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# Editorial: Prospects and challenges for the implementation of HTS genetic methods in fisheries research surveys and stock assessments

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## Editorial on the Research Topic

### Prospects and challenges for the implementation of HTS genetic methods in fisheries research surveys and stock assessments

The status of exploited fish stocks requires regular assessment to ensure sustainable fishing practices. These assessments rely on the collection of data from multiple sources, which include fishery-dependent data — catches, landings and biological information — as well as fishery independent data obtained from research surveys (Stomatopoulos, 2002). These traditional methods provide valuable and systematized information regarding exploited fish populations, marine biodiversity, and their environment, and constitute an essential piece in stock assessment and scientific advice. However, they also have important limitations such as high economic costs of research surveys coupled with complex logistics. As a result, fisheries data have a generally limited coverage in space and time and are time consuming in their analysis (Stomatopoulos, 2002), leading to often biased and imprecise estimations (Hilborn and Walters, 2013; Pennino et al., 2016). This can have a great impact on the quality of the scientific advice provided to management bodies and, hence, ultimately on fishing activities. Moreover, traditional methods lack the capacity to provide information on crucial parameters for stock management, such as the delineation of stock boundaries or the connectivity, among others, highlighting the crucial need for innovative assessment tools to aid fisheries management (Valenzuela-Quiñonez, 2016). In addition, most exploited species worldwide lack the data needed to assess their status, despite the increasing trend of overfished stocks in the last four decades (FAO, 2022).

Advancements of high throughput molecular technologies have unlocked the power of genomics to complement traditional methods, reducing uncertainty, improving cost-efficiency of fish stock assessments, and opening the possibility for expanding the range of assessed species. Novel technologies provide the statistical power and resolution required

to solve key issues in fisheries management but despite their potential to improve fisheries advice, the integration of genomic-informed methods into fisheries management practices is still very limited and patchy (Bernatchez et al., 2017; Benestan, 2019). The starting point of this Research Topic has resided in the recognition that there is a pressing need to overcome these barriers (Ovenden et al., 2015; Bernatchez et al., 2017) and bridge the gap between the two fields to secure the sustainability of exploited fish stocks.

This editorial summarizes the contributions to the Frontiers Research Topic “*Prospects and Challenges for the Implementation of HTS Genetic Methods in Fisheries Research Surveys and Stock Assessments*”, established under the Marine Fisheries, Aquaculture and Living Resources section in the Frontiers in Marine Science journal. This Research Topic aimed at exploring recent developments in the field of genomics applied to fisheries. Here, we compile a set of 14 articles structured in two categories, with nine contributions devoted to reviewing the latest developments in methodologies with potential use in fisheries science, whereas the rest represent practical applications in this field. Below, we summarize each of the articles included in this Research Topic and add thoughts on the potential future directions of fisheries genomics.

Rodríguez-Mendoza and Saborido-Rey carry out a review of the bottom trawl research surveys in the EU to determine how genomic techniques can be used to improve survey data, considering the needs of current and future stock assessment in Europe. This information is key for the implementation of novel genomic methods in fisheries research surveys, as this requires a deep understanding on how the surveys are conducted, which data is collected onboard and how these data are used in stock assessment, but also in ecosystem assessment and other purposes. This key step needs to be taken prior to a large-scale implementation of genomics methods in surveys.

Ramírez-Amaro et al. provide an overview of the environmental DNA methodology and explore the capacity of several approaches based on this emerging tool to inform Ecosystem-Based Fisheries Management. They analyze the main aspects affecting eDNA behavior in the marine environment and provide a detailed compilation of eDNA applications in fisheries management. Petit-Marty et al. highlight the lack of consistency across data analysis in eDNA studies and provide a review of the essential steps of eDNA data processing and of the bioinformatics tools to produce sound, reproducible, and comparable results. This article provides essential guidance for a comprehensive application of eDNA-based approaches in fisheries management.

Piferrer and Anastasiadi present a detailed review of piscine epigenetic clocks, an emerging genomic technology for age estimation, a crucial parameter for fisheries management. The authors provide guidelines for clock development, detailing the steps and considerations required to produce accurate, precise, and reproducible clocks that can contribute to better fisheries management practices. This article is complemented by a second review focused on the computational steps and tools required for the construction of epigenetic clocks in fish and for age prediction (Anastasiadi and Piferrer).

Casas and Saborido-Rey provide an overview of the Close-kin mark-recapture (CKMR) method, an emerging methodology

grounded in genomics, to estimate abundance and other demographic parameters (e.g., population trend, survival rates, connectivity) that are essential in fisheries assessments. The authors assess the readiness, viability, and maturity of the method in a fisheries framework, evaluate technical considerations and requirements for a successful implementation and provide advice for planning a CKMR study. A second review provides guidance to address the genomics and bioinformatics steps required to analyse CKMR data, using a simple terminology to reach potential users with no previous expertise in genomics (Casas and Saborido-Rey).

Rodríguez-Rodríguez et al. assess the cost-effectiveness of the three techniques above (eDNA, epigenetic clocks, and CKMR) applied on marine ecosystems and fisheries and for stock assessment purposes. The authors provide a comparison of the information and cost provided by surveys and novel methodologies, highlighting the striking shortage of systematic cost analysis studies of genomic techniques despite the general assumption of their cost-effectiveness and efficiency in terms of effort and time.

Baltazar-Soares et al. present a Perspective article addressing one of the potential limitations of the implementation of genomics methods in fisheries assessments. Although the establishment of modern genomic approaches and subsequent large-scale genomic datasets can clearly enhance our understanding of stock spatial distributions, it may also compromise the temporal depth analysis and consequently the forecasting ability of stock distribution. To resolve this, the authors propose an interesting approach integrating genomic information on temporal projections of species distributions computed by Species Distribution Models (SDMs) that accounts for habitat selection given the current evolutionary potential of the stock.

Kasmi et al. present a practical application of a real-time PCR-based eDNA approach to assess quantitatively the abundance of cod in the North and Baltic Seas. The authors comparatively analyse the concentrations of eDNA with bottom trawl fisheries catches, showing a significant correlation (95%) between eDNA and cod biomass. This study highlights the potential of this non-invasive tool to assess abundance of fish stocks.

Ferchaud et al. provide an excellent example of the utility of novel genomic techniques to inform fisheries management. The authors use whole-genome data of over 1300 individuals of Greenland Halibut, *Reinhardtius hippoglossoides*, sampled across the Northwest Atlantic to infer geographic population structure and local adaptation. The analysis revealed a panmictic population across the Northwest Atlantic with the exception of the Gulf of Saint Lawrence that presents significant genetic differentiation, mainly attributed to environmental variables, suggesting that this stock might be particularly vulnerable to environmental changes.

Pampín et al. use genomics (2b-RADseq) and transcriptomics to identify single nucleotide polymorphisms (SNP) markers associated with resilience to the protozoan parasite *Marteilia cochillia* that infects bivalves causing a disease known as marteiliosis. Populations of the common cockle (*Cerastoderma edule*) in Galicia (Northwest Spain) constitute a valuable socioeconomic resource for coastal communities but have been decimated by this parasite. The authors produce a robust genotyping SNP tool set that can be applied in marker-assisted

selection programs for restoring affected cockle natural bed ecosystems and recovering their production.

López et al. use RAD-seq to investigate the population structure of vendace (*Coregonus albula*), a small salmonid fish, in the Bothnian Bay, the northernmost part of the Baltic Sea. Their analysis rejects the hypothesis of panmixia as a clear genetic differentiation is found at one of the studied locations. Additionally, they reveal a weak structuring between samples from the Swedish and the Finnish coasts. The study demonstrates the power of RAD-sequencing to detect low but significant genetic structuring relevant for fisheries management.

Lastly, Zelenina et al. demonstrate the usefulness of a panel of SNP markers developed from a RAD-sequencing project to study the intraspecific polymorphism of the complex stock structure of pink salmon, *Oncorhynchus gorbuscha*, in the Okhotsk basin. The complexity is the result of the existence of two allochronous lineages. The developed methodology provides an efficient tool to reliably differentiate regional stocks and determine the proportion of fish from the main reproduction areas in these mixed stocks.

We hope that this Research Topic can contribute to the perception of the potential of new emerging genomic technologies to improve scientific advice and enhance fisheries assessments. The application of genomics tools in fisheries management should not be delayed further, but demands an improved communication and reciprocal training among geneticists, fishery biologists and managers. In addition, the uptake of genomic information for assessment and advice should be progressive, starting with an implementation in parallel with traditional assessment to ensure the preservation of data series and a proper standardization of novel methodologies.

## Author contributions

The idea of the Research Topic was developed during a Project meeting under Service Contract “Improving cost-efficiency of fisheries research surveys and fish stocks assessments using next-generation genetic sequencing methods [EMFF/2018/015]”. LC and FS-R wrote the first draft of the editorial article and all authors contributed equally to the discussion-conclusions and in writing the final manuscript. All authors contributed to the article and approved the submitted version.

## References

- Benestan, L. (2019). *Population genomics applied to fishery management and conservation* (Cham: Springer), 399–421. doi: 10.1007/13836\_2019\_66
- Bernatchez, L., Wellenreuther, M., Araneda, C., Ashton, D. T., Barth, J. M. I., Beacham, T. D., et al. (2017). Harnessing the power of genomics to secure the future of seafood. *Trends Ecol. Evol.* 32, 665–680. doi: 10.1016/j.tree.2017.06.010
- FAO. (2022). *The State of World Fisheries and Aquaculture 2022. Towards Blue Transformation*. (Rome, FAO). doi: 10.4060/cc0461en
- Hilborn, R., and Walters, C. J. (2013). *Quantitative fisheries stock assessment. 3rd ed.* Eds. C. J. Walters and R. Hilborn (Dordrecht: Springer Science & Business Media).
- Ovenden, J. R., Berry, O., Welch, D. J., Buckworth, R. C., and Dichmont, C. M. (2015). Ocean’s eleven: a critical evaluation of the role of population, evolutionary and molecular genetics in the management of wild fisheries. *Fish Fish.* 16, 125–159. doi: 10.1111/faf.12052
- Pennino, M. G., Conesa, D., López-Quílez, A., Muñoz, F., Fernández, A., and Bellido, J. M. (2016). Fishery-dependent and -independent data lead to consistent estimations of essential habitats. *ICES J. Mar. Sci.* 73, 2302–2310. doi: 10.1093/icesjms/fsw062
- Stomatopoulos, C. (2002). *Sample-based fishery surveys: A technical handbook*. FAO Fisheries Technical Paper. No. 425. (Rome, FAO). 2002. 132. Available at: <https://www.fao.org/3/Y2790E/Y2790E00.htm>.
- Valenzuela-Quíñonez, F. (2016). How fisheries management can benefit from genomics? *Brief. Funct. Genomics* 15, 352–357. doi: 10.1093/bfpg/ewl006

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## Conflict of interest

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