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The state of the art in cost-benefit of HTS methods for stock assessment: An overview

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Over the past two decades, enormous progresses have been made in high-throughput sequencing (HTS) method development. This fact unveiled the potential usefulness of HTS methods in a wide range of fields such as fishery assessment and management, for which their application has been extensively discussed. As a consequence of the rapid development, sequencing costs have continuously declined, leading to a general claim that HTS methods are cost-efficient compared with traditional ones. Within this context, the underlying research objective is to assess the cost-effectiveness of genomic techniques through a review of the state of the art (SoA) on three HTS methods: i) environmental DNA (eDNA); ii) epigenetics method for age determination through DNA methylation (DNAm), and; iii) close-kin mark-recapture (CKMR) applied on marine ecosystems and fisheries and for stock assessment purposes. The SoA review of the literature on HTS methods was performed through the snow-balling systematic reviewing approach. The analysis has considered the set of processes and variables necessary to perform the stock assessment and compared the capacity of current and HTS methods for providing the required data. Research reveals that HTS methods constitute a promising tool for fishery research and, particularly, for improving scientific advice. Nevertheless, up to now, only one research, on a non-commercial species, has been conducted on the application of HTS methods for stock assessment purposes. Although some partial data are present in the literature, no systematic analysis on costs has been found. This paper suggests that the future research agenda should attempt to straddle both the scenarios for the transition process, considering complementary implementation and substitution possibilities and their cost-efficiency. Clarifying these questions is likely to pave the way for the effective and step-wise implementation of these methods in fishery management; thus, further research is recommended to encompass the transition process.

KEYWORDS

fisheries, stock assessment, HTS methods, close-kin mark-recapture, eDNA, DNAm

Highlights

- HTS methods have been claimed to be cost-efficient; nevertheless, very few publications have systematically and accurately addressed the issue.
- Most cases that claim cost-efficiency are not referred to stock assessments but to other objectives such as biodiversity observation or traceability of fishes, and, hence, cost-efficiency in stock assessment cannot be directly inferred from those.
- As a matter of fact, most of the research on HTS methods that claims to be cost-effective is eDNA metabarcoding in non-marine habitats such as rivers, lakes, or ponds.
- Even those very few cases referred to stock assessment, these works are focusing on species that differ from most of the commercially exploited species.
- In terms of information outputs, traditional surveys provide a broader scope of variables needed for stock assessment, whereas HTS methods provide more accurate data for very specific variables. Therefore, in this context, both groups of methodologies seem to be more complementary than substitutes. The guideline for future substitution could be based on the evolution of the cost-efficiency.
- Despite the fact that fishing surveys responsible authorities regularly collect cost-related data as a systematic endorse system, there is a clear shortage not only of published cost-efficiency studies on the use of HTS methods for stock assessments but also a general lack of published systematic cost analysis reviews, both for currently used and new methodologies. Therefore, further specific research on cost-efficiency is encouraged.
- HTS methods can provide additional valuable information outputs for managing not only the fisheries but the marine ecosystems.

1 Introduction

Society places multiple pressures on marine ecosystems, threatening their capacity to keep providing the multiple services and benefits that they are yielding (Costello et al., 2012). Consequently, improving the understanding of the marine resources is key to manage them (Thomsen et al., 2012). Responding to such challenges will require not only diverse types of knowledge (Rodríguez-Rodríguez et al., 2021) but cost-effective monitoring tools that enable the collection of accurate data to assess the health status of large marine areas (Borja et al., 2016).

Furthermore, fishery management under the Common Fisheries Policy (CFP) aims to ensure that fishing and aquaculture are environmentally, economically, and socially sustainable and that they provide a source of healthy food for the European Union (EU). Since the inception of the first CFP in 1983, the primary fishery management instrument has been the setting of annual TACs (Total Allowable Catches), which are assigned to different EU member states (Casey et al., 2016). In the Mediterranean, fishery management has tend to rely mostly in input control and technical measures (Carpi et al., 2017). In any case, both the CFP and the ecological, social, and economic sustainability of the European stocks currently rely on a robust and accurate scientific advice (Hoydal, 2007; Carpi et al., 2017). In other words, accurate data are a requirement for fulfilling the aims of the CFP by setting up accurate and robust management measures according to the stock status (Thomsen et al., 2012; Thomsen and Willerslev, 2015; Jerde et al., 2019). TACs are set annually (or every 2 years for demersal stocks) by the EU council of fishery ministers taking as basis scientific advice on stock status from advisory bodies [such as the International Council for the Exploration of the Sea (ICES) or the Scientific, Technical and Economic Committee for Fisheries (STECF)] (Daw and Gray, 2005; European Union, 2013). Within this context, some authors—such Chen (2003); Chen et al. (2003); Cope and Punt (2011)—assessed and highlighted the benefits of employing the most accurate available data in fishery stock assessment for reducing subjective uncertainties in determining current fishery status (Chen et al., 2003).

Regarding the marine species research, the data are largely surveyed using selective and invasive methods, which are mostly limited to commercially exploited species and restricted to particular areas. To ensure consistency, information of marine species could be derived from two main sources, namely, fishery-independent data (scientific surveys at sea) and fishery-dependent data (commercial catches analysis and sampling by observers on board) (Pennino et al., 2016). Both sources of information have complementary information that can be jointly used for fishery evaluation and management purposes (Pennino et al., 2016).

Fishery-dependent data are significantly cheaper to obtain, given the fact that the information can be captured in the process of fishing (Dennis et al., 2015). However, negative factors associated to commercial fleet catches data collection such as hyperstability [understood, as defined by de Mitcheson and Erisman (2012), as the phenomenon in which an observed index of stock abundance remains stable while the stock abundance is declining], spatial variability of fishing effort, variable fishing capacity, or erroneous data collection stated the necessity of including fishery-independent information into stock assessment data collection framework. Inherent features of fishery-independent data such as the employment of fishery scientists, the use of a specific fishing vessel and gears or the samples analysis make it invariably more expensive to attain per unit data unit than fishery-dependent data. Despite this fact, many authors—such as Caddy and Cochrane (2001); Punt et al. (2002), or Dennis et al. (2015)—highlighted the need for fishery monitoring systems that are both robust to the inherent uncertainty associated to the stock assessment process and cost-effective in the relationship between the productivity of the information obtained and its cost.

While it is true that fishery-independent data contain critical information for stock assessment, it is also true that marine scientific surveys are costly, in which cost-efficiency and eventual alternatives open debates (Dichmont et al., 2017; Zimmermann and Enberg, 2017). Along the years, sampling mechanisms have been kept unchanged for both sources of information to maintain homogeneous estimates of stock populations (Stamatopoulos, 2002). At the same time, technical innovations and development of genetic-based methods have supposed a revolution in stock assessment field. Concretely, high-throughput sequencing (HTS) methodologies have been signaled as a breakthrough, able to overcome the traditional methods of data collection and, consequently, to better support institutions and managers in the fishery management (Ovenden et al., 2015; Bravington et al., 2016; Casey et al., 2016; Deiner et al., 2017; Martinsohn et al., 2019; Friedman et al., 2022). Also known as next-generation sequencing (NGS), HTS refers to technologies that sequence DNA and RNA in a rapid and increasingly accessible manner (Nkrumah-Elie et al., 2018). Different advantages with respect to traditional methods have been pointed out in the scientific literature: simplicity, higher precision and accuracy, non-invasiveness, or less time-consuming have been the most highlighted features of HTS methods (Bourlat et al., 2013; Thomsen et al., 2016; Mauvisseau et al., 2017; Hansen et al., 2018). In general, it is assumed that genomic techniques are cost-effective and also efficient in terms of effort and time (Bourlat et al., 2013; Rees et al., 2014; Smart et al., 2016; Gillet et al., 2018; Hering et al., 2018; Lugg et al., 2018; Waples et al., 2018). Genetic analyses have much to offer fishery managers, especially in the provision of tools enabling unequivocal specimen identification and assessment of stock structure (Ward, 2000).

Nevertheless, because of the lack of available information regarding cost-benefit on the implementation of genetic techniques, the very limited published research related to genetic methods for stock assessment purposes (Kolody and Bravington, 2019), although there is an increasing number of papers using genetic studies to present stock structures of different species (Bravington and Grewe, 2007; Pita et al., 2016; Papa et al., 2021) and the high operational costs of implementing those methods in fishery-dependent and fishery-independent data acquisition, makes it necessary to check the evidence supporting such statements. Questions such as the scope for application in terms of gears, species, environments, or fishing areas; the links with policy objectives and the stages covered during the assessment process; the limitations taken into consideration or the benefits of the implementation of HTS methods for stock assessments are key for evaluating the performance of the genetic methods. It constitutes the main objective of this review. In general terms, this implies reviewing what has been stated on the cost-efficiency of HTS methods, which are the current limitations of the available knowledge and the controversies about the suitability for their cost-efficient use in stock assessments.

For that reason, the main purpose of this report is to review the state of the art (SoA) on the cost-benefit/cost-effectiveness of the application of HTS methods for providing biological data for stock assessments. On the basis of the FishGenome project requirements, this review will focus on three relevant HTS methodologies for stock assessments data acquisition process: 1) environmental DNA (eDNA), 2) close-kin mark-recapture (CKMR), and 3) epigenetic age determination based on DNA methylation (DNAm), and it will go from general to the specificities, with particular focus to bottom-trawl fishery-independent surveys and to some of the most representative demersal species subject to TACs, like cod, hake, and wrasse, because cost-efficiency may vary significantly between species (highly migratory, demersal, pelagic, etc.).

Ultimately, the FishGenome study is intended to help getting better and broader scientific knowledge to support future decisions such as an upgrade in the design of the surveys within the European CFP Data Collection Framework (DCF). Therefore, the focus can be put not only on the technology but also on how the current genomic technologies can efficiently contribute to policy and management needs, reducing the gap between science and policy (Casey et al., 2016).

2 Methodology

The SoA review of the existing literature on HTS methods was performed through the snow-balling systematic reviewing approach. The search of literature shown in this report has been conducted using Google Scholar and Thomson Reuters' Web of Science. A search on these academic platforms was performed between 15 April to 20 June 2019 using the following core concepts and terms: i) NGS; ii) epigenetic age determination method (DNAm) (NGS_1); iii) eDNA studies (NGS_2); iv) CKMR studies (NGS_3); v) cost-effectiveness; vi) NGS_1, NGS_2, and NGS_3 combined with "cod", "hake", and "wrasse"; vii) NGS_1, NGS_2, and NGS_3 combined with "North Sea", "North-West Iberian Peninsula", "Balearic Islands", and "Mediterranean"; viii) NGS_1, NGS_2, and NGS_3 combined with "Trawl", "Trawlers", and "Demersal"; ix) fishery research surveys/traditional surveys; and, finally; x) fish stock assessments.

2.1 SoA browsing results and literature review limitations

Table 1 shows the results of the key terms searched on the Thomson Reuters' Web of Knowledge. It should be highlighted

TABLE 1 Combination of terms and search sequence in Thomson Reuters' Web of Knowledge.

NGS	Search	Papers	Reviewed
eDNA	eDNA + Fisheries + Marine	9	8
	eDNA + Fisheries + Marine + Cod	2	2
	eDNA + Trawling	3	3
	eDNA + Cod	4	2
	eDNA + Hake	0	0
	eDNA + Wrasse	0	0
	eDNA + Cost-effectiveness	5	3
	eDNA + Fisheries + Marine + Costs	1	1
	eDNA + Surveys	55	18
	eDNA + North Sea + North-West Iberian Peninsula + Balearic Islands +Mediterranean	0	0
Next Generation Sequencing	NGS + Fisheries + Marine	20	3
	NGS + Fisheries + Marine + Cod	3	0
	NGS + Fisheries + Marine + Hake	2	0
	NGS + Fisheries + Marine + Wrasse	0	0
Close-kin Mark-recapture	CKRM	7	4
	CKRM + Fisheries	3	3
	CKMR + Demersal	0	0
	CKMR + Trawling	0	0
	CKMR + Cod	0	0
	CKMR + Hake	0	0
	CKMR + Wrasse	0	0
	CKMR + Cost-effectiveness/CKMR + Fisheries + Marine+ Costs	0	0
	CKMR+ surveys	1	0
	CKMR+ North Sea + North-West Iberian Peninsula + Balearic Islands +Mediterranean	0	0
DNA Methylation	DNAm + Fisheries	6	3
	DNAm + Marine	1	0
	DNAm + Demersal	0	0
	DNAm + Trawling	0	0
	DNAm + Cod	12	3
	DNAm + Hake	0	0
	DNAm + Wrasse	1	1
	DNAm + Cost-effectiveness + Fisheries + Marine/DNAm + Fisheries + Marine+ Costs	0	0
	DNAm + Surveys	4	0

that there are limited pieces of research on some of the core searching topics. As a general trend, it was common to find research about HTS methods focused on species such as reptiles, amphibians, birds, earthworms, mammals, invertebrates, phytoplankton, and fish, which were analyzed in different habitats as terrestrial, air, freshwater, or marine systems (Deiner et al., 2017). However, very few papers or reports addressed specific conditions closer to those typical of stock assessment and specifically to the conditions selected for the FishGenome project: trawling techniques and demersal representative species as hake, cod, and wrasse.

In this way, Jerde et al. (2019) performed a similar literature review, searching in Google Scholar and Web of Science to collect published papers using the metabarcoding approach to estimate fish biodiversity. The authors used tags such as "environmental DNA", "metabarcoding", and "fish", finding n = 46 works on freshwater systems and just n = 7 on marine habitats. The underlying fact is that the literature on freshwater systems is currently much more advanced than focused on the marine ones (Hering et al., 2018). In this regard, the novelty of the use of eDNA metabarcoding on seawater samples to account for marine fish biodiversity is such as recent that it was unprecedented until 2012 (Thomsen et al., 2016).

As for the results of the search, no publications have been found on cost-benefit of the application of HTS methods (CKMR; eDNA and DNAm) in stock assessments or even marine fisheries. It should be noticed that cost-benefit analysis (CBA) is not limited just to monetary values and, ideally, involves more variables of environmental and societal nature, including its costs and benefits (Bateman et al., 2003;

Sartori et al., 2014; Martinsohn et al., 2019). However, at least the identification of certain costs of HTS methods was possible through the literature review. In the same way, no published research in cost-efficiency–related research was found. Thus, it was approached using the available material, which included research on non-marine systems and gray literature (ICES, 2014; ICES, 2015; ICES, 2018; IEO, 2018).

Finally, it also can be highlighted that there is still insufficient research when the contexts of application of the HTS methods are marine or coastal environments. In this regard, the CKMR method on coastal systems is limited to a few papers, like the ones signed by Bravignton and his team (Bravington et al., 2014; Bravington et al., 2016; Waples et al., 2018) who focus their research on just one species (Blue Tuna). In the same context, the cases of study based on DNAm method are quite limited (Table 1). On the contrary, e-DNA methods are better documented.

3 Traditional marine evaluation surveys vs. HTS methods

3.1 Efficient, for what?

Before any evaluation or review, it is necessary to identify and keep in mind for what the methods evaluated are intended to be efficient. In this case, they should serve for carrying out stock assessments. The purpose of a stock assessment is to provide support for decision-making by (1) describing alternative possible states of nature, (2) determining the consequences of taking different management actions under different states of nature, and (3) calculating the probability of different states of nature (Hilborn, 2003). In the case of European waters, stock assessments are the base for TAC allocation that is a key pillar of the CFP. Each EU member state receives a fixed proportion of whatever TAC is agreed for each fish stock (Casey et al., 2016).

Current methods of stock assessment tend to use all available information in a unified framework and may simultaneously include surveys, catch per unit effort (CPUE), age-distributions, length distributions, and tagging (Hilborn, 2003).

Therefore, a key question in terms of efficiency is whether all of these methods are able to provide the information required for a stock assessment. To the best of our knowledge, no comparisons have been done between the results of traditional versus HTS methods. Thus, a first attempt was needed for this review. In that sense, Table 2 shows the type of information obtained with the traditional fishery surveys and by HTS methodologies.

Table 3 shows the parameters obtained from traditional methods versus the alternative provided by HTS methodologies. From a quantitative point of view, the first direct observation is that traditional methods are currently providing all the parameters needed for a stock assessment, either directly as a part of the survey (species, weight and size, number, age, sex, maturity, fertility, abundance, trophism, etc.) or indirectly through the models, as is the case of the stock status and its distance to management target reference points. On the other hand, HTS methodologies do not provide all the required variables and parameters. For instance, they do not provide information on weight and size. The CKRM method is able to provide key parameters for stock assessment: stock status and biodiversity, whereas eDNA can accurately determine the species and provide information on diversity, and EAD (epigenetics for age determination) supplies accurate data on age and sex.

At this point, it should be noticed that the interest in HTS methodologies stems, on a broad level, from its potential to provide unique understandings of ecological processes in marine environments and supports more precise approaches for ecosystem-based management (Ovenden et al., 2015) and going down to each methodology for the potential to provide efficiently accurate (specific) data. This is the case for CKMR, which is expected to widen the scope of population-level inference relative to currently used monitoring programs (Conn et al., 2020). In the same vein, epigenetic clocks have proven themselves to be accurate (Simpson and Chandra, 2021), with recent studies revealing new examples of DNAm age association in several new species increasing the potential for developing DNAm age biomarkers for a broad range of wild animals (De Paoli-Iseppi et al., 2017). eDNA sampling can be a highly sensitive method for detecting aquatic taxa (Smart et al., 2016); however, its cost-efficiency has been scarcely studied.

Toward the end, currently used methodologies provide a broader scope of variables, whereas HTS methodologies focus on the improvement of certain key variables. At the same time, currently used methodology ensemble is the outcome of a long process of adaptation to the goals and needs of stock assessments, whereas HTS methodologies are scientific developments dealing with their innovation path for fitting with the stock assessment specific needs, which may pose a path-dependent problem.

3.2 About the information outputs of the HTS methods

Once the broad picture of the information outputs provided by the two big groups of methodologies regarding stock assessment has been identified, it is necessary to go deeper into the properties of the HTS methods. The more extensive body of literature in this field is devoted to eDNA. Regarding this method, Deiner et al. (2017) carried out a literature review on eDNA metabarcoding on animals and plants, observing that environmental metabarcoding of DNA can, in some cases, complement and even improve the results of conventional

TABLE 2 Information provided by the traditional fishery surveys, compared with the potential information provided for the combination of the following HTS methods: CKMR + eDNA + epigenetic age determination.

Method	Specie	Weight and Size	Species abundance	Age	Sex	Maturity	Fertility	Stock	Abundance	Biodiversity	Trophism	Additional Information (marine litter, pictures, etc.)
Traditional Survey	✓	✓	✓	✓	✓	✓	✓	?	✓	?	✓	✓
CKMR + eDNA + DNAm	✓	✗	✗	✓	✓	✗	✗	✓	✓	✓	✗	✗

Columns in table refer to different parameters and variables obtained during the traditional fishery surveys and by HTS methods in a fishery-independent survey. This information is as follows: i) species as the identification of existent marine species in the survey area; ii) weight and size as stock weight and size structure; iii) species abundance as the amount of species in a given target area; iv) age as stock age structure; v) sex as target stocks sex proportion; vi) fertility makes reference to the target stock reproductive ability; vii) stock as different stocks identification in a given area; viii) abundance as the target stocks abundance and biomass estimation; ix) biodiversity as the variety of species in the survey area; and x) trophism as information on the structure of fish community and its trophic interactions.

TABLE 3 Information provided by traditional fishery surveys and by HTS methods.

Method	Specie	Weight and Size	Species abundance	Age	Sex	Maturity	Fertility	Stock	Abundance	Biodiversity	Trophism	Additional Information (marine litter, pictures, etc.)
Traditional Survey	✓	✓	✓	✓	✓	✓	✓	?	✓	?	✓	✓
CKMR	✗	✗	✗	✗	?	✗	✗	✓	✓	✗	✗	✗
eDNA	✓	✗	✗	✗	✗	✗	✗	✗	?	✓	✗	✗
Epigenetic Age Determination	✗	✗	✗	✓	✓	✗	✗	✗	✗	✗	✗	✗

Theoretically, the method could offer information on this issue but partially or subjected to other additional processes. Columns in table refer to different parameters and variables obtained during the traditional fishery surveys and by HTS methods in a fishery-independent survey. This information is as follows: i) species as the identification of existent marine species in the survey area; ii) weight and size as stock weight and size structure; iii) species abundance as the amount of species in a given target area; iv) age as stock age structure; v) sex as target stocks sex proportion; vi) fertility makes reference to the target stock reproductive ability; vii) stock as different stocks identification in a given area; viii) abundance as the target stocks abundance and biomass estimation; ix) biodiversity as the variety of species in the survey area; and x) trophism as information on the structure of fish community and its trophic interactions.

methods by identifying different species, sampling greater diversity, and increasing the resolution of taxonomic identifications. This literature review included n = 21 studies in different ecological systems, and only n = 3 related to fish species in marine environments. The results showed that the number of marine species detected by eDNA metabarcoding could be complementary, similar, or even more significant.

A recent study presented by Yamamoto et al. (2017) showed that the level of identification is similar between the traditional evaluation methodology (long-term observation) and the genomic method (eDNA, surface, water column, and ocean sediment), implying that each technique identified more or less the same number of individuals, but each method detected some specific species that the other could not reveal. In particular, they demonstrated that eDNA metabarcoding is a more time-efficient method for examining a whole fish community than a visual census, having a very high detection performance among the HTS methods. This and the next one are two of the cases where it is particularly relevant to bear in mind what we are comparing when assessing the efficiency.

In the same vein, Port et al. (2016) compared another technique, scuba-diving, with eDNA (water column) being the latter much more effective, identifying a higher number of species than the traditional assessment technique. The most consistent study with the purpose of this review is the one carried out by Thomsen et al. (2016). They compared traditional techniques (trawl catch data) with eDNA samples (bottom sediment and water column) obtaining similar family richness. Whereas the eDNA identified species that do not frequently enter the nets, the trawling technique detected other species that were not recognized, at the species level, by the eDNA analysis.

Interestingly, the only assessment based on the CKMR methodology not only provides key parameters needed for stock assessment (abundance) but also requires traditional measures (weight, sex, etc.), suggesting the complementarity between both methods. In fact, different studies suggest the complementarity between traditional and HTS methodologies, because they seem to offer a broader picture of the state of the oceans and their resources (Deiner et al., 2017; Evans et al., 2017; Gillet et al., 2018; Stat et al., 2019).

3.3 Unraveling the value of a sample: Are the HTS methods cheaper than the traditional evaluation methods?

3.3.1 Value of bottom trawl surveys

The identification of costs and economic information related to the bottom trawl surveys has been unsuccessful. Although the literature on currently used methods of evaluation has been explored, with a particular interest in bottom trawl surveys, the consulted manuals do not present economic data regarding costs, salaries, hours of work, or any similar variables. In this sense, the manuals on bottom trawl surveys were reviewed using keywords such as expenses, costs, or outputs. Those terms appeared only on two occasions (ICES, 2014; IEO, 2018), revealing the difficulty of accessing economic information on evaluation projects. Manuals were useful to identify general survey practices, on-board processes, materials, and even the observation personnel necessary for the data collection but do not obtain the data required to establish the bases of cost analysis. Therefore, one of the revealed aspects along the literature review process was the lack of (published) cost studies on this topic.

Dennis et al. (2015) compared the cost-benefit ratio of fishery-independent versus fishery-dependent methods in the small-scale Torres Strait lobster fishery (between Australia and Papua New Guinea). Although the sampling method, randomly allocated stations, is not directly comparable with bottom trawl surveys, the paper yield some interesting insights. The authors based their analysis on the premise that fishery-independent surveys' higher cost would be economically justified when the profit attained due to an additional catch allocation estimated by the fishery model at least matched the survey cost and assuming that the fishery-independent outputs were incorporated by managers to set the TAC. Results show a positive net present value on the long term. Beyond the specificities of this case, the paper demonstrates, on the one hand, the contribution of CBA for decision-making and, on the other, the intrinsic relevance of accurate data.

3.3.2 Value of HTS methods

Only n = 3 works were found, in which the value of an HTS method sample was defined, answering the following question: How much does it cost to generate the information using a genomic technique? Three for eDNA and three for CKMR (but being part of the same project). In addition, one paper has been found on DNA analysis that, although it does not fall exactly within the scope of this review, may be representative of the costs of DNA sequencing.

The group of papers based on eDNA methodology share certain similarities and results (Table 4). All of them are on fish species but in freshwater systems. They were compared with currently used methodologies but only at the survey stage (they do not compare the total cost from sampling to modeling). These works suggest that the cost-efficiency of genomic techniques is based on the reduction of effort and work time in observation campaigns. Therefore, if conducting a biodiversity analysis, then these techniques may be adequate and cost-effective, but they do not provide enough information for a stock assessment of commercial fisheries. At the same time, the sampling process differs significantly in rivers, lakes, ponds, and oceans.

Indeed, these works suggest that the cost-effectiveness of genomic techniques is based on the reduction of effort and work time in observation campaigns. This factor, although reasonable

TABLE 4 Cases of study where the costs of getting information with traditional evaluation methods are compared.

Reference	Traditional Survey	HTS	Samples	Sample Value	Effort/Time	Are HTS much cheaper?
(Evans et al., 2017) Freshwater Namekagon River (EEUU)	• Triple-pass electrofishing • Single-pass electrofishing • Presence-absence electrofishing	eDNA	42	$ 16,14	• eDNA approach required (6.8 person/h) • Triple-pass electrofishing (90 person/h) • Single-pass electrofishing (30 person/h) • Presence-absence electrofishing (20 person/)	• (YES) Triple-pass electrofishing. (e-DNA 67% Cheaper) (YES) Single-pass electrofishing • (E-DNA ± equal) (NO) Presence-absence electrofishing • (e-DNA 33% more expensive) COST: eDNA 42 Samples • A = Materials = Cost of selecting dPCR samples was $ 4.02 per sample + cost of DNA extraction at $ 8.49/sample = $ 525 • B = Labor (6.8 h/person * 22.5 $/h) = $ 153 • Total Cost 42 e-DNA samples = $ 678. • eDNA sample = $ 16.14
(Qu & Stewart, 2019) Freshwater/ Yangtze River/ China	• Traditional Surveys, Capture and Visual Monitoring	eDNA • CPCR • qPCR	45	eDNA (CPCR): €211 eDNA (qPCR): €25.2 Annual value for Visual and Capture monitoring	E-DNA (CPCR) sampling, E-DNA (qPCR): sampling, Visual Monitoring (7 days, 1 boat, 3 personnel) Capture Monitoring (10 days, 15 boats, 40 personnel)	• E-DNA (CPCR) sampling, including labor, filtering water collections, extractions, amplifications, and sequencing. Total cost: 9,531.90. • eDNA (qPCR): sampling, including labor, filtering water collections, extractions, amplifications, and sequencing. Total cost 1,134.07 euros• Visual Monitoring (7 days, 1 boat, 3 personnel). Total cost: 4,466.59 euros/year• Capture Monitoring (10 days, 15 boats, 40 personnel). Total cost: 41,874.29 euros/year.
(Stein et al., 2014) Freshwater /EEUU	• Bioassessment	eDNA • Sanger Sequency	¿?		Substantially less: not necessary to sort specimens, clip tissues, and place extracts into individual wells on a plate	• Potentially, fish traditional method = $850 (Sorting $350 + Taxanomic ID $400) • ADN barcoding using Sanger sequencing includes sorting and, when required, clipping tissue samples. Sanger = $2,900 (Sorting $400 + Taxanomic ID $2,500) • ADN barcoding NGSr = $500–1,000 (Sorting $0 + Taxanomic ID $500–1,000)

from the economic point of view, is not the only one that influences the decreasing cost of the use of genomic techniques. In this sense, possible economies of scale associated with the processes, the number of samples needed, or how many of them are processed will influence the costs of obtaining the information (Smart et al., 2016; Lugg et al., 2018).

On the reduction of effort, it was argued (Stein et al., 2014) that "Next-Generation Sequencing costs are substantially less than those associated with Sanger sequencing because it is not necessary to sort specimens, clip tissues, and place extracts into individual wells on a plate". In this sense, it was observed that, for the identification of fish/invertebrates/algae in freshwater systems:

- Fish traditional method = $850 (Sorting $350 + Taxonomic ID $400).
- ADN barcoding using Sanger sequencing includes sorting and, when required, clipping tissue samples. Sanger = $2,900 (Sorting $400 + Taxonomic ID $2500).
- ADN barcoding using NGS = $500–1,000 (Sorting $0 + Taxonomic ID $500–1,000)

Qu and Stewart (2019) conducted a study on the Yangtze River freshwater system (China) where they compared the costs of the traditional surveys (capture and visual monitoring) with two eDNA protocols (cPCR and qPCR) to identify the status of a specific aquatic mammal (*Neophocaena asiaeorientalis*). Table 5 shows the results of their research, indicating that the technical eDNAs were cheaper than the traditional evaluation methodologies.

In that sense, the value of eDNA (cPCR) taking into consideration literature review about sampling, including labor, filtering water collections, extractions, amplification, and sequencing, had a total cost of €594.20 (for 45 samples).

Regarding the currently used evaluation methods, the difference was the effort invested in the information gathering. Visual monitoring method demanded more time and resources (boat and personnel) implying at less 7 days of works, rent of a boat, and paid three experts who addressed the evaluation processes. The total cost of the operation if it was to be implemented monthly would be €1,116.65. If the same study was replicated seasonally (3X), the estimated value would be €3,349.95; whereas if it was carried out 12 times a year, it would amount to €13,399.78 per year.

The method of capture monitoring was much more expensive, because it demanded 10 days of work, 15 boats, and 40 personnel doing the monitoring work. This operation had a total cost: €41,874.29 year.

In this case, as expressed by Qu and Stewart (2019), "Visual surveying on a monthly basis thus costs 1.88× that of eDNA

TABLE 5 Cost comparison eDNA vs. traditional evaluation methods in a freshwaters system (Qu and Stewart, 2019).

Survey method	Details	Cost
cPCR	eDNA collection labor	€69.09
	Filter papers + consumables	€25.12
	Extraction QIAGEN DNEasy blood and tissue kit	€237.43
	Amplification	€56.53
	Confirmation (visualization)	€94.22
	PCR labor	€67.84
	Total	€594.20
qPCR	eDNA collection labor	€69.09
	Filter papers + consumables	€25.12
	Extraction MOBIO DNEasy PowerWater kit	€516.59
	Amplification and quantification	€32.12
	qPCR labor	€150.75
	Total	€793.66
Visual monitoring	X = 7 days, 1 boat, 3 personnel	
	Per month (1X)	€1,116.65
	Per season (3X)	€3,349.95
	Per year (12X)	€13,399.78
Capture monitoring	X = 10 days, 15 boats, 40 personnel (EFFORT)	
	Per year (1X)	€41,874.29

collections utilizing cPCR (species detection) at the same temporal schedule. If, however, eDNA sampling using cPCR occurred only once per season (3X), then visual surveys would approximate 5.64× more expensive. Similarly, visual surveys compared to eDNA sampling utilizing qPCR would equate to 1.41× on a monthly sampling schedule and 4.22× on a seasonal sampling schedule".

Evans et al. (2017) illustrated how the same genomic technique can be more expensive or cheaper, depending on the traditional method with which it is compared. As a novelty, in this paper, it emphasized the identification of the workforce, the number of employees, salaries, and work time. Precisely, the reduction of effort is the fundamental factor that lowers the costs (Evans et al., 2017).

The closest research to the purpose of this review is the group of publications stemming from the research in the estimation of the spawning biomass of bluefin tuna using close-kin genetic markers (Bravington et al., 2014; Bravington et al., 2016; Waples et al., 2018), because the objectives of their project were i) to provide a fishery-independent estimate of the number of adult Southern bluefin tuna and ii) to provide direct estimates of age-specific fecundity and a better definition of spawning stock biomass (Bravington et al., 2014). The three publications linked to this research suggested that CKMR is a cost-effective method. The sources of cost reduction (comparing with currently used methods) are as follows (Bravington et al., 2014): i) sample sizes are likely to be lower; ii) possibility of re-using samples reducing the cost of sampling in future; iii) progressive reduction of genotyping cost; and iv) no ship or aircraft time.

Nevertheless, no systematic or specific data about cost is presented. Interestingly, they suggest a limitation for the application of this methodology to most of the marine fish species: They are too abundant to make the method cost-effective, so that it will be necessary a further reduction of genotyping costs (Bravington et al., 2014).

In this project, all fish sampled for genetics had their length measured and were sexed by checking for residual female gonads, as a part of the regular catch sampling program. A portion of the fish genotyped form part of the otolith collection set and therefore will be of known age (Bravington et al., 2014), which, as a matter of fact, is suggesting complementarity between traditional and HTS methods.

To the best of our knowledge, one of the most detailed papers about costs of the application of DNA analysis in fisheries is the one by Martinsohn et al. (2019). This paper considered both total cost of monitoring and approximate costs associated with laboratory setup in a monitoring and forensic context based on a number of previous fishery and aquaculture compliance investigations. Results suggest that the application of such methodologies is i) affordable because the costs of sequencing have been dropping over the last years and ii) economically justifiable given that in all cases examined in their study, and analytical costs (including administrative costs) were lower than the value of confiscated catches, illegal imports, and associated fines. Nevertheless, in this case, DNA analysis is providing information that no other method can provide, and, furthermore, the application of this technology responds to quite different policy and management objectives (fishery control, enforcement, and traceability) to those that we are considering.

4 Discussion

A critical requirement of stock assessment is the availability of data as precise as possible. Precision is based on an optimal trade-off between bias (approximation error) and variance (errors in estimating parameter values from the limited data available) as the errors of prediction are influenced by both (Dennis et al., 2015). Up till now, the key way for efficiently increasing accuracy was to combine dependent and independent data; nevertheless, with the significant reduction of sequencing cost, HTS methodologies have become a promising way to provide accurate data efficiently and to reduce the error of estimated TACs. Under the precautionary approach applied to fishery management framework, increased precision would reduce the risk of severe and irreversible damage to the fishery resources and the environment while maximizing economical profits and more steady management scenarios.

Fishery stock assessment usually requires a large number of historical information sets to characterize various fishery aspects (Chen et al., 2016). As stated by some authors, time-series length reflects the completeness of information collection for targeted variables, which is highly correlated with fishery economic/social/ecological importance (Chen et al., 2003; Rotherham et al., 2007; Chen et al., 2016). The continuity in fishery-dependent and (specially) in fishery-independent data collection programs and the gradual implementation of HTS methods applied for stock assessment purposes would suppose a revolution in how decision-making process will change in relation to the data (Hilborn, 2003). This revolution, understood in the sense of evolution, would be focused on providing the best possible technical support toward the stock assessment process development and, subsequently, an improved fishery management for policy making. These improvements would be mainly focused on the following: i) gathering and integration of new stock information (i.e., stock identification and new stock borders); ii) reducing uncertainty on stock assessment estimation process (improvements on community age structure information and reproductive parameters); iii) significant improvement on assessed species number due the reduction of on-sea data gathering techniques time and cost (i.e., data gathering from commercial landings for abundance estimation); vi) data quantity increase and, subsequently, increase on reference points calculation number; and v) inclusion of environmental information in the stock evolution (through the eDNA data incorporation in stock assessment process and policy-making process).

Under the presented context, HTS methods have been claimed to be a breakthrough in marine science (Ovenden et al., 2015; Bravington et al., 2016; Casey et al., 2016; Martinsohn et al., 2019; Friedman et al., 2022), raising the interest in its application in stock assessments. Hence, to check its suitability in terms of cost-efficiency, an SoA review was carried out. Several gaps appear that prevent to support the cost-efficiency by now.

4.1 Lack of research related on the applications of HTS techniques for stock assessment

First of all, only one project addresses the application of HTS methods to stock assessments (Bravington et al., 2014; Bravington et al., 2016; Waples et al., 2018). This research deals with an application of the CKMR method to estimate the spawning biomass of the Southern bluefin tuna, proving to be a suitable and also a cost-efficient method. Nevertheless, although certain possible sources of costs reductions are identified, i) no systematic cost analysis has been presented and, in addition, ii) characteristics of these species differ from most commercial species (lower number of individuals, no need for catching individuals for the assessment, etc.). It means that, for other commercial fisheries or different target species, a higher number of samples are needed (as the number of individuals is higher), increasing the cost of sampling (boat and crew time). Therefore, even with the same purpose, results are not directly transferable. Furthermore, recent contributions (Friedman et al., 2022) based on expert's advice also pointed out that cost-effective studies on the use of genetic technologies should be conducted.

4.2 Current application of new genetic techniques

The remaining literature dealing with the application of new genetic methodologies to fisheries is oriented to objectives that are different from stock assessments. Results in terms of efficiency or efficacy of any method depend on the purposes that they are used for.

In other words, eDNA seems to be efficient when compared with direct observations, scuba observations, etc. Nevertheless, for the moment, there is no evidence about their efficiency for stock assessments when compared with currently used methodologies. Stock identification remains one of the most confusing but relevant challenges in fishery science (Cadrin et al., 2014). Within this context, understanding intraspecific stock subdivisions remains a challenge in fishery science. Despite this, molecular genetic techniques such as eDNA appear to be a robust tool in conservation biology for identifying key aspects such as reproductive isolation between stocks, permitting delineation of management units, and allowing assessment of conservation priorities from an evolutionary perspective (Begg and Waldman, 1999). In particular, coastal and demersal species represent the main target on the application of eDNA techniques because of the species characteristics.

Epigenetic (DNAm) age determination seems to be a very accurate method to obtain sex and age, but it is a small part of the information required. Despite the short amount of information provided by DNAm for stock assessment purposes, it is key to estimate the fishery current status (population age structure, reproductive analysis, stock recruitment relationships, etc.). This information is generally difficult to obtain by means of traditional techniques (i.e., otoliths analysis), or, in other cases, measures are inaccurate. In addition to the benefits on the application of epigenetics on stock assessment processes, from an ecological point of view, these techniques will therefore improve our understanding of the mechanisms underlying natural variation in ecologically important traits and will provide insights into the mechanisms that allow organisms to respond to the environment (Bossdorf et al., 2008). In addition, in general terms, epigenetic processes may increase the evolutionary potential of organisms in response to abiotic stress and other environmental challenges, which could potentially be highly relevant in the context of global environmental change (Bossdorf et al., 2008). Therefore, understanding epigenetics in fishery populations could constitute a key tool in adaptive management toward the mitigation of climate change negative implications.

Despite the lack of variety on research studies about the application of CKMR methods for stock assessment purposes, it seems to be a promising HTS method in fishery research area. As stated by some authors, CKMR can be used effectively and cheaply as a mid/long-term monitoring tool for stock assessment. Some features—such as i) the ability of performing long-term forecasts; ii) the independent estimation of selectivity, fecundity, and mortality; iii) the capacity to estimate accurately stock abundance; and iv) accurate estimation of stock-recruitment relationship—place CKMR as a promising tool for stock assessment. Despite this, in marine context, most fish species are simply too abundant to have made the method cost-effective, although this may change as genotyping costs continue to drop (Bravington and Grewe, 2007).

In general terms, optimal levels of spatial and temporal replication according to fishery characteristics, target species, or the benefits of increasing sample sizes, etc., should be taken into account on deploying CBA (Underwood, 1996). This fact implies the inclusion of an inherent stage of the surveys that will determine appropriate compromises between survey precision and the collected information amount (Bravington and Grewe, 2007).

4.3 Surveys

Despite the fact that there remains a need to measure the relative importance of different types of fishery data for stock assessment in allocating sampling effort to ensure the optimal data collection (Chen et al., 2003), the inclusion of HTS techniques in stock assessment data collection frameworks and, subsequently, in management processes would suppose a revolution in the fishery-dependent and fishery-independent sampling.

A common practice while obtaining biological information about a fishery resource during a fishery-dependent sampling is to complement catch and effort data with biological observations of caught individuals. Traditional mechanisms for measuring sex, maturity, or age are highly invasive and generally require to purchase a wide number of individuals. HTS techniques put over the table a non-invasive mechanism for obtaining wide amount of information from a single fin-clip, eliminating (to a great extent) the need to engage trawl or acoustic surveys for determining stock size. Related literature on this topic is unclear, but some manuals recommend a minimal sample size of 50~100 individuals to obtain relevant biologic information (Martinsohn et al., 2015). Performance and benefits of implementing HTS methods on biological fishery-dependent information sampling are highly determined by target species' commercial value.

Related with fishery-independent surveys, many authors such as Caddy and Cochrane (2001) or Dennis et al. (2015) highlighted the need and benefits for fishery monitoring systems that are both robust to inherent uncertainty and cost-effective. Despite this, the general intuition is that new HTS methods could reduce costs and improve efficiency and precision of fishery information. In addition, despite the further work needed, genetic response to environmental changes such as climate change information could be obtained by means of HTS methods. It would offer wide amount of information to the application of a climate-based adaptive management in fishery research area (Frost et al., 2012).

4.4 On the benefits of including genetic information on stock assessment

Literature revision on the benefits of including HTS information on fishery data for stock assessment highlighted the value of the new techniques. Those could be summarized in i) precise stock identification; ii) accurate sex, maturity, and age determination; and iii) reduction of the associated uncertainty of parameter estimation and, subsequently, improvement of fishery model outcomes for stock assessment precision, which could lead to a more accurate management measures.

Stock identification is a key aspect in modern fishery stock assessment. However, considering the importance of identifying the target species stock structure, there is a scarcity of assessments that actually include stock identification requirements (Begg et al., 1999). Understanding the genetic variation between stocks provides a reliable source of information for management purposes (Begg and Waldman, 1999).

Many authors addressed the fact that a large amount of biological knowledge is potentially useful in stock-assessment and management context. Sex, age, and maturity parameter estimation involves a wide number of processes and methods for sampling. In addition, sometimes, the big number of samples and the difficulties to obtain precise observations (i.e., otoliths sampling) increase the process uncertainty (observer error). In addition, differing by species and region, this kind of information could not be sampled (e.g., otoliths observation in tropical species and/or small-pelagic individuals cannot be performed). The inclusion of HTS techniques and, concretely, the use of DNAm methods could suppose a revolution in the ability to estimate precise fishery parameters and, subsequently, improve the scientific advice—the latter through reducing the sources of uncertainty in fishery stock assessment and, therefore, potentially improving management.

4.5 HTS method limitations

In addition, just a few works expose the limitations of such novel techniques, putting in the spotlight the need of delving into the study of the HTS methods to advise them as substitute measures to traditional methodologies (Bravington et al., 2014; Bravington et al., 2016; Yamamoto et al., 2016; Evans et al., 2017; Yamamoto et al., 2017; Harper et al., 2018; Qu and Stewart, 2019). Moreover, there are very few works that go beyond analyzing the HTS methods from a critical point of view questioning their alleged cost-efficiency in a broader analytical frameworks (Stein et al., 2014; Hansen et al., 2018; Jerde et al., 2019).

4.6 Further applications of HTS methods

Finally, it is worthy to point out that HTS can provide additional information that could be of interest for marine research beyond stock assessment, contributing, for instance, to move toward ecosystem-based fishery management. HTS-based methods such as CKMR in the estimation of biomass and species abundance, epigenetic analysis as an alternative to traditional ageing techniques, genotypic analysis of marine species, and eDNA sampling could enable a more adaptive management, contributing to mitigate negative climate change implications.

5 Conclusions

Once the literature is revised, the HTS method seems to be a promising methodology for marine science and, particularly, for stock assessment. Nevertheless, no complete evidence of their cost-efficiency/cost-benefit for marine fish stock assessments has been provided up to now. Almost all available analysis focuses on specific components or activities, but there is a lack of full-stream assessments.

An eventual cost-efficient analysis comparing currently used versus HTS methodologies should take into account, on the one hand, the information provided (and its suitability for stock assessment) and, on the other, the cost of gathering such information considering the sampling process, data collection, and the processing of the information until the assessment is done. In addition, different commercial species should be considered as costs can vary significantly depending on the abundance, the habitats, etc.

As it is not possible to assess the efficiency without taking into consideration the outputs (both intermediate and final), it would be convenient to identify the amount and quality of information generated by the genomic techniques individually and compare them with the data obtained in traditional sampling, to confirm whether the use of HTS methods is more efficient.

Finally, the future research agenda should attempt to straddle both the scenarios for the transition process, considering complementary implementation and substitution possibilities and their cost-efficiency. A key requirement in this regard is that fishery stock assessment usually requires a large number of historical information sets. Clarifying these questions is likely to pave the way for the effective and step-wise implementation of these methods in fishery management; thus, further research is recommended to encompass the transition process.

Author contributions

GR-R provided the original idea. HB, ES-L and GR-R designed the manuscript content and outline. GR-R, HB, ES-L, RB and RO contributed to writing and re- viewing the manuscript. All authors contributed to the article and approved the submitted version.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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