1970 when it formed part of the Common Agricultural Policy. Its formal inception as a stand-alone regulation occurred in 1983 and since that time, the CFP has undergone reforms in 1992, 2002 and 2013, each time bringing additional challenges to the scientific advisory process as the scope of the advice increased in response to changing objectives arising from E.U. regulations and commitments to international agreements. This paper reviews the influence that genetics has had on fish stock assessments and the provision of management advice for European fisheries under successive reforms of the CFP. The developments in genetics since the inception of the CFP have given rise to a diverse and versatile set of genetic techniques that have the potential to provide significant added value to fisheries assessments and the scientific advisory process. While in some cases, notably Pacific salmon *Oncorhynchus* spp., genetics appear to be very well integrated into existing management schemes, it seems that for marine fishes, discussions on the use of genetics and genomics for fisheries management are often driven by the remarkable technological progress in this field, rather than imminent needs emerging from policy frameworks. An example is the recent suggestion to use environmental (e)DNA for monitoring purposes. While there is no denying that state-of-the-art genetic and genomic approaches can and will be of value to address a number of issues relevant for the management and conservation of marine renewable natural resources, a focus on technology rather than policy and management needs is prone to widen the gap between science and policy, governance and management, thereby further impeding the effective integration of genetic and genomic information into the fisheries management decision making process. Hence, rather than focusing on what is technically achievable, this review outlines suggestions as to which modern genetic and genomic approaches are likely to help address some of the most pressing fisheries management challenges under the CFP.

Key words: European fisheries; genomics; marine conservation; renewable resources; stock assessments.

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INTRODUCTION

HOW CAN GENETICS HELP?

A number of recent reviews have addressed the prevailing lack of integration of genetic information into fisheries management schemes, which appears to be in stark contrast with the current swift progress in the fields of genetics and genomics (Hauser & Carvalho, 2008; Kochzius, 2008; Waples *et al.*, 2008*a*, *b*; Seeb *et al.*, 2011; Zelenina *et al.*, 2011; Garner *et al.*, 2016; Valentini *et al.*, 2016). For the purpose of this paper, the attempt to direct the focus on needs emerging from a major policy framework, the E.U. Common Fisheries Policy (CFP), a recent review by Ovenden *et al.* (2015) of genetic analytical approaches that are relevant to fisheries management, provides a valuable guideline. The review discusses the application and value of genetics under 11 themes: (1) species identification, (2) fisheries stock structure, (3) resolving mixed-stock fisheries, (4) DNA as a biomarker for age, (5) ecosystem monitoring, (6) estimating harvest rates and abundance, (7) genetic diversity, population abundance and resilience, (8) evolutionary responses to fishing, (9) genetic effect of stock enhancement, (10) detection of pathogens and invasive species and (11) product provenance and fisheries surveillance.

Ovenden *et al.* (2015) concluded that genetics offers a diverse collection of versatile and useful tools for informing fisheries managers about issues that have a biological basis. They also note that currently, the use of genetic tools focuses on a narrow set of fisheries management issues, but suggest that the diversity of genetic tools and the novel issues they can address indicates that uptake will grow, particularly if communication between geneticists and end-users improves, a conclusion similar to that drawn by Waples *et al.* (2008*a*, *b*) and further examined in depth by Dichmont *et al.* (2012).

The potential application of the technologies and techniques available have differing applications, so the aim is to focus on those that might be of most relevance to fisheries management under the CFP, particularly on themes (2), (3) and (6), which are highly relevant for a number current fisheries management issues.

FISHERIES MANAGEMENT UNDER THE E.U. COMMON FISHERIES POLICY

Fisheries management under the CFP aims to ensure that fishing and aquaculture are environmentally, economically and socially sustainable and that they provide a source of healthy food for E.U. citizens. Implementation of the policy is the responsibility of the European Agriculture and Fisheries Council (AGRIFISH, comprising ministers from each of the 28 E.U. member states) and the European Parliament (EP), who, following the adoption of the Lisbon Treaty in 2007 (E.U., 2007), adopt fisheries management regulations under a process known as co-decision. Co-decision applies to all fisheries legislation except for the setting of annual total allowable catches (TAC), which are the sole responsibility of AGRIFISH. The European Commission (EC), as the E.U.'s executive body, initiates and proposes legislation under the CFP remit and also monitors its implementation.

The EC's department with responsibility for making legislative proposals for fisheries management is the Directorate-General for Maritime Affairs and Fisheries (DG MARE). The CFP explicitly requires 'taking into account available scientific, technical and economic advice' (Article 6 of E.U., 2013). Accordingly, legislative and regulatory proposals initiated by the EC must be based on scientific advice. Advice on fisheries management is provided by a variety of scientific bodies including for European waters, the International Council for the Exploration of the Sea (ICES) and the Scientific Advisory Committee of the General Fisheries Council for the Mediterranean (GFCM-SAC). The European Commission's own but independent scientific advisory committee is the Scientific, Technical and Economic Committee for Fisheries (STECF) that annually convenes more than 20 expert working groups, involving some 400 scientists and which provides advice in direct response to requests from DG MARE.

While the CFP scientific advisory process is well established, the systematic incorporation of genetic information is conspicuously absent and reference to genetics in the advice emanating from scientific forums is rather infrequent and largely relates to fish stock identification. An example is the 2014 review of scientific advice, where genetics is mentioned in relation to stock delineation of commercially important marine fishes including European anchovy *Engrauslis encrasicolus* (L. 1758), Greenland halibut *Reinhardtius hippoglossoides* (Walbaum 1792) and cod *Gadus morhua* L. 1758 (STECF, 2014; ICES, 2014).

MANAGEMENT INSTRUMENTS

Since the inception of the first CFP in 1983, the primary fisheries management instrument has been the setting of annual TACs, which are allocated to different E.U. Member States using a fixed allocation key; a process known as relative stability. In other words, each member state receives a fixed proportion of whatever TAC is agreed for each fish stock. Such allocations were negotiated during the creation of the 1983 CFP, although they were revised and updated as additional member states with a fishing interest joined the E.U. In addition to TACs, technical measures such as minimum mesh sizes, minimum landing sizes, regulated areas or seasons have also been employed in an attempt to control exploitation rates.

MANAGEMENT NEEDS

Until the 2013 reform of the CFP, the primary need for the north-east Atlantic Ocean, North Sea, Irish and Baltic Sea, the marine area covered by ICES, was for advice on appropriate levels of catch that could be used as a basis for AGRIFISH to negotiate and set annual TACs. Already, however, with the 2002 CFP reform through the introduction of the concept of recovery and management plans, the notion of conservation and rebuilding stocks was emerging. Such plans were largely attempts to control exploitation rates to rebuild stock biomasses on a species or stock basis, *e.g.* the recovery plans for hake *Merluccius merluccius* (L. 1758) and *G. morhua* (EC, 2004*a*, *b*, 2005, 2008, 2012) and were mainly implemented through harvest control rules (HCR) that specified a limit on the annual TACs according to the status of the stocks and their exploitation rates. In effect, recovery plans were a means to legislate for the maximum level of catch that could be taken annually and in practice reduced the ability of the E.C. Fisheries Council to negotiate a TAC higher than that given by the HCR. In addition, limits on the maximum level of fishing effort that could be deployed by fishing vessels deploying certain gears were also introduced following the 2002 reform, again in the form of HCRs.

The 2013 reform of the CFP brought with it a shift in emphasis from single species management plans to the implementation of regional fishery management plans that should take into account the multi-species nature of many fisheries. In addition, the obligation to land all catches, the so-called landing obligation (LO) was introduced together with more specific objectives and targets for E.U. fisheries management, notably the aim to ensure that exploitation of living marine biological resources restores and maintains populations of harvested species above levels which can produce the maximum sustainable yield (MSY; Article 2 of E.U., 2013). MSY is defined in Article 4 of E.U. (2013) as 'the highest theoretical equilibrium yield that can be continuously taken on average from a stock under existing average environmental conditions without significantly affecting the reproduction process'. Furthermore, in order to reach the objective of progressively restoring and maintaining populations of fish stocks above biomass levels capable of producing maximum sustainable yield, the maximum sustainable yield exploitation rate (F_{MSY}) shall be achieved by 2015 where possible and, on a progressive, incremental basis at the latest by 2020 for all stocks. Nevertheless, while the emphasis of how fisheries management is to be implemented in the E.U. has changed since the inception of the CFP in 1983, particularly with the 2002 and 2013 reforms, there remains the need for advice on the status and exploitation status of individual fish stocks. So, what constitutes a stock under the CFP?

STOCKS AND THE CFP

The concept of stock has long been discussed by many authors (Carvalho & Hauser, 1994; Waples & Gaggiotti, 2006; Cadrin *et al.*, 2014), but according to Ward (2000), the most commonly quoted biological definition of a stock is that proposed by Ihssen *et al.* (1981): 'a stock is an intraspecific group of randomly mating individuals with temporal and spatial integrity'.

Under the CFP, however, a stock is explicitly defined as 'a marine biological resource that occurs in a given management area' (Article 4.14, E.U., 2013). Although management area is not defined, management areas in the north-east Atlantic Ocean and adjacent seas (FAO region 27) are areas for which fishing opportunities or TACs are set and which correspond to single or a combination of ICES statistical divisions. In this sense, the definition of stock under the CFP corresponds to what is termed by Smith *et al.* (1990) as a 'fishery stock'; a group of fishes exploited in a specific area or by a specific method. In the Mediterranean and Black Seas (FAO region 37), stocks relate to species in one or more combinations of 30 geographical sub-areas (GSA), although with the exception of bluefin tuna *Thunnus thynnus* (L. 1758), no TACs are set for any of the stocks in the Mediterranean and management is through effort controls and technical measures. For the Black Sea, the E.U. unilaterally fixes TACs for turbot *Scophthalmus maximus* (L. 1758) and sprat *Sprattus sprattus* (L. 1758) that apply exclusively to its fishing fleet. The stock concept in fisheries management is not solely an EU problem and recently the Australian Government has attempted to improve its understanding of stock status on a national scale especially for those that are shared across two or more jurisdictional boundaries (Flood *et al.*, 2016).

ADVICE ON FISHERIES MANAGEMENT UNDER THE CFP

Irrespective of the measures to be used for the management of fisheries, fundamental to the provision of management advice under the CFP is knowledge of stock status and the associated exploitation rates. Such information is necessary because of the CFP objective described above, *i.e.* to ensure that exploitation of living marine biological resources restores and maintains populations of harvested species above levels that can produce the MSY, which requires fishing at the maximum sustainable yield exploitation rate (F_{MSY}). Given that there are 238 combinations of management areas and species in the ICES area (Jardim *et al.*, 2016) and hence 238 nominal stocks, this is rather a tall order.

STOCK IDENTITY AND STRUCTURE

Here, it is suggested that the first priority theme under which genetics can inform fisheries management under the CFP is fisheries stock structure (Theme II from Ovenden *et al.*, 2015). Ideally, the assessment of stock status should relate to the biological unit stock so that appropriate action to control the exploitation rates on such stock units can be implemented and their effects can be assessed and monitored. For the north-east Atlantic Ocean, the fisheries management areas are based on ICES areas which were originally set up for the purposes of reporting statistical data. As a result, there may be a mismatch between the biological unit stock as defined by Ihssen *et al.* (1981) and the management area for which TACs are set. For example, Reiss *et al.* (2009) investigated 32 putative stocks in the ICES area and found sufficient evidence of a mismatch for six species namely *G. morhua*, haddock *Melanogrammus aeglefinus* (L. 1758), whiting *Merlangius melangius* (L. 1758), blue whiting *Micromesistius poutassou* (Risso 1827), *M. merluccius* and herring *Clupea harengus* L. 1758. Mismatches can occur under a number of circumstances and two contrasting examples from the ICES area relate to stocks of *M. merluccius* and Norway lobster *Nephrops norvegicus*.

MERLUCCIUS MERLUCCIUS AND *NEPHROPS NORVEGICUS*

Merluccius merluccius in the north-east Atlantic Ocean is distributed from Mauritania northwards along the European Atlantic seaboard to the Norwegian coast and into the North Sea, Norwegian Trench and the Skagerrak. For assessment purposes, however, it is considered by ICES as two separate stocks; a northern stock distributed over ICES areas IV, VI, VII and divisions IIIa, VIIIa, b, d and a southern stock distributed over ICES divisions VIIIc and IXa (see Fig. 1 for ICES areas). While the management area for the southern stock corresponds with the assessment area of the stock, and for which a single TAC is set, for the northern stock, separate TACs are agreed for four different management areas defined as follows: (1) ICES division IIIa (Skagerrak and Kattegat and E.U. waters of subdivisions 22–32 of the Baltic Sea); (2) E.U. waters of ICES division IIa and subarea IV; (3) ICES subareas VI and VII and E.U. and international waters of division Vb and the international waters of subareas XII and XIV; (4) ICES divisions VIIIa, VIIIb, VIIId and VIIIe.

Merluccius merluccius was one of the target species of the EC 7th Framework Programme (FP7) project FishPopTrace (https://fishpoptrace.jrc.ec.europa.eu/) that aimed at uncovering the genetic population structure of four major commercially

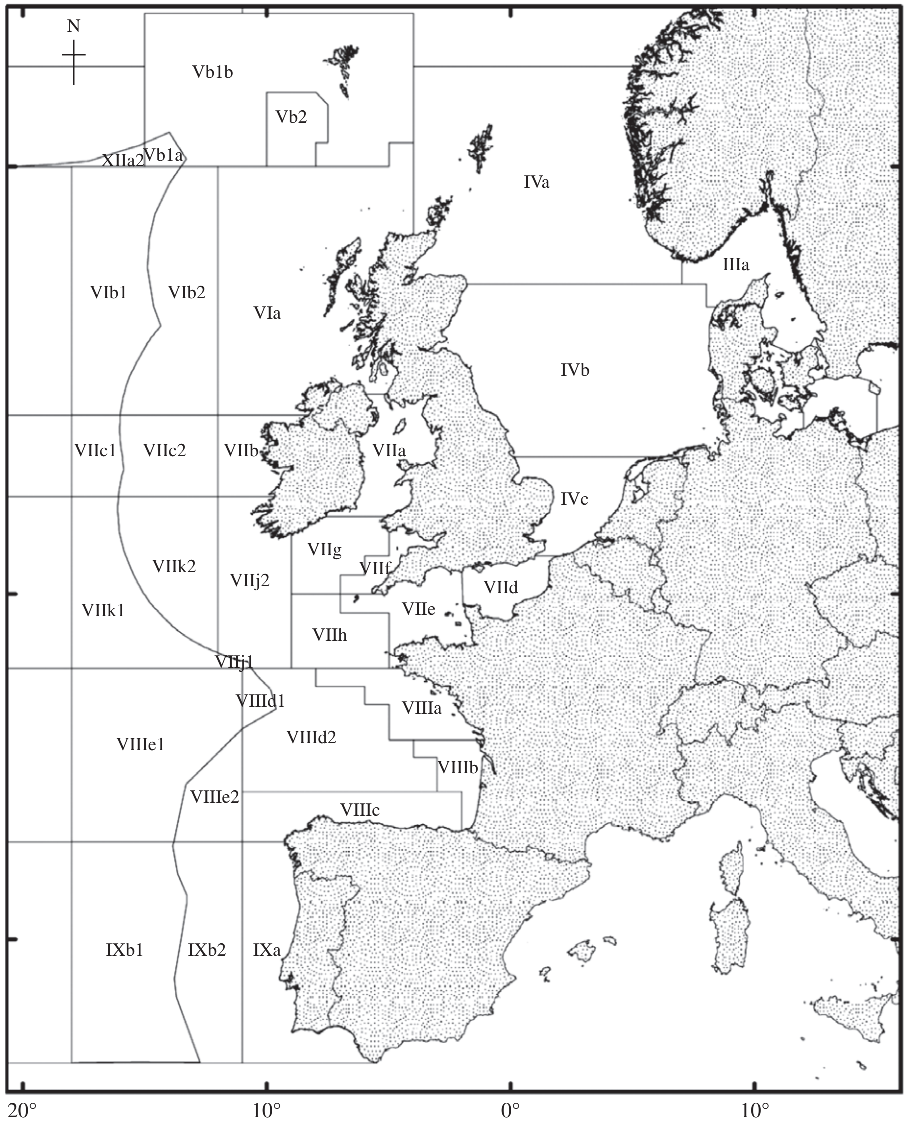

FIG. 1. ICES statistical subareas (roman numerals) and division (lower-case letters) off the western European seaboard (after ICES: www.ices.dk).

exploited marine fish species in European waters. Using single nucleotide polymorphism (SNP) markers under selection, it was possible to reveal fine-scale genetic structuring across *M. merluccius* populations (Milano *et al.*, 2014). Particularly in the Mediterranean, where *M. merluccius* is heavily overexploited and its stock structure a matter of debate (Cardinale *et al.*, 2015), such information could prove invaluable in supporting the development of fisheries management plans that aim to achieve sustainable and profitable exploitation of *M. merluccius* in line with the recently launched E.U. Mediterranean Strategy (https://ec.europa.

eu/fisheries/inseparable/en/medfish4ever#quicktabs-medfish4ever=4/). To date, however, no practical use has been made of the information already available in the management of *M. merluccius* fisheries. Furthermore, in combination with other available information such as habitat mapping (Druon *et al.*, 2015), knowledge on genetic population structure of *M. merluccius* or other commercially exploited fish could prove to be highly informative.

Nephrops norvegicus occur on muddy substrata where they live in burrows throughout the Atlantic waters of the E.U., from the Azores to the North Sea and also in the Mediterranean. The populations of *N. norvegicus* in the E.U. waters of the North Sea (ICES subarea IV) are distributed over eight distinct areas known as functional units (FU) that are regarded as separate stocks for assessment purposes. The management area, however, is the whole of Subarea IV (North Sea) and for which a single TAC is set.

These examples illustrate two different problems for the management of exploitation rates on each of the stocks of *M. merluccius* and *N. norvegicus*. In the case of *M. merluccius*, a single TAC is set to limit the catch from the stock as a whole and which is allocated to four separate management areas based on historical proportions of the overall annual catches reported from the different management areas. In such circumstances, even if the TAC limits the overall catch, the exploitation rate on the stock components in the different management areas may be quite different. The situation is further complicated by the fact that investigations into the population genetics of *M. merluccius* in the north-east Atlantic Ocean and Mediterranean Sea indicate that the population structure within the Atlantic Ocean is more complex than the discrete northern and southern stocks as assessed by ICES (Roldán *et al.*, 1998). In addition, Pita *et al.* (2013) provide evidence that a large genetic connectivity exists for *M. merluccius* in the north-east Atlantic Ocean, which is mediated by significant migration between the Celtic Sea and adjacent Atlantic grounds. Therefore, the spawning biomass of the northern *M. merluccius* population could play a crucial role at ensuring the sustainability of the southern *M. merluccius* fishing grounds. So for *M. merluccius* there are potentially at least three kinds of mismatch: a mismatch between the biological stock units and the assessment units, a mismatch between the biological stock units and the management units and a mismatch between the assessment units and the management units.

In the case of *N. norvegicus* in the North Sea, the status and exploitation rate for each of the separate stocks (FUs) are assessed separately and the adjustments in exploitation rates needed to achieve the CFP objectives for each FU may be quite different. Because the TAC relates, however, to the maximum permissible catch from the combined FUs, without additional management measures that are FU-specific, such a TAC does not necessarily restrict the catches from individual FUs or the associated exploitation rates. While the main mismatch in the case of *N. norvegicus* in the North Sea is considered to be that between the management unit (TAC management area) and the individual stock units (FUs), there is also a potential mismatch between the biological stock units and hence the assessment units if the individual FUs are not reproductively isolated (genetically distinct).

Given that, the principle of relative stability is so enshrined in the CFP that it is highly unlikely that the management units adopted will be revised at least for the lifetime of the current CFP, how can genetics help? Genetic techniques can potentially inform on the management of fisheries that exploit *M. merluccius* and *N. norvegicus* in two related ways. The case of *M. merluccius* is essentially a mixed-stock issue, in that catches taken across five separate management units originate from at least two different spawning components (northern and southern stocks as assessed by ICES) that have different reproductive potentials. With appropriate sampling of catches, genetic analysis could be used to further investigate the mixed-stock scenario and identify the respective contributions of the various spawning components across the different management areas. Such information would provide valuable input to the stock assessment process and could be taken into account in allocating TACs across the different management areas in an attempt to achieve the desired exploitation rates for the different stock components. With regard to *N. norvegicus*, genetic techniques can be used to determine whether the different functional units are genetically distinct and, on the basis of the results, strengthen the argument for specific TAC allocations to each FU rather than remaining with a single TAC for the North Sea as a whole.

While there is no TAC-based management for fisheries applied in the Mediterranean, the same line of argument and approach is highly relevant also to *N. norvegicus* in GSA 17 and 18, the Adriatic Sea. There is an unresolved debate on the stock structure in these GSAs, impeding proper assessments (Cardinale *et al.*, 2016) and clearly genetic stock identification (GSI) could help to resolve this issue. Ultimately, GSI might lead to the redefinition of management units, but in the interim, knowledge on genetic stock structure would help to provide appropriate stock assessments and equally importantly, to rationalize sampling efforts that underpin such assessments.

MIXED-STOCK ANALYSIS

A second but equally important and priority theme under which genetics can inform fisheries assessment and management is in resolving issues associated with mixed-stock fisheries (Theme III from Ovenden *et al.*, 2015). Mixed-stock fisheries contain catches of individuals from two or more biological unit stocks of the same species when such stocks are present on the same fishing grounds at the same time. The complexities associated with the management of mixed-stock fisheries are well known and genetic mixed-stock analysis has been applied to address issues in the north-east Atlantic Ocean (Bekkevold *et al.*, 2015). Under the CFP, the static nature of the stock definitions, and the mismatch with TAC management areas, means that mixed-stock issues are a rather common phenomenon, even if such issues are only rarely explicitly addressed.

A current example from the ICES area is the ICES division VIa and VIIb,c herring genetic stock identification baseline project, a 12 month collaborative project between the European Association of Fish Producers Organisations (EAPO) and University College Dublin to develop the genetic baseline with which to compare future mixed-fishery and survey samples from the stocks of *C. harengus* to the west of Britain and Ireland (ICES divisions VIa and VII b,c; https://www.researchgate.net/project/VIa-and-VIIb-c-Herring-Genetic-Stock-Identification-Baseline-Project/). The *C. harengus* in these areas are believed to constitute at least two separate stocks that have temporally and spatially-discrete spawning seasons. *Clupea harengus* from different spawning components, however, are known to form mixed aggregations on common feeding grounds where they are simultaneously exploited in a mixed-stock fishery. A dedicated research survey also takes place when the stocks are mixed. A major obstacle to ICES in undertaking assessments and providing pertinent management advice for such stocks is the inability to distinguish individuals from the different stocks in commercial mixed catches or research surveys. As a result, ICES is only able to undertake a combined assessment and provide advice for a single TAC to cover catches from both stocks. Such a TAC does not ensure that the exploitation rate on either stock will be controlled and if the component stocks are of dissimilar productivity and size, there is a risk that the smaller components will be subject to exploitation rates that may result in their decline.

ESTIMATING ABUNDANCE AND SPAWNING STOCK BIOMASS

While the former themes relate to the identification of stocks and the analysis of stock structure, both of which are prerequisites for stock assessment, to monitor progress towards achieving the biomass capable of delivering MSY, reliable estimates of changes in stock biomass over time are required. Hence, a third theme worth consideration as a priority to inform fisheries management in the E.U. is theme VI from Ovenden *et al.* (2015): estimating harvest rates and abundance, specifically the use of genetic markers to identify close-kin relationships to provide fishery-independent estimates of spawning stock biomass (SSB). Bravington *et al.* (2016) provided a fishery-independent estimate of spawning stock biomass of southern bluefin tuna *Thunnus maccoyii* (Castelnau 1872) through identification of close kin using genetic markers. For fish stocks that are of minor importance, either because their biomass is naturally small or depleted or they are commercially unimportant, there is generally a paucity of reliable and representative fishery-dependent data available for input to stock assessments. To monitor and assess whether the CFP objective to restore and maintain stock biomasses at levels capable of delivering the MSY is being achieved, however, requires that reliable estimates of spawning stock and a fishery-independent estimate of SSB derived from close-kin genetic analysis would be useful in this respect.

Close-kin analysis, however, is not without its drawbacks. The technique is not suited to all fish populations as it relies on being able to distinguish parental and offspring generations and also requires that the different generations can be independently sampled. Furthermore, a major limitation is that for large populations a large number of samples, proportional to the square root of the true population abundance, need to be processed to detect sufficient numbers of parent–offspring pairs (POP) for the technique to be feasible. Consequently, such large samples imply high effort and high costs. In addition, the costs associated with development of new molecular markers for each species to be studied means that initially the technique will most likely be restricted to high-value and long-running research and monitoring programmes (Ovenden *et al.*, 2015). Nevertheless, as discussed elsewhere (Martinsohn *et al.*, 2015), there may be scope to apply close-kin analyses to selected stocks in E.U. waters especially those that are commercially important and for which there is a paucity of reliable fishery-dependent data and information. Obvious candidates worthy of further investigation are the commercially important species of anglerfish *Lophius piscatorius* L. 1758 and *Lophius budegassa* Spinola 1807 that are caught all along the western European continental shelf. These species are caught in mixed fisheries but their biological stock structure is not precisely known.

SUMMARY

Based on the themes described by Ovenden *et al.* (2015), it is suggested that for the application of genetic approaches priority should be given to the following areas relevant for fisheries management under the E.U. Common Fisheries: theme II, fisheries stock structure; theme III, resolving mixed-stock fisheries; theme VI, estimating harvest rates and abundance, specifically the use of genetic markers to identify close-kin relationships to provide fishery-independent estimates of spawning stock biomass.

The suggestions mentioned above are based on the immediate needs emerging from the CFP regulation (E.U., 2013) and genetic approaches that appear to be feasible, practicable and cost efficient. In this paper, it is argued that for the efficient and routine integration of genetics and genomics into fisheries management it is recommendable to start out by focusing on the most immediate needs and to pay attention to guidelines and obligations laid down in legal and policy frameworks. This will also contribute to a better dialogue between managers, decision makers, fisheries scientists and geneticists, a precondition for an enhanced application of fisheries genetics as often highlighted (Martinsohn, 2011). Obviously, the utility of close-kin analysis for estimating spawning stock biomass and abundance requires further investigation to determine on a case by case basis, whether such an approach is likely to be cost-effective, which in turn is likely to be dependent on the value of the species under consideration.

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