

STOCK IDENTIFICATION METHODS WORKING GROUP (SIMWG)

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i Executive summary

In 2025, representing the third year of its current 3-year term, the Stock Identification Methods Working Group (SIMWG) met in Faro, Portugal, from 9-11 Sep 2025, with hybrid sessions to connect WG members who could not attend the meeting physically.

SIMWG has continued to provide annual updates on recent applications of stock identification methods to species assessed by ICES and on advances in stock identification methods. Based on the wide expertise of SIMWG members, we provide reviews of recent literature on genetics, life history parameters, morphometrics/meristics, tagging, otolith morphometry, chemistry of otoliths and other archival structures, parasites and interdisciplinary approaches (ToR a).

A key activity of SIMWG is to address requests by ICES expert groups for technical advice on issues of stock identity. In the current term, we reviewed documents and information on

- King and queen scallops (ToR b, WGScallop request);
- ‘Other soles’ in Divisions 8c and 9a (ToR b, WGBIE/WKOS request);
- West Greenland inshore cod (ToR d, NWWG request).

SIMWG members participated actively in the Scallop Assessment Working Group (WGScallop) and the Workshop on Other Soles in ICES Division 8c and 9a (WKOS) to provide advice on stock structure and guidance for future work. There also is a strong link to the Working Group on the Application of Genetics for Fisheries and Aquaculture (WGAGFA).

SIMWG contributes to the general understanding of the biological features of the north Atlantic ecosystem through its work to describe fish population structure. Additionally, SIMWG’s annual reviews on advances in stock identification methods keep ICES members abreast of best practices in this field of study. SIMWG expert reviews on questions of stock structure for particular ICES species are directly relevant to the appropriate definition of stock and contribute to the accuracy of stock assessment and effectiveness of management actions. We see an important role for SIMWG in the future as ICES copes with the shifting distributions of fishery resources and questions re-garding the appropriate definition of fish stocks. Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock can be contemplated and SIMWG will continue to work with with ICES expert groups to address pressing stock identification issues.

ii Expert group information

Expert group name	Stock Identification Methods Working Group (SIMWG)
Expert group cycle	Multiannual fixed term
Year cycle started	2022
Reporting year in cycle	3/3
Chair	Christoph Stransky, Germany
Meeting venues and dates	By correspondence in 2023; Online meeting 17-19 June 2024 (originally planned in Faro, Portugal); Faro, Portugal, 9-11 Sep 2025

1 Review recent advances in stock identification methods (ToR a)

Stock Identification Methods Working Group 2025 report

Over the past years, there has been a wide use of applications of stock identification methods to ICES stocks, as well as several notable advances in stock identification methods, with many results relevant to ICES science and advice. SIMWG has committed to providing annual updates on recent applications of stock identification methods to ICES species and on advances in stock identification methods. The group has focused on summarizing research in the focal areas listed below:

- a) Genetics
- b) Life-history parameters
- c) Morphometrics/meristics
- d) Tagging
- e) Otolith morphometry
- f) Chemistry of otoliths and other archival structures
- g) Parasites
- h) Interdisciplinary approaches

SIMWG's annual reviews on advances in stock identification methods keep ICES members abreast of best practices in this field of study. This review activity has served as a valuable contribution to the field and has formed the foundational material for two editions of the book "Stock Identification Methods: Applications in Fishery Science". This book was first published in 2005. SIMWG members S. Cadrin, L. Kerr and S. Mariani edited the 2nd edition (2014), and several SIMWG members contributed chapters to this book. A 3rd edition is planned for 2026, again involving several SIMWG members (see Section 4).

The details of annual reviews of advances in stock identification methods are summarized in Annex 3.

2 Technical reviews and expert opinion on matters of stock identification (ToR b)

Stock Identification Methods Working Group 2025 report

SIMWG provides expert feedback on questions of stock structure for ICES stocks to ICES expert groups. In 2025, SIMWG contributed to ICES advisory needs by providing expert feedback on the status of the stock structure of

- King scallops (*Pecten maximus*) and queen scallops (*Aequipecten opercularis*);
- Senegalese sole (*Solea senegalensis*) and sand sole (*Pegusa lascaris*) in Division 8c and 9a;
- Cod (*Gadus morhua*) in NAFO Subarea 1 (West Greenland Inshore Spawning Cod).

The detailed reviews are provided in Annex 4.

Moreover, SIMWG members participated in the Scallop Assessment Working Group (WGScallop) and the Workshop on Other Soles in ICES Division 8c and 9a (WKOS) to discuss stock structure and provide a way forward to improve data/information for stock identification collaboratively.

SIMWG expert reviews on questions of stock structure for ICES stocks are directly relevant to the appropriate definition of stock and contribute to the accuracy of stock assessment and effectiveness of management actions. Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock can be contemplated, and SIMWG will continue to work with ICES expert groups to address pressing stock identification issues. We see an important role for SIMWG in future as ICES copes with the shifting distributions of fishery resources and questions regarding the appropriate definition of fish stocks.

SIMWG's advice has been well received by the requesting groups, and there is a growing number of requests from different groups, which underlines the importance of the service that SIMWG provides to the ICES community. SIMWG's expertise should continue to be used to address specific questions of stock structure and should be considered in the advisory process in the context of whether the stock units are appropriate for accurate assessment and sustainable management of ICES fishery resources.

An overview of past SIMWG reviews is provided in Annex 5. The group suggests that this table should be provided as an Excel file to replace the outdated PDF (from 2016) that is currently downloadable on the SIMWG's homepage.

(<https://www.ices.dk/community/groups/Pages/SIMWG.aspx>).

3 Advances in mixed-stock analysis (ToR c)

Stock Identification Methods Working Group 2025 report

In 2024, the group discussed several ongoing applications and provided practical recommendations for implementing mixed-stock composition analyses (ICES 2024), as a follow-up to Section 3 of the SIMWG 2022 report (ICES 2022). Apart from work on North Sea cod, no new developments were reviewed this year.

3.1 North Sea cod

WKNSCodID (ICES 2020) provided recommendations for genetic sampling to support stock composition analyses. However, uncertainties remain regarding the three putative stock components ('Viking', 'Dogger', and 'Celtic'). A new project (GenDC) has been initiated to enhance genetic sampling coverage and address these uncertainties.

In response to a special request from the UK, Norway and the European Commission (DG MARE), two workshops, WKCODSCOPE and WKCODSAMPLING, were planned for 2025 to further investigate the substock structure of Northern Shelf cod and to synthesize findings from the GenDC project. Results from these workshops were not yet available at the time of the SIMWG meeting and will be summarized in next year's report.

3.2 References

- ICES 2020. Workshop on Stock Identification of North Sea Cod (WKNSCodID). ICES Scientific Reports. 2:89. 82 pp. <http://doi.org/10.17895/ices.pub.7499>
- ICES 2022. Stock Identification Methods Working Group (SIMWG). ICES Scientific Reports. 4:72. 66 pp. <http://doi.org/10.17895/ices.pub.20937001>
- ICES 2024. Stock Identification Methods Working Group (SIMWG). ICES Scientific Reports. 6:85. 249 pp. <https://doi.org/10.17895/ices.pub.27110470>

4 Update on stock ID book (3rd edition)

Stock Identification Methods Working Group 2025 report

Elsevier invited a 3rd edition of the book 'Stock Identification Methods: Applications in Fishery Science' with substantial revisions and new information. In 2022, SIMWG confirmed that there have been advances in many of the topics covered in the second edition (e.g. genomics, spatial Management Strategy Evaluation, spatial integration of multidisciplinary information), and climate change is an emergent topic that influences several aspects of stock identification. The editors and SIMWG proposed a substantial revision to consolidate some current chapters and add some new chapters. All chapters will be revised to deemphasize traditional or outdated methods, retaining brief descriptions to support integration and consider challenges of climate change. The currently proposed plan for the book chapters is:

Background Concepts:

- Overview
- Structure and Connectivity
- Variation in Quantitative Traits

Individual Methods:

- Early Life Stages
- Life-history Parameters
- Morphometrics
- Growth Marks
- Parasites
- Chemistry of Hard Parts
- DNA barcoding
- Population Genomics
- Conventional and Electronic Tagging

Application:

- Interdisciplinary Sampling
- Interdisciplinary Synthesis
- Integrating Spatial Structure into Stock Assessment
- Addressing Complex Structure in Management Strategies
- Testing Implications of Stock Structure-Simulation Modelling

The proposed timeline foresees drafting of the chapters during 2026, with input from a (proposed) Theme Session on 'Advancing Stock Structure Science: From Identification to Application' at the ICES Annual Science Conference in September 2026.

Annex 1: List of participants

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Annex 2: Resolutions

The **Stock Identification Methods Working Group (SIMWG)**, chaired by Christoph Stransky, Germany, and generate deliverables as listed in the Table below.

	Meeting dates	Venue	Reporting details
Year 2023	Work by correspondence		
Year 2024	June	Online	
Year 2025	9–11 September	Faro, Portugal	

ToR descriptors

ToR	Description	Background	Science plan codes ¹	Duration	Expected deliverables
a	Review recent advances in stock identification methods	a) Tracks best practices in stock ID b) Promotes new technologies relevant to all ICES species	1.4, 1.8, 5.2	3 years (and continued)	EG report, revised stock ID book chapters
b	Provide technical reviews and expert opinions on matters of stock identification, as requested by specific Working Groups and ACOM	Ad hoc advice requests to be addressed at short notice	1.4, 1.8, 5.2	3 years (and continued)	EG report, contribution to ASC
c	Review and report on advances in mixed-stock analysis, and assess their potential role in improving precision of stock assessment			3 years	EG report
d	Review of the suggested splitting of the West Greenland inshore stock (cod) into two separate stock units, based on available biological	Advisory requirement	1.4, 1.8, 5.2	1 year	Brief review report provided to NWWG and ACOM (clear response required) Chapter in EG report

¹ Note: these resolutions refer to the former Science Plan codes approved in 2018. The current Science Plan codes are available here: https://www.ices.dk/about-ICES/how-we-work/Documents/SciencePlanCodes_2025.pdf

ToR	Description	Background	Science plan codes ¹	Duration	Expected deliverables
	(tagging), catch trends and survey trends				

Supporting information

Priority	Understanding stock structure is a fundamental requirement before any assessment or modelling on a stock level can be contemplated. SIMWG liaises with ICES expert groups and working groups on stock identification issues and continues to review new methods as they develop
Resource requirements	None.
Linkages to ICES committees or groups	SIMWG has recently worked closely with a range of ICES working groups including HAWG, WGBIE and WGHANSA; benchmark workshops including WKELASMO, workshops on cod stock structure (WKNSCodID, WK6aCodID, WKSIDAC). In previous years, SIWMG connected with many more ICES groups to fulfil requests.
Linkages to other organizations	There are no obvious direct linkages, beyond the SIMWG members' affiliation and commitment to their own employers. Depending on the request, SIMWG's scope might expand beyond the ICES area to address straddling stocks e.g. in the NAFO, NEAFC, CECAF and other RFMO areas.

Annex 3: Review recent advances in stock identification methods (ToR a)

Advances in Stock Identification Methods in 2025

In 2025 (review period mid-2024 to mid-2025), there were several notable advances in stock identification methods and a proliferation of applications, with many results relevant to ICES science and advice. Here, we summarize advances and results accounting for research in genetics, life-history parameters, morphometrics, tagging, otoliths, parasites and interdisciplinary approaches.

Genetics (Contributors: Florian Berg, Rita Castilho, Ilaria Coscia, Áki Jarl Láruson, Tuomas Leinonen, David Murray)

Over the past two decades, there has been a significant shift in the genetic markers and approaches used in fisheries research, reflecting technological advancements and research priorities. Beginning in the early 2000s, microsatellites (micros) were the predominant markers used due to their high polymorphism and informativeness for population studies. However, the number of papers employing microsatellites began to decline after peaking around 2018, as Single Nucleotide Polymorphisms (SNPs) started gaining prominence.

In particular, microsatellite papers exhibited a noticeable upward trend between 2021 and 2025, peaking at 167 papers in 2015. Following that peak, the numbers fluctuated with a notable decline in recent years, particularly in 2025, when the number dropped to 57 papers. On the other hand, at the beginning of the millennium, the number of papers focusing on SNPs was almost negligible. However, there has been a substantial increase in the number of SNP-related papers since 2011, with a peak in 2022 at 107 papers. This indicates a growing academic interest and likely advancements in SNP-related methodologies and applications. Papers using emerging markers such as structural variants (e.g. copy number variants; CNVs) started from single counts in 2001, but numbers are still low compared to the two other marker types and are not common. Yet, it is expected that with the rise of available genomes (see section below), these markers will become easy to identify and to incorporate into future studies. The shift towards genomics since 2018 marks a significant milestone, as depicted in the increasing number of publications from this period, illustrating the field's adaptation to cutting-edge genetic technologies. This evolution of genetic markers not only mirrors technological advancements but also the growing complexity of questions addressed in fisheries science.

In summary, while microsatellite-based research publications saw a rise and then began to taper off in the recent years, SNP-related research has been gaining traction, especially in the past decade. The advent of reference genomes and the decrease in cost for obtaining genomic sequences anticipate a future increase in the use of alternative markers such as copy number variations and other structural variant types. The data paint a picture of the evolving landscape of the use of different genetic marker types for population structure analyses for stock identification.

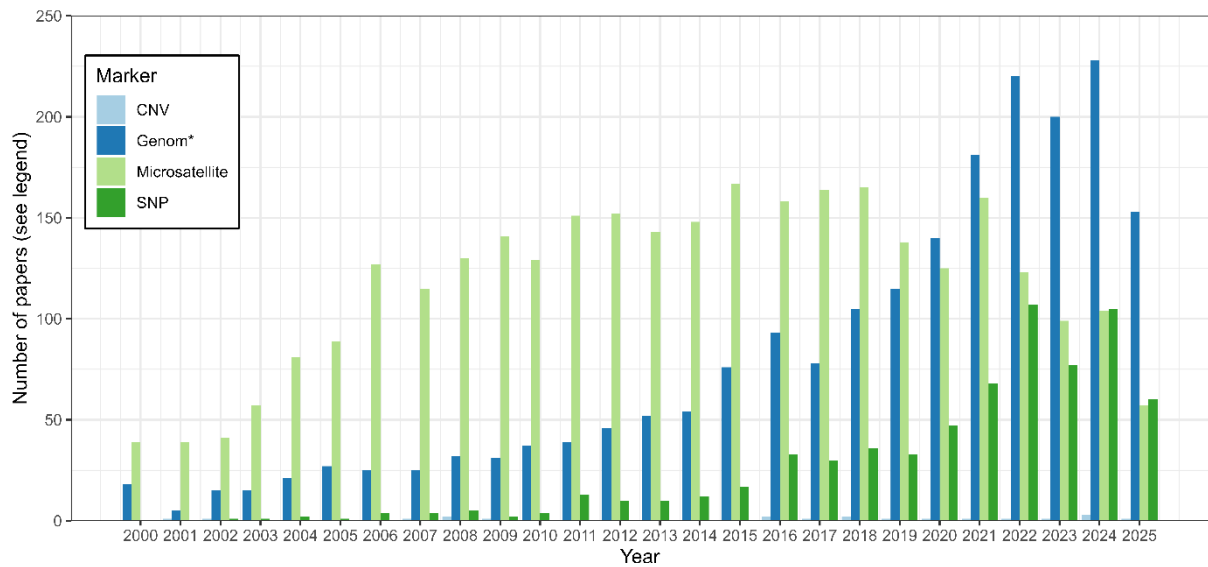


Figure A3.1. Scientific publishing trend since 2000, comparing outputs of studies using microsatellite, SNPs and CNVs, as listed in the Clarivate Analytics Web-of-Science. The search criteria were: “fish* AND gene* AND (population OR stock) AND ‘molecular marker*’, where ‘molecular marker*’ means “Microsatellite*”, “SNP*”, “CNV*” or “Genom*”. Search link for microsatellite (<https://www.webofscience.com/wos/woscc/summary/b5c80b49-662b-4525-b4c1-865c22f99b20-a52e48cd/relevance/1>); SNP (<https://www.webofscience.com/wos/woscc/summary/c4da2151-03b7-4ed7-b153-12deb40c9041-a52f4b87/relevance/1>); CNV (<https://www.webofscience.com/wos/woscc/summary/7ee22b70-0976-4fe3-9098-4da0373aa33b-a52f88dd/relevance/1>); Genom (<https://www.webofscience.com/wos/woscc/summary/bed1f912-d011-44e4-a5f4-bb564cfe4b06-a236a758/relevance/1>). Only papers in the following Web of Science categories were considered: ‘Fisheries’, ‘Environmental Sciences’, ‘Ecology’, ‘Biodiversity Conservation’, ‘Marine & Freshwater Biology’ and ‘Oceanography’. Data for 2025 only represent papers published through to the present date (September 2025). Note: There is the caveat that some of the as genom* identified papers may also be considered as SNP papers and may be counted twice.

Comprehensive review papers

The selection of the 2024-2025 papers as examples of advances in genomics for fish stock discrimination reflects the subjective choice of the contributors. While they highlight significant progress and innovation, other important studies may also exist. The choice is influenced by the contributors' perspectives on what constitutes genuine advancement in this field, making the selection inherently subjective.

Carvalho (2025) published a comprehensive review on the impact of ‘omics’ technologies on fish ecology, management, and forecasting. The paper synthesizes when, how, and why genetics and genomics have influenced marine fisheries management and been taken up by policy-makers. Carvalho emphasizes that future progress depends on effective communication among scientists, practitioners, and policy-makers, as well as broader dissemination of evidence beyond the “grey literature” of agency reports, framed within sustainability and economic benefits. The combination of increasingly accessible genomic tools, clear scientific and economic gains, and the urgent conservation needs of global fisheries is expected to drive greater awareness and sustained investment.

Examples of genetic stock identification (GSI)

A total of ~30million SNPs were obtained by Pujolar *et al.* (2025) from whole-genome sequencing (WGS) to analyse the population structure in European anchovy (*Engraulis encrasicolus*; n=40). Anchovies were collected from ICES divisions 3.a, 4.b-c, 7.f-g, j and 9.a. Using sliding-window FST scores, the study detected strong signatures of selection (i.e. adaptive markers) on chromosomes 3,4,6,18 and 19, which were used to examine genetic groups. The paper found evidence of three distinct 'genetic clusters': 1) Northern cluster, including anchovy from the Kattegat and North Sea (Divisions 3.a, 4b-c), 2) Southern cluster, including anchovy from Ireland, Central Portugal and North Sea (Divisions 4.c, 7.f-g, J and 9.a), 3) Cadis cluster which are individuals collected from southern Iberia (Division 9.a). The authors make no suggestions regarding realignment of stock boundaries due to mismatches with 'genetic clusters'.

Sabatino *et al.* (2025) investigated the role of chromosomal inversions in shaping the population genomics of the European sardine, a highly fecund, widely distributed pelagic fish. Using WGS of 34 populations across the Atlantic and Mediterranean, researchers identified nine large inversions spanning over half the sardine genome. These inversions correlate strongly with life-history traits and environmental gradients, such as temperature and productivity. Despite widespread gene flow at neutral loci, inversion regions show pronounced genetic differentiation, even between geographically close populations. Demographic modelling revealed reduced migration and effective population sizes within inverted regions, supporting their role in local adaptation. The results have significant implications for fisheries management, indicating a mismatch between the locally adapted genetic stocks detected in the study and the current stock boundaries. In the Atlantic (samples coverage from the tip of Cornwall the western portions of 7e and 7f), no genetic difference was found between the Northern and Central stocks, which formed a single genetic cluster extending into the Cantabrian Sea. The Southern stock was also shown to include different genetic clusters, notably one in NW Iberia and another in southern Iberia extending into northern Moroccan waters and the adjacent Mediterranean Sea.

In McKeown *et al.* (2025), RAD-seq was used to identify ~3500 SNPs for analysing the population structure of European sardine (*Sardina pilchardus*; n=288). Samples were collected from ICES divisions 4.b-c, 7.d-f, 8.a-b. Within the Northeast Atlantic samples, genome-wide patterns confirm restricted gene flow between the Biscay (Divisions 8.a-b) and North Sea (Divisions 4.b-c) sardine. Using FST, individual assignment, and introgression analysis of outlier loci (also known as adaptive markers) revealed further structuring, identifying a North Sea-Eastern channel (Divisions 4.b-c, 7.d) group which is genetically distinct from Bay of Biscay (Divisions 8a-b), Celtic Sea (Division 7.f), and western English Channel (Division 7.e) sardines. The authors state that there is a mismatch between 'management units' and the genetic population structures.

Using a panel of 41k SNPs, Taylor *et al.* (2025) investigated the genetic population structure of sea bass (*Dicentrarchus labrax*) within the Northeast Atlantic region (ICES divisions 3.a 4.b-c, 6.a, 7.a-b, 7.d-g). Sea bass were split by season to analyse 'spawning' and 'feeding' samples separately and combined. Genetic differentiation was low irrespective of sample type (Spawning $F_{st}=0.00022$; Feeding $F_{st}=0.00032$). Average F_{st} was larger between spawning samples, suggesting some, as yet undetected, biologically meaningful population structure. However, there was no statistically significant evidence to suggest that sea bass in different ICES divisions comprise genetically differentiated populations. Evidence from this peer-reviewed paper was presented at the ICES Sea bass stock identification Benchmark in 2023 and contributed to defining the current stock unit boundaries.

Using a curated SNP baseline spanning multiple NE Atlantic herring populations and running GSI on mixed catches, Seljestad *et al.* (2024) show that current management boundaries cut across biological population structure. Practically, this means standard assessment areas can pool distinct genetic units, biasing allocation and status signals; methodologically, the paper is a clean template for (i) baseline curation, (ii) mixture assignment/uncertainty, and (iii) translating assignment outputs into concrete advice on stock boundary revision.

Johansson *et al.* (2025) present the development of a single-nucleotide polymorphism (SNP) genotyping panel for genetic stock identification (GSI) of Atlantic salmon (*Salmo salar*) in the Teno River system, one of the most genetically diverse salmon populations globally. The researchers genotyped over 1,200 individuals from 37 locations using more than 33,000 genome-wide SNPs to identify 22 genetically distinct reporting units. A subset of 180 informative SNPs, along with a sexing marker, was selected for a genotyping-by-sequencing (GT-seq) assay. The new SNP panel demonstrated comparable assignment power to the previously used microsatellite panel, with advantages in cost, speed, and cross-platform robustness. Mixed-stock analysis of the 2018 salmon catches confirmed contributions from all 22 units, with catch proportions correlating with independent estimates of spawning female biomass. This validates the panel's effectiveness for stock assessment and management. The study emphasizes the importance of regular GSI for sustainable fisheries management, especially in complex systems like the Teno River, where multiple genetically distinct populations coexist. The SNP panel offers a future-proof tool for monitoring and conserving Atlantic salmon stocks, aligning with international conservation guidelines and bilateral management efforts between Finland and Norway.

Miettinen *et al.* (2021) found population sub-structure in River Tornio, which has a natural Atlantic salmon population, using 18 microsatellites. The River Tornio Atlantic salmon population is treated as a single stock in the ICES stock assessment (ICES 2024a). Miettinen *et al.* (2024) identified River Tornio subpopulations in commercial catches from the Baltic sea with GT-seq of 166 SNPs, including SNPs linked to adaptively important large-effect loci, and found within-season temporal variation in the proportions of the River Tornio subpopulations. There were strong within-season allele frequency changes at *vgll3*, the major locus linked with Atlantic salmon age at maturity: fishing early in the season targeted *vgll3* variant linked with later maturation. Fishing in early season can, therefore, lead to evolutionary changes and a decline in mean reproductive age and size of salmon, especially since the start of the Atlantic salmon fishing season was advanced in 2017 (ICES 2024a).

Bekkevold *et al.* (2024) found seasonal variation in the proportions of native and non-native sea trout in coastal feeding areas of the North Sea-Baltic Sea transition area. They analysed a total of 903 sea trout from feeding areas against a baseline of 3465 sea trout from <100 rivers with a panel of 3.8K SNPs. Based on the analysis of historical samples, the mixing has been consistent since the 1950s. This, together with a weakening contribution of the neighbouring NW Baltic Sea trout, suggests that large-scale stocking has had an impact on the sea trout stocks.

Maes *et al.* (2025) investigated the genetic population structure of common sole (*Solea solea*), a species of significant commercial importance in European waters, using Single Nucleotide Polymorphisms (SNPs). The study analysed over 55,000 SNPs from sole specimens collected across ten ICES divisions: 7d, 4c, 7h, 7f, 7g, 7a, 8a, 8b, 7e, and 7j. Overall, the levels of genetic differentiation detected were very low. Notably, populations from Divisions 7f, 7g, and 7h exhibited no significant genetic differences when assessed with both neutral and adaptive markers, indicating genetic homogeneity across this region. In contrast, sole from southwest Ireland (Division 7j)—currently managed jointly with 7h—showed weak but statistically significant genetic differentiation compared to other populations. Based on these findings, the authors recommend revising stock boundaries by merging sole from the southwestern Celtic Sea (7h) with those from Divisions 7f and 7g, while treating sole from southwest Ireland (7j) as a separate unit. The absence of genetic structure between the southern Celtic Sea (7h) and the broader Celtic Sea (7f) is further supported by biological metadata, including length and weight measurements.

Another study on the common sole by Corti *et al.* (2025) involved the implementation of a holistic design (genomics + otolith shape + otolith chemistry), resulting in Mediterranean sole population units that demonstrate how multiple markers converge on biologically meaningful boundaries. This study is a “how-to” on integrating genetic assignment with complementary tracers to harden management advice when signals are subtle or spatially complex.

Goodall *et al.* (2024) used whole-genome sequencing to show that multiple populations of large piscivorous herring have evolved in the Baltic Sea. The piscivorous ecotype is much larger, but less abundant than the zoo planktivorous Baltic herring. There is also a clear genetic difference between spring-spawning and autumn-spawning herring ecotypes. The current management is based on geographical differentiation of spring-spawning herring (ICES 2024b), which the results by Goodall *et al.* (2024) challenge.

The work of LeBlanc *et al.* (2025) presents the development and validation of a 233-locus GT-seq SNP panel assigning *Morone saxatilis* to six regions with ~95% accuracy, optimized for cost-effective, large-scale mixed-stock monitoring. In practice, it demonstrates robust simulation-based error evaluation and immediate deployment in coastal monitoring. Methodologically transferable to ICES species needing economical, in-season stock-of-origin tools.

St. John *et al.* (2025) used whole genome sequencing to analyse red king crab populations across four Alaskan regions and identified five distinct genetic clusters with strong differentiation between Gulf of Alaska and eastern Bering Sea populations. The study revealed pronounced signatures of local adaptation, and unique genetic variation in the Gulf of Alaska population that underscores regional divergence. Inbreeding levels were consistently low across populations, reducing immediate genetic management concerns. The genetic patterns reflected both historical demography and regional environmental influences. Based on these findings, the authors recommend that broodstock for stock enhancement should be sourced locally to prevent genetic mismatches. The study demonstrates that regional management strategies are essential to conserving the species' observed genetic diversity. These results provide crucial insights for the sustainable management of Alaskan red king crab fisheries.

The paper by Beemelmans *et al.* (2025) reports the development of cost-effective SNP panels for three salmonid species central to Indigenous fisheries in northern Canada: Arctic Char, Brook Trout, and Lake Whitefish. Using low-coverage whole-genome sequencing (lcWGS) of 418 individuals from multiple regions, the authors designed and optimized species-specific GT-seq panels, each targeting ~400–460 informative loci (plus a sex marker for Arctic Char). These panels captured fine-scale population structure and achieved high accuracy in genetic stock identification (average assignment accuracy ~83%, with Brook Trout and Lake Whitefish >97%). Results revealed clear regional genetic clusters, identified migrants and admixed individuals, and provided reliable baselines for mixed-stock fisheries monitoring. Importantly, the study highlights the advantages of lcWGS over reduced-representation methods for SNP discovery in salmonids and demonstrates how these genomic tools, when integrated with Indigenous knowledge, can strengthen co-management, stewardship, and food security strategies for northern communities.

Fully annotated and assembled genomes to support fisheries management

From a fisheries management perspective, having a fully annotated and assembled genome provides substantial resolution for selecting population markers and therefore, assisting with determining biologically relevant stock units (Andersson *et al.*, 2024). For example, cod, herring and horse mackerel genomes have provided greater insight into the biological connectivity, and boundaries, of populations throughout the Northeast Atlantic, see the following for examples: Bekkevold *et al.* (2023), Fuentes-Pardo *et al.* (2023), Pampoulie *et al.* (2023), Manuzzi *et al.* (2024) and Cunha *et al.* (2024). Furthermore, the availability of an organism's entire genome can highlight potential responses of populations to environmental impacts, such as heatwaves and climate change (Benestan *et al.*, 2016).

In addition to providing insight into the genomic architecture of potentially useful genetic variants used in stock identification, the generation of assembled genomes allows for the identification of uniquely useful markers to develop smaller scale genetic tracking approaches. For example, Baerwald *et al.* (2022) used 203 reference genomes to design an early and late migrating CRISPR mediated assay targeting uniquely informative markers to distinguish specific runs in a

subpopulation of Chinook salmon in California. In the same system, Anderson *et al.* (2025) describes the development of a comparatively cheap high throughput microhaplotype chip with parent-offspring scale resolution, made possible by the categorization of 204 microhaplotype amplicons from over 3,500 whole genome sequences that also showed sex and phenotype specific associations.

As genetic research continues to advance, there are indications that a single reference genome from a single individual from one population/ecotype is insufficient to capture the full genetic diversity within a species (Thorburn *et al.*, 2023). The pangenome represents the complete set of genes of a species; it is composed of core genes, present in all individuals, and variable genes, which are specific to certain populations (Thorburn *et al.*, 2023). While there are ongoing efforts to provide a single reference genome for certain marine species, for some commercially important species, reference genomes are beginning to be assembled that represent individual populations.

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Life-history parameters (Contributor: Richard McBride and Florian Berg)

From June 2024 to September 2025, there was only one paper investigating population or stock structure and their dynamics based on life-history parameters. In all studies, life-history parameters were estimated to demonstrate differences between groups, however, none used the estimated parameters for direct identification of individuals.

Lindegren *et al.* (2025) investigated the stock structure of Greenland halibut (*Reinhardtius hippoglossoides*) using standardized data from several bottom-trawl surveys collected from 1996 to 2017 in the North Atlantic Ocean. Their direct analyses applied a spatial-temporal statistical approach (the VAST software package) to model abundance and fish size (length). They demonstrated two overall clusters separating the Northwest and Northeast Atlantic, each with presumptive spawning and nursery grounds. Although a centrally-planned trawl study of life-history traits would be too costly to propose today, pooling the data from these many existing trawl surveys is pragmatic: it complemented the previously published findings of weak but significant genetic differences, as well as within stock boundary movements by marked and recaptured individuals. By themselves these life-history results could not identify finer-scale stock structure, but in future, they may aid in the design and application of additional disciplinary studies for Greenland halibut, or even the redesign of future genomic and tagging studies, because these previous studies had limited sample sizes that could be augmented in future because costs for such approaches have been generally declining.

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Morphometrics/meristics (Contributors: Steven Cadrin, Eglė Jakubavičiūtė, Emma White)

When applying morphometric and/or meristic methods to a stock identification study, we are using variables that are under simultaneous control by genetics and/or environmental factors. Identifying spatial differences in these measurable (morphometric) and countable (meristic) traits, can provide information on population structure and connectivity. Morphometric and meristics methods are less commonly used in the field of stock identification but these cost-effective methods are still relied upon in many studies and can be used in combination with other stock identification methods to determine differences between populations. The following case studies demonstrate that the approach is still being widely applied, with some iterative advancements in methodology.

Kelly *et al.*'s (2025) work provides a scientometric analysis and a systematic mapping of the application of geometric morphometrics in fish. They look at the trends and scientific impacts of geometric morphometry since the 1990s and the study concludes the ongoing relevance of geometric morphometrics in ichthyological research by expanding our knowledge of morphological diversity in aquatic environments.

Luo (2024) presents a detailed protocol for conducting geometric morphometric analysis of fish morphology. The author provides instructions on the use of different free software available and packages in R that are used to analyse shape data. The process includes details on extracting outline coordinates, converting and scaling data, defining landmarks, creating data objects, analysing outline differences and visualizing the results.

Vasconcelos *et al.* (2025) used a combination of geometric morphometrics and wavelet functions to identify four distinct morphotypes of horse mackerel (*Trachurus trachurus*) from the Ibero-Mauritanian coastal stock in the South European Atlantic Shelf ecoregion. The study revealed that environmental conditions in the area influenced the local populations. It was clear that fish from the northern population had a more elongated body shape, whereas fish from the southern population had a wider body shape. These results could be used to improve management in the area, taking into consideration the local adaptations.

Morphometric and meristic characters used to discriminate between genetically distinct groups of golden redfish (*Sebastes norvegicus*) in Norwegian waters by Bruvold *et al.* (2025). They found that beak length and eye diameter sufficiently discriminated between these proposed cryptic species and from the sympatric specimens of *S. mentella* and *S. viviparus*. They recommend that the presence of an additional redfish species that can be identified by morphological and genetic characters should be considered in stock assessment and fishery management.

Currie *et al.* (2024) used morphometric and meristic character variation to determine differences between three species of flounder; sand flounder (*Rhombosolea plebeia*), greenback flounder (*R. tapirina*) and yellowbelly flounder (*R. leporina*) in New Zealand. The study found evidence that the flounder populations were reproductively isolated, which is also supported by previous genetic analysis. It is reported that environmental variation and adaptive physiology of juvenile flounder are influencing the morphometric and meristic variation found among estuaries and years.

A study aimed at identifying squid populations off the northern and southern Java coast was conducted using morphometric analysis (Ervinia *et al.*, 2024). Three populations of squid were identified based on differences in body morphometric variables. Differences in growth rates were also reported which reflects variation in ontogenic development, trophic ecology and environmental conditions in Indonesian waters.

Linear and geometric morphometric analysis was applied to distinguish between two species of guitarfish (*Pseudobatos horkelii* and *Pseudobatos percellens*; Leite *et al.*, 2024). Certain areas, including the head and posterior region differed significantly between the species. This work contributed to the improvement of fisheries management strategies for these species.

Mekkawy *et al.* (2025) looked at variations in interspecific geomorphometric and in meristics of radii of scales from three species of gerreid fish from the Red Sea, Egypt. The size and shape of the scales were clearly different between the three species. This demonstrates the potential use of scales in the identification of stocks and subsequently appropriate fisheries management.

Third and Parsons (2024) applied landmark-based geometric morphometrics to investigate the population structure of the commercially and recreationally important snapper species *Chrysophrys auratus* off New Zealand, aiming to help prevent the overexploitation of vulnerable groups within existing stocks. Their analysis revealed notable morphological variation both within and among current *C. auratus* stocks, with the most distinct differences found in head curvature, body depth, eye size, and caudal peduncle width.

Morphometric analysis revealed that the Mediterranean horse mackerel (*Trachurus mediterraneus*) in the Adriatic Sea should not be managed as a single stock, as evidence suggests the presence of at least two morphologically distinct populations in the basin (Vasapollo, 2025).

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Tagging (Contributors: Steve Cadrin, Douglas Zemeckis)

Several recent case studies applied tagging for stock identification in ICES areas and other regions. Conventional or electronic tagging data were often combined with other sources of information. New tag technologies continue to be developed as well as advances in analytical techniques. The recent case studies described below offer examples of the continued application of tagging for stock identification.

Most geolocation from archival satellite telemetry uses light, sea surface temperature data which are not available for deep-sea fishes. To address this challenge Arostegui *et al.* (2024) developed a three-dimensional geolocation base on temperature, depth and oceanographic models for fishes in mesopelagic (200–1000 m) and bathypelagic (1000–4000 m). They compared geolocation results for deep-water shark species to known locations from acoustic telemetry, identified limitations and solutions to reliably derive location.

Özgül *et al.* (2024) reviewed case studies in European waters to assess their utility for fishery management. They found that acoustic tagging has contributed improved understanding of stock dynamics, habitats, and migration routes to evaluate effectiveness of conservation measures. However, they concluded that information from the European Tracking Network could be more broadly applied.

Wright *et al.* (2024) evaluated seasonal migrations of the European sea bass (*Dicentrarchus labrax*) in UK and surrounding waters. Archival tags were internally deployed on 171 sea bass in the English Channel, southern North Sea, and Irish Sea to record temperature and depth, and 48 tags were recovered after deployments averaging 370 days with movements averaging 172 km. Reconstructed tracks were similar to 237 mark-recapture observations from 1970 to 2020. Seasonal movements were between shallow areas in summer and deeper spawning areas in winter. They found high connectivity between the Celtic Sea/Irish Sea and the North Sea, and a portion of residents in the North Sea throughout the year.

Delgado *et al.* (2025) acoustically tagged 847 cod (*Gadus morhua*) from inshore and offshore locations off Newfoundland and Labrador. They identified four migratory phenotypes that 1) moved throughout the region, 2) resided in a north of Newfoundland, 3) resided in the southern portion of the region, and 4) resided inshore. Whole-genome sequences of 77 tagged cod indicated genetic differences between cod in northern and southern areas during the spawning season.

Piper *et al.* (2024) analysed data from acoustic telemetry, stable isotopes, genetics and scale banding patterns to study movement patterns and population structure of sea trout (*Salmo trutta*) in two rivers of East Anglia, UK. They observed movement within rivers, but little anadromy, and most residence in lower reaches of rivers. Few tagged fish migrated to the North Sea, but 10% strayed between rivers.

Henslee *et al.* (2024) used acoustic telemetry to estimate stock composition of coho salmon (*Oncorhynchus kisutch*) in a coastal fishery off Alaska. They deployed 578 tags over two seasons to assign 341 individuals to a stock of origin based on natal site fidelity. Stock composition was estimated using sex, location of capture, and date of capture.

Goddard *et al.* (2025) analysed tag-recapture data to evaluate population connectivity of yellow-tail kingfish (*Seriola lalandi*) off Australia and New Zealand. From 1974 to 2022, 63,432 fish were tagged and 4,636 recaptures were recorded. Most were recaptured within 10 km of their original release location, some up to 14 years after tagging, but 14% were recaptured over 100 km from their release location, and one moved 2,834 km in 702 days. Network analysis estimated no connectivity between western and eastern Australia, which is consistent with genetic differences. However, there was extensive connectivity between eastern Australia and New Zealand. They

recommend increased collaboration between state and international fisheries jurisdictions for stock assessment and fishery management.

Gunton *et al.* (2005) documented movement patterns of yellowfin bream (*Acanthopagrus australis*) off Australia with 24,000 conventional tag releases and 2,036 reported recaptures over 19 years. Many tagged fish (37%) were recaptured at their release location, and few (9%) moved further than 100 km, with occasional long-distance movements. Generalized additive models indicated that movement was positively influenced by time at liberty, body length, tagged in autumn, tagged in the south, and moved in a northerly direction. Based on these results, they recommend stock assessment and fishery management at a finer spatial scale than the current state-wide approach.

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Otolith morphometry (Contributors: Florian Berg, Kélig Mahé, Christoph Stransky, Valerio Visconti)

From June 2024 to June 2025, there were 19 papers dedicated to otolith shape. For marine organisms, especially for fish, the otolith is the main calcified structure used to identify the stock structure.

Since the early 2000s, the use of otolith morphology and related techniques has continued to increase. Consequently, the number of papers published each year has increased from two or three to around 40 in the period of 20 years (Figure XXX). In recent years, this increase can also be explained by the development of deep learning and machine learning analyses and the emergence of three-dimensional in otolith shape analysis.

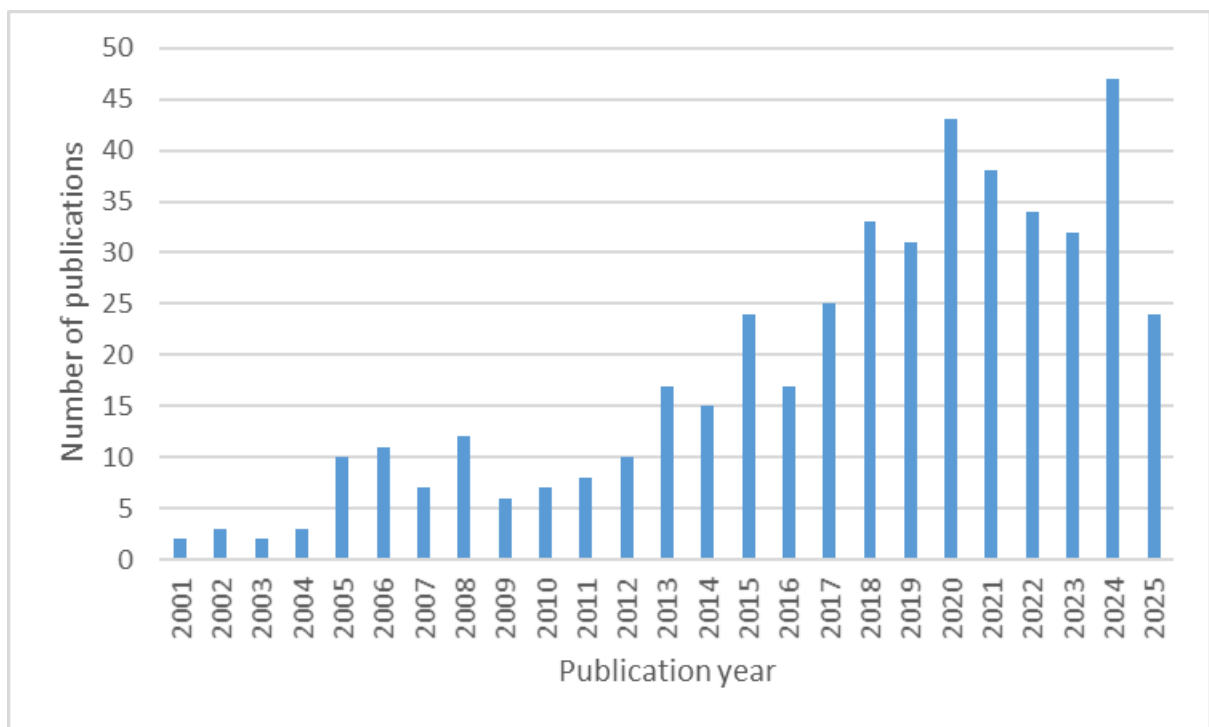


Figure A3.2: Publications number per year extracted to Web of Science with to keys-words “stock” and “otolith shape” (on 10 Sep 2025).

The number of papers in 2025 only includes those published in the first half of the year, so the final number should be comparable to that measured in 2024.

Otolith shape as tool for stock identification

Species/stocks in the ICES area

Vasconcelos *et al.* (2025) tried to address the challenge of distinguishing between two cryptic deep-sea scabbardfish species, *Aphanopus carbo* and *A. intermedius*, in the northeastern Atlantic. The shape contour analysis employed for this study was a wavelet function developed by the AFORO team to identify local morphological variation along the x-axis of the otolith contour. A total of 512 equidistant Cartesian coordinates were extracted from each otolith projection, with the anterior tip of the rostrum used as the starting point. These coordinates were then analysed using wavelet transformed (WLT; sensu Parisi-Baradad *et al.* 2005). Otolith samples collected from Madeira and the African coast over four decades revealed that both species have coexisted in the region, with *A. carbo* generally dominating catches except for a notable decline in 2010. The study found that *A. intermedius* was more prevalent in offshore areas, possibly linked to

higher salinity near Madeira during the spawning season. Environmental factors such as temperature and salinity at depths greater than 800 metres, along with the expansion of the longline fishery, were identified as likely influences on species distribution patterns.

Species/stocks outside the ICES area

Ben Ghorbel *et al.* (2024) investigated the stock structure of the annular sea bream (*Diplodus annularis*), in Tunisian waters by analysing the morphometrics and microchemical composition of otoliths (*sagittae*) from populations on Djerba and Kerkennah Islands (Gulf of Gabes). The morphometric measurements included otolith length, width, area, and perimeter, and assessed differences in these dimensions and in the concentrations of a few chemical elements (i.e. K, Cs, Pb) between individuals from each island. Authors also examined fluctuating asymmetry (FA) in otolith size as a potential indicator of stock structure and connectivity. The results revealed significant asymmetry in all otolith size dimensions between left and right otoliths among males and females within and between the two islands (this was attributed to fluctuating asymmetry). There were also marked differences in otolith microchemistry, with Djerba fish showing lower K and Cs but higher Pb compared to Kerkennah fish. Differences were linked to factors such as fish age, environmental conditions, and biological traits. Principal component and discriminant function analyses confirmed that individuals from the two islands formed distinct clusters, indicating discriminant stock structure and limited connectivity between the populations. Ben Ghorbel *et al.* (2024) concluded that the observed differences in otolith morphometry and microchemistry reflect environmental stress, developmental history, and geographical isolation, supporting the need for separate management strategies for Djerba and Kerkennah stocks of *D. annularis*.

On the same species, Spani *et al.* (2025) investigated the population-level shape variation and otolith asymmetry based on the geometric morphometrics methods (GMM) of otoliths collected in the Gulf of Asinara (Porto Torres, Sardinia) and the northern Adriatic Sea (Le Tegnue). In short, GMM focuses on the geometric relationships of homologous points, known as landmarks and semi-landmarks, and these proved to be useful to assess shape variation and otolith fluctuating asymmetry (FA). The authors found significant differences in otolith shape and size between the two populations, with Le Tegnue fish having larger and differently shaped otoliths compared to those from Porto Torres. The research also examined fluctuating asymmetry (FA) as an indicator of developmental stability and environmental stress, revealing that Porto Torres fish showed posterior otolith asymmetry, while Le Tegnue fish exhibited anterior asymmetry. No sexual dimorphism was detected in otolith shape or size. The findings highlight the sensitivity of GMM for detecting subtle morphological differences, suggesting that both environmental and genetic factors influence otolith morphology. The study concludes that otolith shape analysis is a valuable tool for understanding population structure and environmental adaptation in marine fishes, with implications for fisheries management and ecological monitoring.

Sen *et al.* (2025) carried out a study on the otolith shape and morphometry of the Bogue (*Boops boops*) in the Aegean Sea and the Marmara Sea. Otolith samples collected during the fishing season of 2024 (244 individuals in the North of Aegean Sea and 188 individuals from the Southwest of Marmara Sea) were measured for the length (OL), width (OW), radius (OR), perimeter (OP), area (OA) and weight (W) for both the right and left otoliths of each individual. Otolith shape indices used include Aspect ratio (AR), Ellipticity (E), Form factor (FF), Roundness (RD), Circularity (C), and Rectangularity (R) as defined by Tuset *et al.* (2003b) and Ponton (2006). The results showed significant differences in several otolith shape indices and dimensions between the two regions, with area and circularity of the left otolith, roundness and rectangularity of the right otolith, and form factor of left and right otolith being significantly different ($p < 0.05$). Also, the principal component and canonical discriminant analysis indicated that roundness, area, and width of the otoliths were key factors distinguishing the stocks, with over half of the individuals correctly classified to their region of origin. The findings suggest that *Boops boops* in these two areas may represent distinct stocks.

Yedier *et al.* (2025) investigated the stock structure of garfish (*Belone belone*) from three Turkish seas (Aegean Sea, Black Sea, and Sea of Marmara) using both morphometric and wavelet analyses of sagittal otoliths. Fish samples were collected from each region, and their otoliths were measured and analysed for shape differences. While traditional morphometric analysis could distinguish stocks with moderate success (overall classification rate 57.6%), wavelet analysis of otolith contours proved much more effective, achieving a classification success rate of 93.81%. The greatest shape variation among stocks was found in the postero-ventral, antero-ventral, and dorsal regions of the otoliths. No significant differences were found between sexes or between left and right otoliths, allowing all samples to be pooled for analysis. Both studies from Vasconcelos and Yedier demonstrate that wavelet-based otolith shape analysis is a powerful tool for discriminating fish stocks (especially when combined with other methods), providing valuable information for fisheries management and stock assessment.

TenBrink *et al.* (2025) used the stock spatial structure of dusky rockfish (*Sebastes variabilis*). In this study, otolith shape analysis was used to evaluate the stock structure of dusky rockfish across five geographical subareas exhibiting ecological differences in the GOA and Bering Sea and Aleutian Islands (BSAI), where dusky rockfish are managed as two separate stocks. A combination of size and shape indices, wavelet, and elliptic Fourier descriptors were examined from left and right-side otoliths collected from these regions ($n = 522$). Individual variation existed across subareas. Wavelet and elliptic Fourier descriptors indicated that mean otolith shapes were partitioned between the two management regions but also showed a high degree of overlap among subareas. Classification accuracies of otoliths to their subarea of origin through linear discriminant analysis (LDA) were variable (6.3 - 73.5 % and 15.4 - 65.8 % correctly classified for the elliptic Fourier and wavelet analyses, respectively). The highest classification rates were found between the western GOA and eastern Aleutian Islands, contributing to the observed differences between management regions and providing some support for current management paradigms. Dusky rockfish exhibited low to moderate overall classification rates (43.9–52.2 %), suggesting minimal stock structure within Alaska waters. This study highlights the utility of otolith shape analysis as a stock discrimination tool, and results will help refine further investigations and support fishery management in Alaska.

Yildiz *et al.* (2024) applied shape analysis to differentiate two red mullet (*Mullus barbatus*) stocks in the western Black Sea and assessed the generalized linear model (GLM) for age prediction based on otolith dimensions and weight. Sagittal otoliths from 259 fish were collected by commercial bottom trawl vessels in İğneada and Şile, Türkiye, between October 2017 and April 2018. Otolith shape was described using wavelet transformation (contour shape) along with four morphometric characteristics (otolith length, area, width, and perimeter) and six shape indices (circularity, rectangularity, form factor, roundness, ellipticity, and aspect ratio) to reveal differences between the two regions. Shape indices were explored using multivariate statistical methods, including multivariate analysis of variance (MANOVA) and canonical discriminant analysis (CDA). Canonical analysis of principal coordinates (CAP) provided an overview of the differentiation in the otolith outline shape between the two stocks by using the wavelet coefficients. The GLMs predicted age using otolith size parameters, shape indices, and otolith weight. The MANOVA showed no significant differences between sexes but notable differences between right and left otoliths. The CDA achieved a discrimination rate of 65.7% for age 1 and 64.8% for age 3, indicating distinct local populations. The otolith contours varied between Red Mullet sampled in the two regions, with CAP achieving an overall accuracy of 67.1% for both regions, 68.12% accuracy for İğneada, and 66.20% accuracy for Şile. The GLMs identified otolith length, weight, width, and perimeter and fish sex as key factors, with otolith length being the most significant predictor for age estimation. The close alignment of observed and estimated ages highlights the potential for using otolith length in age estimation.

Houeto *et al.* (2024) examined the right and left otoliths of 174 individuals of *Pseudotolithus senegalensis* from the Porto-Novo lagoon, Lake Nokoué and the Atlantic coast. The results show a significant variation in the population according to geographic location. Mixed-effects linear analysis showed no significant variation by site, side or sex ($p > 0.05$). Analysis of otolith shape using ANOVA showed significant differences for length, width and area ($p < 0.05$), but not for perimeter ($p > 0.05$). Canonical discriminant analysis revealed significant differences between sites ($p < 0.05$). Finally, shape analyses showed significant differences between sites ($p = 0.0001$) and between right and left sides ($p = 0.007$), but no difference by sex ($p = 0.395$). The study of otolith morphology is therefore proving to be a valuable tool for differentiating stocks and understanding ecological variations.

Otolith three-dimensional shape as tool to stock identification

There have been no new papers applying three-dimensional (3D) shape analysis after the method was introduced by Andrialovaniria *et al.* (2024). Currently, these analyses are still predominantly conducted using two-dimensional (2D) images, offering only a partial representation of the otolith's shape.

Otolith morphometry (e.g. growth marks, annuli, etc.) as tool for stock identification

The utilization of growth marks in calcified structures for stock identification has decreased over the last years and has been mainly replaced by studies involving their shape or chemical composition. During the review period (mid-2024 to mid-2025), only one study was published that used growth marks in calcified structures for stock identification.

Kerr *et al.* (2025) evaluated the effectiveness of otolith-based stock identification techniques for distinguishing sympatric Atlantic cod (*Gadus morhua*) populations in the Gulf of Maine that differ in spawning season (winter vs. spring). They found significant differences in both otolith structure and microchemistry, with the highest classification accuracy achieved when both features were considered. In particular, otolith structure revealed marked differences in age-one growth: winter-spawning cod had a larger first annulus than spring spawners. Moreover, the width of age-one growth varied significantly with the interaction of spawning time and year class. From 2008 to 2011, winter spawners showed greater variability of age-one growth, whereas spring spawners displayed more consistent growth across cohorts. Growth at age one did not differ significantly by capture location (Massachusetts vs. Ipswich Bay) or by the interaction between location and spawning time. These differences in early otolith growth are linked to spawning phenology and the definition of the first annulus. Since one opaque and one translucent zone are counted as a year, winter-spawned fish (November–December) undergo nearly a full year of growth before forming their first annulus, whereas spring spawners (May–June) have only a partial growing season before the annulus is set in January.

Otolith shape as tool for species identification

Otolith shape as tool for species identification is more and more used to discriminate different species of the same family (Morawicki *et al.*, 2025, Saygin, 2025, Vu *et al.*, 2025, Barani *et al.*, 2024; Wang *et al.*, 2025, Vasconcelos *et al.*, 2025) or to identify the preys of animals as seals with the machine learning approach (Mion *et al.*, 2024).

Automated processes for otolith shape analysis

The automated processes are developed by some institutes/universities to identify the species or stocks from the otolith shapes in 2D and/or 3D formats and to estimate the age from the otoliths images (i.e. external, as shape, and internal information as nucleus and growth increments). In the chapters presented before (i.e. “Otolith 3D shape as tool to stock identification” and “Otolith shape as tool for species identification”), several studies used the different automated methods (Andrialovanirina *et al.*, 2024; Mion *et al.*, 2024).

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Chemistry of otoliths and other archival structures (Contributors: Lisa Kerr, Kirsteen Mackenzie, Patrick Reis-Santos, Susanne Tanner)

In the past year, Otoliths (ear bones) in fishes are used, along with other archival structures such as scales, fin spines, and vertebrae, and statoliths in cephalopods, for a variety of research and fisheries management applications (Panfili *et al.* 2002). These calcified structures are especially useful for age reading, growth determination, and stock identification. Among these structures, otoliths are of particular interest as they contain unaltered chemical and physical records of the entire life history of the fish, thus chemical compositions can be measured during each period of life. These chemical compositions can be used to determine and differentiate natal origins, nursery, feeding, and breeding grounds, and to distinguish between stocks using different areas during temporally explicit durations throughout their lives.

In the past year, otolith chemistry has been applied as a stock identification tool to discern stock structure of fish species around the world. Below is a summary of applications over the past year (June 2024 - September 2025) using chemical analyses of otoliths and other archival tissues to support fish stock identification in ICES regions or species of interest, as well as an update on recent advances in the field.

A synthesis on the advances and challenges reported on at the 7th International Otolith Symposium (IOS 2023, October 2023, Viña del Mar, Chile) was published in 2025 (Cerna *et al.* 2025). A total of 205 delegates from 39 countries participated in the IOS 2023, with scientific presentations covering numerous topics related to otolith research. These included: otolith formation and composition, evolutionary biology of fish, life-history studies, and aquatic ecosystem ecology. Studies using chemical composition of otoliths were seen to be providing valuable insights into habitat use, demographic patterns, trophic ecology, palaeo-reconstruction of ichthyofauna, physiological processes, and fish migration pathways. In addition, case studies using otolith-based biochronologies demonstrated the usefulness and application of this technique to help reveal biological patterns at annual to centennial time-scales to potentially provide long-term ecological insights into the impacts of climate change on aquatic ecosystems.

Otolith chemistry

Gauthier *et al.* (2025) analysed the elemental composition of Atlantic halibut (*Hippoglossus hippoglossus*) otoliths from individuals captured in the Gulf of Saint Lawrence, Canada, to determine their natal/nursery ground and subsequent movement patterns. Using only Sr, Ba, and Mg, the authors found three potential primary early-life sources, but overall mixing of natal origin stocks throughout the Gulf as adults. Analyses of four cohorts (2006, 2007, 2009, 2010) showed no association between natal origin and later migration strategies, suggesting a well-mixed population. While these findings advance understanding of early life history and spatial structuring, interpretation is limited by small sample sizes per cohort and the absence of otoliths from very young halibut, which constrain the ability to generalize results to stock scale.

Heimbrand and Limburg (2025) measured levels of boron (B:Ca) in the otoliths to assess the possible provenance of a unique population of Atlantic cod (*Gadus morhua*), found in the low-salinity Åland Sea region of the northern Baltic Sea. By examining both lifetime chronologies and concentrations in the core region (corresponding to birth and early life), they found that B:Ca concentrations in cod from Åland Sea were 31 to 348 times higher than in other populations. These concentrations were unexpectedly high given that boron is linearly, positively proportional to salinity (highest in the southern Baltic Sea), and other populations displayed very low concentrations by comparison. Otolith B:Ca suggested Åland Sea cod may form a distinct

population with a separate spawning area, which may mix with other populations. The source of elevated boron remained unknown, but its widespread presence indicated a broad, nonpoint origin.

Ryan *et al.* (2025) investigated nursery fidelity and the ability to differentiate estuarine nurseries of sea bass *Dicentrarchus labrax* using otolith chemistry. The study focuses on sea bass near its northern distribution limit in the southern Irish coast. Multi-annual otolith chemical signatures showed strong estuary discrimination for age 0 juveniles (89-95% overall correct classification). These multiyear chemical signatures provide reliable baselines to retrospectively assign adult *D. labrax* to their nursery of origin, even when year classes are not matched. Given the low occurrence of 0-group sea bass in Irish waters, identifying and protecting the estuaries that contribute most to adult stocks will be critical to safeguard the region's stock.

Focusing also on sea bass *D. labrax*, Antunes *et al.* (2025) used life-history chemical signatures across otolith growth axis to assess the seasonal occurrence of sea bass in a freshwater habitat within the Minho River, Portugal, and to estimate the duration of these incursions. Otolith chemical analysis suggested that nearly 50% of the individuals began their lives in brackish environments, suggesting that coastal habitats may also serve as spawning grounds and raising the hypothesis of partial migratory behavior in this population. The documented, continuous use of freshwater habitats over an extended period (> 1 year) should be considered in fisheries management.

Zipp *et al.* (2025) evaluated the influence of alternative stable isotope baselines (adults and yearlings) and different random forest input parameters and decision thresholds on the stock assignment of Atlantic Bluefin Tuna (ABFT) caught in the Gulf of Maine, a key commercial fishing area where substantial mixing occurs between two ABFT stocks. Results showed that when samples from one baseline were reclassified using a random forest model trained on another baseline, their assigned stock identities did not match their original classifications. Also, baseline selection and model settings influence classification performance metrics, and thus affect estimates of mixing proportions and age structure in the Gulf of Maine. Findings highlight that careful evaluation of baselines and robust methods for handling new ones are essential, as their inclusion can shape stock perceptions in regions with heavy fishing and stock mixing.

Chou (2025) evaluated the potential of using otolith chemistry, specifically stable oxygen isotopes coupled with individual-based migration models, to reconstruct the migration history of individual small fish and to establish a connection between the theoretical movement predicted by the model and the empirical data obtained from the otolith isotope-based method. Three main approaches were taken: i) a drift case study using Atlantic mackerel, where simulated ocean currents and hydrography were used to predict otolith isotope records, evaluating $\delta^{18}\text{O}$ profiles as low-cost "natural tags" for stock discrimination and geolocation; ii) a thermal physiology case study using juvenile Atlantic mackerel where stable isotope analysis was applied to infer thermal performance, showing that ecological factors such as food or competition may influence metabolism more strongly than temperature; and iii) a larval migration case study using European eel where drift analyses incorporating different swimming behaviours assessed whether otolith $\delta^{18}\text{O}$ could distinguish between successful and failed drifts and tested the influence of NAO on migration. Overall, the thesis demonstrated how integrating otolith stable isotopes with migration models can enhance understanding of early fish life histories and support conservation and fisheries management.

Multi-marker studies with otolith chemistry

The report from the Workshop on the evaluation of Northeast Atlantic mackerel stock components (WKEVALMAC, 2023 meeting) was published in 2024 (Bekkevold *et al.* 2024). The objective of WKEVALMAC was to review information on stock identification of NEA mackerel and develop a consensus understanding of the Atlantic mackerel population structure and key uncertainties. The evaluated data and studies centred on genetics, tagging, otolith approaches; egg and larval dispersal models; commercial landings and perceptions from the industry. Recent directed genetics, tagging, otolith chemistry investigations, ongoing surveys, catch data, fisher perspective, and preliminary modelling studies all failed to support the three-component concept for NEA mackerel.

Corti *et al.* (2025) applied a multi-tracer approach to assess population structure of the common sole *Solea solea* across the mediterranean sea. They integrated otolith chemistry (core and edge), otolith shape, and neutral and outlier genetic markers, and then applied two integrative approaches to bring all the complementary data together: the semi-quantitative Stock Differentiation Index (SDI) and a quantitative multivariate analysis based on principal component analysis (PCA) of each tracer. Both approaches consistently revealed strong spatial separation, identifying at least three major subregional stocks (Eastern Mediterranean, Adriatic Sea, and Western Mediterranean) with additional intra-stock complexity within the Western Mediterranean, namely between the Northern Spain/Gulf of Lion and Tyrrhenian Sea. The authors highlighted that these integrative analyses successfully simplified the complexity of information extracted from multiple markers, providing a clear and interpretable outcome for fisheries managers and other stakeholders.

Lee *et al.* (2025) synthesized current evidence on population structure of blue whiting (*Micromesistius poutassou*), a key mid-trophic species in the Northeast Atlantic, revealing a complex metapopulation made up of both resident and migratory subpopulations. Although currently managed as a single stock, this management unit overlooks important biological structuring and may reduce management effectiveness. The evidence collated supports partial migration, with resident and migratory contingents shaping spatial complexity. Genetic, otolith, parasite, and life-history studies pointed to distinct northern and southern subpopulations, mixing zones, and local resident groups. These findings highlighted the need for adaptive, spatially explicit management and identified key gaps in understanding fine-scale structuring, life-history stage dynamics, and connectivity pathways that may be tackled using integrative methods that combine genomics, otolith chemistry, and biophysical modelling.

Brûlé *et al.* (2025) used a combination of otolith chemistry and scalimetry to determine migratory behaviours within a population of Atlantic salmon (*Salmo salar*) in the Ungava Bay region of Canada. Patterns of trace element variations along otolith transects were used to determine timing and duration of residence in freshwater, brackish, and marine environments. These patterns were used to identify and to quantify estuarine summer residence behaviour vs. marine anadromy. The results were compared with patterns of scale growth, with a 98.8% correspondence between life-history patterns from both methods. This study found different proportions of estuarine summer residence between different river origin stocks, with 22% estuarine residency in the aux Mélézes River and 74% in the du Gué River.

Capelin on the Newfoundland and Labrador shelf are currently managed as a single stock. Tripp and Davoren (2025) tested the trace element chemistry of newly-hatched capelin, raised experimentally in intertidal and subtidal habitats using natural abundance and barium-137 enriched seawater, to determine the influence of temperature, salinity, and maternal contributions to otolith chemical compositions. This study found no clear influence of salinity, but a strong influence of temperature on the chemical composition, notably on barium concentrations, in the otoliths, although this effect varied by family. The variability of the incorporation of trace elements into the embryonic otolith due to temperature differences led to habitat-specific chemical compositions in the otoliths. This study determined that there is an influence of ambient water on the

chemical composition of pre-hatch capelin otoliths, although it is unlikely that this influence would mask the larger maternal contribution. Results were compared with those of previous studies on microsatellite markers, body and egg morphometrics, life-history traits, acoustic tags, and monitoring of spawning sites for egg traits and larval and environmental conditions in the same capelin population. The authors determined that selection between intertidal and subtidal sites by spawning capelin was largely facultative based on temperature, and that there was no stock separation between these spawning sites.

Other archival tissues

Bobowski *et al.* (2025) used statolith chemistry to identify the occurrence of different stocks of southern shortfin squid *Illex coindetii* and long-finned squid *Loligo forbesii* in the North East Atlantic (North Sea, West of Scotland, Celtic Sea) and Mediterranean Sea (West Sardinia, East Sardinia, Ionian and Adriatic Seas). Statolith core and edges were analysed for 11 trace elements. For *I. coindetii*, four stocks were identified, including three region-specific stocks and one mixed-stock in Italian waters, suggesting temporary ontogenetic separation but overall connectivity. For *L. forbesii*, five stocks were detected, with some connectivity among North East Atlantic populations. Authors linked chemical data to previous stock inferences from statolith shape data to make final inferences on stock structure highlighting their study showed the potential but also limitations of statolith chemistry for stock discrimination and that a single approach is likely insufficient to comprehensively discriminate all stocks in this case.

Hayne *et al.* 2025 used vertebral elemental chemistry to assess stock structure and connectivity in blacktip sharks (*Carcharhinus limbatus*). They detected regional differences in chemistry (Ba, Mg, Mn, Sr, Zn) and high classification accuracy when comparing sharks collected across eastern and western regions of the northern Gulf of Mexico. Findings indicate individuals tend to remain in their natal regions, and region-specific differences in vertebral edge also suggest that connectivity is low, consistent with described philopatric behaviour. Overall, the results supported current multi-stock management efforts and the use of vertebral chemistry to inform stock structure.

Biogeochemical tags database

Ding *et al.* 2024 presented a global, open-access database of Migratory Fish's Biogeochemical Tags (MFishBT - <https://fish-ecology.shinyapps.io/mfishbt/>) containing biogeochemical records measured across various fish biological archives, including otoliths, scales, eye lenses, and vertebrae. The database appears to be updated regularly, and authors encourage the addition of more datasets to this database in future. MFishBT is the most comprehensive open-access database on biogeochemical tags in migratory fish to date, and can serve a variety of needs in scientific research, conservation, and management.

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Parasites (Contributor: Ken Mackenzie)

Introduction

Nine papers published in the past year have described the actual or potential use of parasites as biological tags in population studies of marine fish and squid. Six of these describe original studies, two are reviews of previous research and one is a comprehensive update of the methodology used in this method of stock identification. Four of the six original studies and one review are based on fisheries in South American waters, one original paper is from Japan and two reviews are based on research in the North Atlantic. Parasites used as, or selected as potential, biological tags range from single species of larval nematode, larval cestode and adult trematode to assemblages of long-lived parasites.

Summaries of papers

For fisheries management purposes, stock assessments of most marine fish are based on the assumption that stocks are perfectly mixed panmictic closed units, but the reality is usually more complex than this. The extent of such intra-stock variability in the hake *Merluccius hubbsi* in the Argentine Sea was investigated by Braicovich *et al.* (2025) using parasites as biological tags. Three stocks of this hake are currently recognized, of which the southern or Patagonian stock is by far the most abundant, representing nearly 90% of the species total biomass. Samples of hake were collected from stations in the northern, central and southern parts of this stock's area and examined for long-lived parasite species - larval helminths parasitising the body cavity and tissues and adults of the nematode *Ichthyofilaria argentinensis*. The data collected were analysed by multivariate methods based on Bray–Curtis dissimilarities. Significant differences between parasite assemblages in different samples revealed clear latitudinal patterns in their similarity, reflecting the strict dependence of many parasites on oceanographic conditions. In this case, the oceanographic conditions within the study area generate a temperature gradient over the continental shelf which creates a number of marine fronts affecting the entire biota, including parasites. The authors recommend that, when using parasite tags for stock identification, sampling should cover most of the known or suspected distribution area of the population or stock. Otherwise, incomplete spatial coverage may overestimate differences between samples. For example, in the present study, if the two central samples had not been taken the recommendation would be to divide the current southern stock into two separate stocks.

Squid have proven to be difficult subjects for stock identification studies using parasites as biological tags because of their short lifespans, variable growth rates and the strong dependence of their reproduction and recruitment on environmental conditions. Gutiérrez *et al.* (2024) found this to be the case when they attempted to evaluate the temporal variability of parasites for a highly migratory stock of squid and to assess interstock differences in a mixing area between stocks. The subject of this study was the Argentine shortfin squid *Illex argentinus*, which supports one of the world's most productive fisheries. Four spawning stocks of this squid have been proposed on the Argentine shelf and slope based on size structure, reproductive seasons and ground and migratory patterns. Uncertainties remain, however, regarding the demographic independence between some spawning groups, particularly summer spawning stock and the south patagonian stock. Samples of squid totalling 333 specimens were caught at 9 stations in December 2020, March 2021 and February 2022 and examined for parasites. Ten parasite taxa were found, only 6 of which showed a prevalence of >10% in at least one sample, with larval cestodes in the digestive tract representing 82.5% of the overall parasite load. Multivariate analyses of the parasite data showed a similarity in parasite assemblage composition and structure between both stocks caught in the mixing area on the same date. The similarity was related to the presence of

short-lived trophically transmitted parasites associated with recently consumed food items and, indirectly, to the oceanographic conditions. While the value of parasites as tags for squid stock identification remains doubtful, the authors suggest that their variability could serve as a valuable indicator of changing environmental conditions, particularly climate change.

Chinook salmon *Oncorhynchus tshawytscha* is an invasive species in southern Chile which now supports recreational and incipient artisanal fisheries. Information on the foraging areas of these fish during their marine feeding phase is important for the management of this new fishery. To this end, Figueroa-Muñoz *et al.* (2025) investigated the possibility of using a long-lived marine parasite as a biological tag to trace these migrations. The parasite investigated was the plerocercoid larva of the cestode *Hepatoxylon trichiuri*, which infects the visceral cavities of many marine and anadromous teleost fishes. The authors examined a total of 61 returning chinook salmon from a river system in southern Chile for *H. trichiuri* and compared the new data with that from previous studies in other river systems in southern Chile at varying distances from their study area. They found that prevalences and intensities of infection in different river systems were clearly differentiated and related to geographical distance between them. The adult form of this cestode infects large pelagic sharks, so its geographical distribution depends on the occurrence of these sharks in sufficient numbers to facilitate transmission. There is little information on shark abundance in Chilean Patagonia, but there are marine protected areas along this coast and there is evidence that these may support abundant shark populations. The results of this study highlight the potential for using *H. trichiuri* as a biological tag to identify different chinook salmon stocks in this region.

Lee *et al.* (2025) reviewed the current state of knowledge of the complex stock structure of blue whiting in the Northeast Atlantic. A large section of the review is devoted to assessing the role of different approaches to stock identification, including the use of parasites as biological tags. The authors considered that parasite assemblages offer promise for understanding spatial structure and host connectivity, but that past efforts had been limited by low taxonomic resolution. Recent developments in molecular diagnostics now allow the accurate identification of cryptic species, for example in the *Anisakis* species complex. These methods may further support inferences about trophic separation and site fidelity in different contingents, thus expanding the potential use of parasites in elucidating blue whiting population structure.

Marcotegui *et al.* (2024) examined the stability of the stock structure of Argentine anchovy *Engraulis anchoita* in the Argentine Sea some 20 years after a previous study had identified two distinct Northern and Southern stocks in this study area. Since then, a possible discrete stock in the San Matias Gulf, in the transitional region between these two stocks, and from which samples were not available in the earlier study, had been proposed. This new study, in which 295 anchovies were examined for parasites, included samples from the transitional zone and from the Northern and Southern stocks. The structure and composition of both parasite infracommunities and component communities were analysed by univariate and multivariate statistics. The results showed the existence of three groupings, with the Northern and Southern stocks remaining clearly identifiable but including a central stock in the San Matias Gulf extending outside the Gulf on the continental shelf. This newly identified stock may have been overlooked in the earlier study because all parasites found were included in the multivariate analyses, whereas the new study was restricted to long-lived parasites, which are recommended as tags for stock identification.

Pubert and Randhawa (2025) described and quantified the metazoan parasite fauna of plaice from sampling stations off the north and south coasts of Iceland and assessed the potential of the parasites found as biological tags for stock identification of plaice in Icelandic Waters. A total of 82 plaice were examined and 11 parasite taxa recorded, including 5 which are new records for plaice in Icelandic Waters. The two parasites identified as potentially useful tags were larvae of the nematode *Anisakis simplex* and the adult trematode *Zoogonoides viviparus*. Plaice in Icelandic

Waters are currently managed as a single stock, but the findings of this study support a complex stock structure in the region. The parasite results are consistent with those from tagging and otolith microstructure studies. A larger sample size is recommended for future studies using these two parasites as tags.

Tanaka and Ohshimo (2024) used larvae of the nematode genus *Anisakis* as a biological tag to investigate the expansion routes of Japanese Spanish mackerel *Scomberomorus niphonius*, the population of which has been expanding in coastal Japan since the 2000s. A total of 50 mackerel from the Sea of Japan and 67 from stations in the northern Pacific Ocean close to the coast of Japan were examined for *Anisakis* larvae. Molecular identification revealed that >90% of these larvae were of *A. pegreffii*, a species known to inhabit the Sea of Japan (East Sea). Of the 246 larvae from the northern Pacific Ocean identified molecularly, only 3 were of other species of *Anisakis* (*A. typica* and *A. simplex* s.s.). This provides strong supporting evidence that these mackerel originated in the Sea of Japan (East Sea) and migrated into the Pacific Ocean via the narrow Tsugaru Strait. The authors recommended that future surveys should be expanded to include mackerel caught in the central regions of the Pacific side of Japan. Such surveys would contribute to understanding the migratory ecology and stock structure of Japanese Spanish mackerel of the Pacific Ocean, the Sea of Japan (East Sea) and East China Sea populations, thereby aiding in accurate stock assessments.

The latest major review of parasites as biological tags for aquatic hosts written by Timi (2025) was recently published as a chapter in a book on Aquatic Parasitology. This publication compiles and updates the published research on parasites as biological tags as indicators of various aspects of host ecology and biology, mostly from the perspective of fisheries, particularly the use of parasites as tags for stock identification of marine fish and invertebrates. The rationale on which the use of parasites as tags are based and the routine statistical techniques employed are analysed, along with the criteria for the selection of suitable parasite tags. The use of parasite genetics as a source of data on spatial and temporal distribution of hosts is described. This publication extends the scope of the methodology from the level of host populations to host communities and biogeography,

Wöhler *et al.* (2025) reviewed the current situation regarding the management of stocks of Patagonian toothfish *Dissostichus eleginoides* in South American waters. There are currently four fisheries for toothfish in waters near the southern tip of South America, each one of which uses different abundance estimates and annual catch allocations. This review examines historical data and recent research, including parasites as biological tags, to explore the potential differentiation between toothfish populations in South American waters. A total of 62 different parasite taxa have been recorded from toothfish. Studies of this parasite fauna indicate different taxonomic richness values between different regions: the highest richness was found around the South Georgia Islands, while that around the Falkland Islands showed intermediate similarities between Chile and South Georgia waters. The adult trematode *Elytraphalloides oatesi* has been suggested as a potential biological tag to study migratory movements and population structure of toothfish: prevalences and abundances of this trematode in all subantarctic islands were much lower than in the Falklands region, indicating lesser abundance in colder regions, while it is absent from toothfish caught in central-southern Chile. This review suggests the existence of distinct stocks of toothfish along the shelf and slope in this region, with little exchange of fish between different fishing grounds.

Comments

The studies carried out in the past year continue the trend of previous years in highlighting the considerable contribution made by parasitologists in South America to the use of parasites as biological tags in studies of marine organisms. They also include a welcome contribution from

the North Atlantic in the form of two publications from Iceland, both of which include suggestions for further research. Two papers (Braicovich *et al.* 2025 and Marcotegui *et al.* 2024) underline the importance of adequate sampling to ensure complete coverage of a study area and one breaks new ground in using parasites to reveal intra-stock variability.

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Interdisciplinary approaches (Contributors: Manuel Hidalgo, Steve Cadrin and Lisa Kerr)

General introduction

The application of interdisciplinary analyses (i.e. the integration of two or more stock identification techniques) has consolidated as a regular approach to provide a holistic view of different facets impacting the stock structure. This has been particularly useful to integrate ecological and evolutionary processes across temporal and spatial scales that contribute to describing the stock structure. Most integrated approaches are still mainly associated with two techniques: genetics/genomics and otolith based methods. From those, genetic methods are generally applied in combination with different techniques, while otolith based methods are generally applied in independent studies combining shape, microchemistry and often growth. In addition, other less common methods such as spatial statistics are being increasingly used (along or in combination with other techniques) to reveal inter- and intra-stock structure. Particularly relevant, many synthesis and reviews studies in topics related with stock structure have been published in 2024-2025, including connectivity, holistic quantitative approaches, or species/fisheries specific reviews combining published information from different techniques.

We here summarize some reviews, integrated approaches and methods development published in the second semester of 2024 and first semester of 2025 that were not included in the review published by SIMWG last year (ICES, SIMWG, 2024) grouped in the following subsections: 1) genetics in combination with other methods, 2) otolith-based methods, 3) combination of other less common methods, and 4) synthesis and reviews. Notably, many of the studies this year focus on different salmon species – they are kept in this review as this species spend part of their life stage in seawaters.

Genetics in combination with other methods

A large number of studies in the last year integrated genetics with other methods, often otoliths-related information or morphometrics. Dueñas-Romero *et al.* (2025) combined information of microsatellite markers and beak morphometric analysis of the upper beak of a Pacific octopus, *Octopus hubbsorum*, in Mexican Pacific waters to identify the population structure. Genetic information provided evidence of six well-defined populations while geometric morphometric results of the upper beaks also provided compelling evidence of morphological differentiation between the localities. Authors conclude that the understanding of the population structure may guide the development of targeted conservation and sustainable exploitation strategies.

Kongmeephol *et al.* (2025) examined the morphological and genetic characteristics of the cuttlefish *Sepia aculeata* populations around Thai-Malay Peninsula using individuals collected across the Gulf of Thailand and the Andaman Sea. Morphometric analysis only revealed sex- but not spatial differences. Genetic analysis revealed shared genetic patterns, though the Andaman Sea population exhibited significantly higher genetic diversity compared to the Gulf of Thailand population. Mismatch distribution and neutrality tests suggested recent population expansion in both regions. These findings suggest implementing sex-specific harvesting strategies would be appropriate. Finally, authors indicate that the higher genetic diversity observed in the Andaman Sea emphasizes the need to prioritize it as a genetic reservoir for conservation planning besides the genetic connectivity supporting a single stock.

Yasue *et al.* (2024) combined genetics and morphometric information of Japanese anchovy *Engraulis japonicus* in the Kii Channel, which includes the boundary between the Pacific (southern side of the Kii Channel) and the Seto Inland Sea stocks (northern side), to clarify the relationship between morphological differences and genetic differences for a better understanding of the

population structure. While sufficient morphological and size differences were identified between areas, the morphological differences among cohorts can be attributed to phenotypic plasticity. There were no genetic differences between samples from the southern side and the northern side of the Kii Channel, suggesting strong genetic connectivity in these areas.

Makhlouf *et al.* (2025) show that integrating complementary information of genetic stock identification and isotope-based methods from otoliths improve the spatial resolution of provenance assignments of Pacific salmon of the Yukon River basin. Authors reconstructed basin-wide estimates of natal origin locations for Chinook salmon in the Yukon River, and corroborated that a watershed scale estimate of natal origin distributions was provided with a greater resolution than from genetic information or isotope data alone.

Nazir *et al.* (2024) combined otolith $\delta^{18}\text{O}$ value and mitochondrial information of Japanese butterflyfish (*Psenopsis anomala*) in coastal waters off northeastern and southwestern Taiwan, as well as in the middle Taiwan Strait, to elucidate the migration pattern and population structure. Their results reveal a seasonal migration pattern between the northern South China Sea and the Yellow Sea, with no geographic population structuring in Japanese butterflyfish samples from Japan and Taiwan. The authors stress that, according to the combined findings from otolith microchemistry and genetic analysis, this species in east Asia shall be managed as a single stock.

Sarakinis *et al.* (2024) combined natural multiple fish markers (i.e. genetics, otolith shape, otolith isotopic composition, and otolith elemental composition) with the aim of increasing the power of assessing population structure and connectivity of black bream *Acanthopagrus butcheri* from in several estuaries across southern Australia. The study also determined the effectiveness of each marker independently and through integration. Their results show that combining genetics and otolith-based techniques was complementary in increasing the accuracy of their results but not all marker integrations were consistently beneficial, highlighting the importance of appropriate marker selection. The maximum classification accuracy to collection site included a combination of genetics, otolith shape, and otolith isotopic composition, evidencing the species' estuarine dependence and limited connectivity across the sampling range.

Corti *et al.* (2025) combined published information to perform a multi-tracer holistic approach, integrating genomic and otolith data of common sole *Solea solea* in the Mediterranean Sea across various spatio-temporal scales using semi-quantitative (Stock Differentiation Index) methods and integrative multivariate analysis. The Stock Differentiation Index indicated a strong spatial structure, with multivariate analysis showing consistent and complementary results across different tracers. The study concludes with the existence of at least three distinct regional stocks within the Mediterranean, and highlighting a complex spatial population structure.

Other numerous studies have combined genetic tools with other diversity of methods and types of data, including biological variables, life-history information, biotelemetry, visual identification through test fisheries. Maes *et al.* (2025) provides novel information of common sole (*Solea solea*) structure in the southern Celtic Sea and southwest of Ireland combining single nucleotide polymorphisms and five biological variables (sex, maturity, age, length, and weight), considering both population structure and their connectivity patterns from the southern North Sea to the Bay of Biscay, which spans 10 ICES areas. They report large-scale genetic differentiation between the southern North Sea and Bay of Biscay. These novel results suggest a current mismatch between the biological populations and stock units in the area, currently managed as a single stock, and provide a solid basis for the re-evaluation of the current stock structure.

Cadiz *et al.* (2025) characterized the fine-scale genetic structure of Atlantic salmon (*Salmo salar*) in the Näätamö River, in the Northern Sami area covering northern Norway and Finland, and evaluated the possibility to assign individuals to their population of origin. They combined genotyped juveniles sampled from eight locations using SNP panel to characterize within-river genetic diversity and structure, with the life-history diversity within each river using a long-term

scale archive of ~22,000 individuals collected over 48 years. Their results show that the genetic structure of the Näätämö River salmon population appears weak possibly due to natural straying. They also identified 59 unique life-history strategies, evidencing the high intra-stock phenotypic diversity. They conclude that information of genetic structure, substantial gene flow and diverse life history need to be considered to protect and manage the self-sustaining salmon population in the Näätämö River.

Howley *et al.* (2025) integrate dispersal behavior (using biotelemetry), genetic analysis of four putative populations and source-sink estimates using Leslie matrix analyses of the demographic status of brown trout (*Salmo trutta*) neighbouring populations connected in a semi-enclosed fjord system, Sognefjord, in Norway. Results showed that Sognefjord brown trout formed a metapopulation consisting of multiple sink populations, primarily supplemented from a single source. Authors also show that a successful dispersal (straying) was performed by 25% of the total spawning population, and that the extensive hydroscape generated directional gene flow from the innermost to outermost populations, with the highest rates observed among neighbouring populations. This study stresses that connectivity patterns observed likely enhance the overall resilience of the metapopulation to variation and shifts in contemporary conditions within the fjord.

Hess *et al.* (2024) combined visual identification through test fisheries with genetic information of Columbia River spring Chinook salmon (*Oncorhynchus tshawytscha*) to evaluate accuracy, resolution, and lead time of predictions for stock-specific run timing and abundance. The study also attempted to maximize the utility of test fisheries by resolving run forecasts into weak- and healthy-stock subcomponents. The study showed that the genetic stock identification resolved the predictive ability as finely as the hatchery broodstock level. The authors described steps to combine these two methods to provide timely in-season information and with prediction accuracy.

Otolith-based methods

Otoliths offer the possibility of a diversity of natural markers and, therefore, it is common to see studies combining several of the methods emerging from these calcified structures. Interestingly, while most studies used to combine trace elements and shape analyses, recent studies also include growth and microstructure information. Lee *et al.* (2024) applied a complementary approach using otolith microstructure and trace element analysis to infer time-resolved elemental profiles that reflect the early ontogeny of age-0+ Patagonian toothfish *Dissostichus eleginoides* from key nursery areas on the Patagonian Shelf. Results revealed significant ontogenetic shifts across the early life history and highlight important considerations in terms of the complexity and protracted nature of early life-history stages as a complex process. They also indicate potential future research directions related to the identification of the stock origin.

Song *et al.* (2024) employed a suite of otolith-based methodologies (otolith microstructure, stable isotope ratios, $\delta^{13}\text{C}$ and $\delta^{18}\text{O}$, and shape analyses) to address the population connectivity of redlip croaker *Larmichthys polyactis* within the southern Yellow Sea region, and particularly between two fishing grounds (Haizhou Bay and Lvsi - considered putative independent stocks). Their findings support the occurrence of population connectivity between the two stocks and propose the existence of a mixed population within Haizhou Bay, likely resulting from the transportation of eggs or larvae originating in Lvsi to Haizhou Bay via prevailing northward currents.

Bellodi *et al.* (2025) combined otolith morphology and a multi-model inference analysis using age-at-length data to estimate growth of large-scaled gurnard *Lepidotrigla cavillone* along the coasts of the two larger Mediterranean islands: Sardinia and Sicily. In both regions, there were no major differences in growth between sexes with slight differences between regions. Also,

shape analysis revealed that otolith morphology distinguishes between Sardinian and Sicilian populations. Authors conclude that these morphological discrepancies are due to a mix of genetic and environmental factors.

Yu *et al.* (2025) used otolith shape analysis and comparison of growth parameters of dotted gizzard shad, *Konosirus punctatus*, in two areas along the Korean coast: the East Sea and the Yellow Sea - western Korean Strait to assess populations differences between the two putative populations. Otolith shape analysis revealed two otolith patterns, which was also confirmed by different growth parameters found for each group. Their results suggest that there are two phenotypic stocks of *K. punctatus* in the Korean coastal waters and they should be managed differently.

Finally, Kerr *et al.* (2025) combined commercial fisheries data with otolith-based stock identification techniques to discriminate between spawning populations of sympatric populations of Atlantic cod with distinct spawning times (winter and spring) in the Gulf of Maine. The authors show clear differences in otolith structure and microchemistry between winter and spring spawners with the highest degree of classification accuracy based on both features. Fluctuating contributions of spring and winter spawners were observed in the 80s and 90s, while the contemporary (2015–2016) commercial fishery is dominated by winter spawners. Authors conclude that otolith-based stock composition has the potential to support monitoring and assessment of cod populations in this area.

The combination of otolith shape and microchemistry analyses persists as one of the most recurrent integrated approaches. De Almeida *et al.* (2024) also combined otolith shape and microchemistry analyses for the black drum, *Pogonias courbina*, in southeastern Brazil lagoon systems. The overall reclassification rate obtained using both techniques was 98% evidencing the existence of two groups associated to the two lagoons investigated. The results suggest a clear spatial discrimination and low connectivity between these groups of two years old *P. courbina* individuals living in the studied lagoon systems.

De Lima *et al.* (2025) also examined population structure through otolith shape and chemistry of white mullet *Mugil cure* in three estuaries in the coastal waters of the Paraíba state, northeastern Brazil. The two techniques applied indicate population differences among sites. Their results underscore spatial structuring and limited connectivity between populations. These patterns also suggest that site fidelity or restricted dispersal plays a role in shaping population structure of this species.

Ghoerbel *et al.* (2024) used size dimensions and microchemical structure of the otoliths of two populations of the annular sea bream (*Diplodus annularis*) collected from the Djerba and Kerkennah Islands in Tunisian waters. The study found significant asymmetry in otolith size dimensions among males and females of the two Islands and the noticeable difference in otolith microchemical elements between individuals of the two groups, that were attributed to factors such as fish age, environmental conditions, and fish biological traits. The authors claimed that these results confirmed the discriminant stock structure and limited connectivity between fish within the two Islands, which should be managed separately.

Combination of other less common methods

Novel combination of species distribution models and discrimination analyses has been proved to be powerful to assess the stock structure of commercial species, leveraging from structural non-commercial monitoring and, therefore, improving knowledge of the temporal variation in stock structure research. Lindegren *et al.* (2025) uses density and size information collected in several and distinct scientific bottom-trawl-surveys in the Northwest and Northeast Atlantic to apply a spatial statistical approach to reveal the Greenland halibut (*Reinhardtius hippoglossoides*) population structure. Their findings demonstrate two overall clusters separating the

Northwest and Northeast Atlantic, which are broadly consistent with recent studies based on available tagging data and genetics. However, the authors also acknowledge whether the results of clustering accurately reflect the true population boundaries, especially at a finer spatial scale, calling for a more holistic approach.

Abad *et al.* (2025) combine distribution modes of nursery areas of four-spot megrim (*Lepidorhombus boschii*) in the north Spanish peninsula to assess how persistent are the recruitment areas over time, with an assessment model based on the spatial findings, in which the advice for this species was divided into two spatial areas. Their results showed significant spatio-temporal variability of nursery areas, with the results of the updated assessment model showing differences in biological reference points compared to the existing global model. They conclude that static spatial management approaches may be ineffective due to environmental variability and that the importance of incorporating spatial structure into the assessment process calls for the potential implementation of spatial stock assessment for this species.

Larval dispersal simulations is a tool of increasing use in stock structure research as it is one of the few techniques informing at low spatial and temporal scale. As a biophysical model, it needs to be fed with lots of parameters informing on life history, growth and behavior to make the simulations more realistic. Cresci *et al.* (2025) integrated information of orientation-swimming experiments in dispersal (Individual Based Model, IBM) simulations of saithe (*Pollachius virens*) dispersal in the Norwegian-North Sea. The study showed that observed swimming and orientation behavior from experiments resulted in higher recruitment to the North Sea saithe stock management unit when implemented in IBM compared to other models, demonstrating the important role of larval swimming and orientation in the recruitment dynamics of saithe populations.

Integrative reviews and synthesis

During the last year, several reviews integrating published or unpublished information have been developed at different levels: species, taxonomic groups (e.g. bivalves) or across species in a given area. Craig *et al.* (2025) has recently revisited a long-lasting hypothesis of three subpopulations of Pacific sardine (*Sardinops sagax*) off US waters. The authors made a critical assessment of this hypothesis reviewing published studies with different techniques including meristics, otolith and body shape, spawning, genetics, growth and demographic analyses. They conclude that many of these studies do not support the hypothesis of subpopulation structure in Pacific sardine.

Lee *et al.* (2025) synthesized available evidence on blue whiting (*Micromesistius poutassou*) population structure in the Northeast Atlantic, revealing a complex metapopulation composed of resident and migratory subpopulations. Genetic, otolith, parasite, and life-history data supports the presence of partial migration, with both migratory and resident contingents contributing to spatial complexity in population, including northern and southern subpopulations, mixing zones, and resident groups. They stress the importance of adaptive, spatially explicit management approaches that account for temporal variability, foster regional cooperation and support stakeholder engagement. The authors also conclude with knowledge gaps in terms of fine-scale population structuring, life-history stage characterization, and connectivity mechanisms.

Talwar *et al.* (2025) Combined information from genetics, artificial tagging, life history, and small-and large-scale fishery-dependent data from across much of the Silky Shark's (*Carcharhinus falciformis*) Pacific Ocean range to synthesize all the information available that helps to elucidate population structure and dynamics of assessed species. The authors conclude that they found preliminary evidence of a three-stock model—southern, central, and northern—in the eastern Pacific Ocean. The authors strengthen the relevance of their synthesis as an example to

comprehensively understand spatial population dynamics of common bycatch species lacking a dispersive larval phase, such as elasmobranchs, by integrating genetic, biological, ecological, and fisheries data.

Griffin *et al.* (2025) revised the entrainment hypothesis, which indicates that migratory routes are socially transmitted from experienced spawners to younger conspecifics resulting in distinct contingents within a population. They use a combination of literature review, life-history data, mark-and-recapture records and electronic tagging of Atlantic tarpon (*Megalops atlanticus*) populations. Authors also evaluated several biological hypotheses related to entrainment mechanisms, habitat conservation and phenotypic plasticity. Their findings provide evidence of migratory connectivity and the role of entrainment in shaping Atlantic tarpon contingent structure across the Western Atlantic. They conclude that research on contingent structure, larval recruitment patterns and abundance trends is needed to inform management measures to ensure the maintenance of migratory knowledge.

Two relevant reviews have been published at taxonomic and geographic level. D'Alessandro *et al.* (2025) analysed 100 articles that examined connectivity patterns of 54 bivalve species across local, regional, basin, and global scales to evaluate the spatial and temporal resolution of these methods. Their findings indicated that geochemical markers have been most successfully used to estimate connectivity at small spatial scales (30–39 km), biophysical models at intermediate spatial scales (29–210 km), and genetic markers at the largest spatial scales (185–1,675 km). They also found that one third of the studies examined use multiple years or generations, highlighting the importance of interannual and seasonal currents patterns in influencing larval dispersal. Authors claim that this synthesis provides quantifiable connectivity estimates across methods and spatial scales, providing useful insights for the integration of marine bivalve connectivity into area-based management. Henriksson *et al.* (2025) reviewed 172 scientific publications assessing connectivity or population structure in close to fifty species in the Skagerrak, a marginal sea in the Northeast Atlantic Ocean. They found that contemporary connectivity with adjacent seas is high, but asymmetric for most species, and most species have multiple distinct populations in the Skagerrak, and separate from those in adjacent seas. Within the Skagerrak, population structure is common both among coastal populations and between coastal and offshore populations, but less frequent among offshore populations. They conclude that population structure is evident despite high connectivity, and temporal variability of population assemblages, challenging area-based protection measures.

Finally, numerous projects focus on a holistic and integrative view of marine connectivity, which includes inter- and interstock structure. This is the case of the SeaUnicorn project in which three recent synthesis and review contributions have been published. Warmuth *et al.* (2025) review the gap between empiricists in this marine connectivity and theoretical ecology modelers in this field. Authors discuss conceptual and mathematical limitations as well as data shortages for the development of integrative meta-population, meta-community, and meta-ecosystem models. Authors stress that enhancing the interaction between marine connectivity modelers and empiricists may play a major role in overcoming several limitations identified, promoting the application of meta-ecology theory and models in ecological connectivity research.

Tanner *et al.* (2025) performed a systematic review of marine connectivity information from more than two hundred reviews to synthesize the current state of marine connectivity research, highlighting the main topics, methods, taxa, geographic areas, and future research priorities. They reveal imbalances in review topics, with certain habitats, taxa, geographic areas receiving disproportionate attention due to variations in funding, field site accessibility, public interest, and/or delays in adopting new concepts and methodologies. Research priorities were broadly grouped into two themes: (i) methods - need to integrate and advance sampling, modelling and novel techniques, and (ii) ecology and application - emphasizing the need to understand drivers and integrate connectivity knowledge into marine conservation and management.

Finally, Daurdane *et al.* (2025) provide in an introduction to a themed article set on marine connectivity with 17 articles that cover a range of approaches and scales applied in contemporary marine connectivity studies and encompass a diversity of ecosystems and taxa. This introduction stresses how marine connectivity knowledge can be better applied to protect marine resources and manage marine and littoral habitats.

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Annex 4: Responses to requests from ICES working groups (ToR b)

SIMWG review of stock structure of king and queen scallops (ToR b, WGScallop request)

David Murray, Steven Cadrin, and Ilaria Coscia from SIMWG attended WGScallop online (on 8 Oct 2025) at the request of WGScallop Chairs Isobel Bloor and Adam Delargy. Within the meeting agenda, SIMWG were specifically asked to provide advice on ToR D (*“Continue to refine stock structure using best available information on genetics and larval dispersal and improve current mapping of scallop stocks”*) and ToR G (*“Identify, list and collate all available data for queen scallops and propose appropriate stock assessment areas”*).

SIMWG attendees listened to ongoing research on methods to identify appropriate stock units for king scallops (*Pecten maximus*) and queen scallops (*Aequipecten opercularis*). From a SIMWG perspective, we are encouraged at the level of consideration WGScallop is giving to what research is required to proactively develop stock units based on biological information. We highlighted that this is one of the few situations we are aware of that biologically relevant research will inform stock unit boundaries, before ICES undertakes assessments and provides advice, rather than retroactively having to realign established boundaries.

There appears to be a substantial amount of biological and ecological research on the population structure of king scallops, including genetics, larval dispersal, and morphological traits (e.g. shell size, meat yield etc). For this species, SIMWG highlighted the importance of taking a holistic approach and to collect a wide range of different data to help inform stock boundaries. We also discussed the importance of considering the strengths and weaknesses of alternative stock identification methods and to consider what data they plan to use in their assessment to inform on the most appropriate methods.

Compared to king scallops, stock identification research on queen scallops is at the nascent stage. However, SIMWG pointed out that the roadmap that WGScallop have undertaken for king scallops would provide an excellent template on how to approach stock identification research for queen scallops (i.e. mapping fishing grounds, resource distributions, management areas, investigating geographic variation in growth, maturity or spawning season to design genetic sampling and larval dispersal studies).

Regarding future opportunities, SIMWG attendees suggested the following:

Existing evidence in king scallops suggest localized population-level biological parameters (e.g. growth, maturity information to estimate yield or spawning potential per recruit reference points), thus biological assumptions for assessments should take this into account.

Careful consideration should be given to gaps in biological information at the geographical scale. SIMWG identified specific areas where there was a perceived unevenness regarding the amount of stock identification evidence available. In cases of spatial heterogeneity, sample data from one area may not be representative of another. This may impact our ability to robustly assess boundaries and would be relevant to both king and queen scallops.

Moving forward, we suggested a closer working relationship with WGScallop as they continue to build their stock boundaries. By working together, we would be able to contribute our Working Groups' substantial expertise which may ensure a more efficient and robust transition to a full ICES assessment and advice. For example, some collaboration on genetic analyses would promote good practice in sampling, analysis and interpretation. SIMWG could provide advice

on genetic techniques (e.g. individual low-coverage whole genome sequencing *vs.* pooled-sequencing), sample types (e.g. baseline *vs.* mixed samples) and *post-hoc* genetic analyses (population assignment models, isolation-by-distance indices and multivariate statistics).

SIMWG review of stock structure of ‘other soles’ in Divisions 8c and 9a (ToR b, WGBIE/WKOS request)

During this year’s meeting (Faro, Portugal, 9-11 Sep 2025), SIMWG reviewed the two documents (Maia *et al.* 2023, Pennino *et al.* 2025) provided by the Working Group for the Bay of Biscay and the Iberian Waters Ecoregion (WGBIE) and requested to be reviewed in conjunction with the Workshop on Other Soles in ICES divisions 8c and 9a (WKOS). Also other relevant literature (e.g. genetic studies) was considered. SIMWG members then attended WKOS on 22 Sep 2025 (online) to discuss stock structure of Senegalese sole (*Solea senegalensis*) and sand sole (*Pegusa lascaris*) and the way forward to improve the data/information basis for stock identification.

SIMWG provided the following advice:

Stock identity remains a key uncertainty. Current evidence does not clarify whether populations in Divisions 8c and 9a are self-contained or connected with areas further south. Genetic and otolith-based studies (morphometrics and chemistry) could help resolve connectivity patterns, ensuring that the assessment units used are biologically meaningful and consistent with the ICES advice framework.

To resolve the issue of stock identity for these species, multidisciplinary approaches are recommended, allowing the combination of genetic and otolith-based studies to capture both evolutionary and ecological aspects of connectivity. Genetic analyses, using samples collected from the divisions of interest (and subareas within these divisions) and from adjacent ICES areas, can provide a broader understanding of gene flow and population structure. Applying high-resolution markers, such as SNPs, could further reveal patterns of connectivity. Otolith-based studies using the same samples can offer valuable insights into stock identity. Otolith shape analyses can help detect population structuring, while otolith chemistry provides information on spawning origins and the role of specific habitats, such as inshore nursery areas, in supporting recruitment, for *Solea senegalensis*. Integrating these methods will ensure that both long-term genetic connectivity and short-term environmental signals are considered, while the integration of other tools, such as larval dispersal models could further strengthen conclusions.

Finally, life-history parameters need harmonization. Existing studies provide estimates of growth, maturity, and reproduction mainly from Portuguese waters, but inconsistencies remain among sources and spatial representativeness is limited. Standardized sampling protocols and joint analyses would help reduce uncertainty and improve biological reference points.

In summary, the pathway towards advice for *S. senegalensis* and *P. lascaris* involves:

1. Validation and harmonization of fishery-dependent indices.
2. Exploration of dedicated coastal surveys to generate independent abundance indices.
3. Studies to resolve stock identity and connectivity.
4. Harmonization of life-history parameters across countries and habitats.

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SIMWG review of stock structure of West Greenland inshore cod (ToR d, NWWG request)

The SIMWG was requested to review the stock structure of inshore cod at West Greenland. Two working documents (Retzel and Nielsen, 2024; Retzel and Buch, 2025) were submitted and summarized at the 2025 SIMWG meeting (Faro, 9-11 Sep 2025). The working group has reviewed these documents and here provides a summary of the main findings, followed by recommendations and conclusions.

Genetic evidence (Retzel and Buch, 2025)

An overview of genetic data used in the Greenland cod assessment process identified four main genetic populations:

- West Greenland Inshore Spawning Cod (WISC)
- West Greenland Offshore Spawning Cod (WOSC)
- East Greenland Iceland Offshore Spawning Cod (EGIOSC)
- Iceland Inshore Spawning Cod (ISI)

For the present review, only the structure of WISC is considered. Genetic analyses from 2000–2024 indicate that WISC occur both offshore and inshore along West Greenland, overlapping with the other genetic populations. However, WISC dominate inshore in the central regions.

Tagging, ecological and fishery evidence (Retzel and Nielsen, 2024)

This working document provided evidence suggesting that WISC may consist of two distinct inshore spawning components (northern and southern). Key findings include:

- **Tagging (2003–2022):** Out of 359 recaptures, only two fish moved between inshore areas, suggesting limited migration among regions.
- **Survey indices:** Data from three inshore areas showed divergent fluctuations in CPUE and biomass indices. However, the analyses could not establish whether these represent true regional differences in stock dynamics or simply reflect variability of survey estimates. Cohort tracking across areas was also inconclusive.
- **Catch data:** Landings were presented by area but contained no explicit information on stock structure.
- **Genetics:** No significant genetic differentiation was observed between northern and southern inshore areas. Nevertheless, the authors argue that ecological separation may exist: migration rates could be high enough to prevent long-term genetic divergence, while still being low enough to create management-relevant differences on shorter time-scales.

Conclusion

Currently, the West Greenland inshore cod stock is assessed as a single management unit, but with two separate assessment models, which already provides some protection against local overexploitation by accounting for potentially distinct biological components. The available information gives clear indications that a split into northern and southern inshore stocks could be justified, but SIMWG does not recommend such a change at this stage. Genetic analyses show

no significant differentiation between northern and southern inshore cod, indicating that they belong to a single biological population, while the strongest argument for separation comes from tagging studies that demonstrate almost no movement between inshore areas. However, the tagging work was limited to inshore sites, with no offshore recaptures, and genetic studies confirm that West Greenland Inshore Spawning Cod also occur offshore, making it unclear whether these individuals originate in northern or southern inshore areas. This uncertainty means that offshore catches may consist of mixed components without any current method to discriminate them.

While SIMWG acknowledges the evidence supporting a potential split and recognizes the importance of this work, the available data remain insufficient to support changing the stock structure at present. Maintaining the current approach is therefore recommended until further evidence becomes available, particularly from offshore tagging, improved survey analyses or alternative methods capable of distinguishing northern and southern components.

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Annex 5: Overview on past SIMWG reviews

SIMWG Annual Report	Species	ICES Stock (s)	Ecoregion	Requested by
2025	Atlantic cod (<i>Gadus morhua</i>)	NAFO Subarea 1 (West Greenland Inshore Spawning Cod)	(NAFO area)	NWWG
	Senegalese sole (<i>Solea senegalensis</i>), Sand sole (<i>Pegusa lascaris</i>)	Divisions 8c and 9a	Bay of Biscay & Iberian Coast	WKOS
	King scallops (<i>Pecten maximus</i>)	Subareas 6 and 7	Greater North Sea, Celtic Seas	WGScallop
	Queen scallops (<i>Aequipecten opercularis</i>)	Subareas 6 and 7	Greater North Sea, Celtic Seas	WGScallop
2024	Blue ling (<i>Molva dypterygia</i>)	1) "bli.27.nea" in Subareas 1, 2, 8, 9, 12 and Divisions 3a and 4.a, 2) "bli.5a14" in Subarea 14 and Division 5a, and 3) "bli.5b67" in Subarea 6-7 and Division 5b	Barents Sea, Norwegian Sea, Greater North Sea, Faroes, Greenland Sea, Oceanic Northeast Atlantic, Celtic Seas, Bay of Biscay & Iberian Coast	WGDEEP
	Horse mackerel (<i>Trachurus trachurus</i>)	Western stock (Subarea 8 and Divisions 2.a, 5.b, 6.a, 7.a-c, and 7.e-k and 3.a & 4.a in quarters 3 and 4); North Sea stock (Divisions 4.b-c, 7.d and 3.a & 4.a in quarters 1 and 2); Southern stock (Division 9.a)	Norwegian Sea, Greater North Sea, Celtic Seas, Bay of Biscay & Iberian Coast	WKBHMB
	European anchovy (<i>Engraulis encrasicolus</i>)	Division 9a	Bay of Biscay & Iberian Coast	WGHANSA
	Dab (<i>Limanda limanda</i>)	Baltic Sea dab (dab.27.22-32) and North Sea dab (dab.27.3a4)	Baltic Sea, Greater North Sea	WGBFAS
	Flounder (<i>Platichthys flesus</i>)	Belt Seas and the Sound (fle.27.22-23) and North Sea flounder (fle.27.3a4)	Baltic Sea, Greater North Sea	WGBFAS
	Plaice (<i>Pleuronectes platessa</i>)	ple.27.21-23 (Kattegat, Belt Sea and the Sound), ple.27.24-32 (Baltic Sea, excluding the Sound and Belt Sea)	Baltic Sea	WGBFAS, WGNSSK
2023	Dab (<i>Limanda limanda</i>)	Baltic Sea dab (dab.27.22-32) and North Sea dab (dab.27.3a4)	Baltic Sea, Greater North Sea	WGBFAS, WGNSSK
	Flounder (<i>Platichthys flesus</i>)	Belt Seas and the Sound (fle.27.22-23) and North Sea flounder (fle.27.3a4)	Baltic Sea, Greater North Sea	WGBFAS, WGNSSK
2022	European hake (<i>Merluccius merluccius</i>)	Areas 3a46, 78abd and 8c9a	Greater North Sea, Celtic Seas, Bay of Biscay & Iberian Coast	WGBIE
	White anglerfish (<i>Lophius piscatorius</i>) and black anglerfish (<i>Lophius budegassa</i>)	Areas 3a46, 78abd and 8c9a	Greater North Sea, Celtic Seas, Bay of Biscay & Iberian Coast	WGBIE
	European anchovy (<i>Engraulis encrasicolus</i>)	Division 9a	Bay of Biscay & Iberian Coast	WGHANSA
2021	Herring (<i>Clupea harengus</i>)	Divisions 6.a, 7.bc	Celtic Seas	HAWG
2020	Greater silver smelt (<i>Argentina silus</i>)	aru.27.123a4, aru.27.5a14, and aru.27.5b6a, and aru.27.6b7-1012	Faroes, Greenland Sea, Icelandic Waters, Norwegian Sea	WKGSS
2019	European sardine (<i>Sardina pilchardus</i>)	1) Subarea 7 (Southern Celtic Seas, English Channel), 2) Divisions 8.a-b and 8.d (Bay of Biscay), 3) Divisions 8.c and 9.a (Cantabrian Sea and Atlantic Iberian waters)	Celtic Seas Ecoregion, Greater North Sea Ecoregion, and Bay of Biscay and the Iberian Coast Ecoregion	WKSAR

	Beaked redfish (<i>Sebastes mentella</i>)	Division 14.b, demersal (Southeast Greenland) and Subarea 14 and Division 5.a, Icelandic slope stock (East of Greenland, Iceland grounds)	Greenland Sea and Icelandic Waters	NWWG
	Atlantic cod (<i>Gadus morhua</i>)	Division 6.a	Celtic Seas	MIACO
	Red gurnard (<i>Aspitrigla cuculus</i>)	Subareas 3-8	Greater North Sea, Celtic Seas, Faroes, Biscay	WGWIDE
2018	European sardine (<i>Sardina pilchardus</i>)	1) Subarea 7 (Southern Celtic Seas, English Channel), 2) Divisions 8.a-b and 8.d (Bay of Biscay), 3) Divisions 8.c and 9.a (Cantabrian Sea and Atlantic Iberian waters)	Celtic Seas Ecoregion, Greater North Sea Ecoregion, and Bay of Biscay and the Iberian Coast Ecoregion	WKSAR
	Beaked redfish (<i>Sebastes mentella</i>)	Division 14.b, demersal (Southeast Greenland) and Subarea 14 and Division 5.a, Icelandic slope stock (East of Greenland, Iceland grounds)	Greenland Sea and Icelandic Waters	NWWG
	Atlantic cod (<i>Gadus morhua</i>)	Div. 6.a	Celtic Seas	MIACO
2017	No species reviewed			
2016	Atlantic mackerel (<i>Scomber scombrus</i>)	Northeast Mackerel Stock Identity in ICES Subareas I-VII and XIV and Divisions VIIIa-e and IXa	Widely distributed and migratory stocks	WGWIDE
2015	Haddock (<i>Melanogrammus aeglefinus</i>)	Haddock in ICES Subareas IV and VIa (North Sea and West of Scotland)	North Sea and West of Scotland	WKHAD
	Megrim (<i>Lepidorhombus whiffiagonis</i>)	megrim in ICES Subareas VIIIc and IXa	Bay of Biscay and Iberic waters	WGBIE
	Anchovy (<i>Engraulis encrasicolus</i>)	European anchovy in ICES Division IXa	Bay of Biscay and Iberic waters	WGHANSA
	Plaice (<i>Pleuronectes platessa</i>)	Plaice in ICES sub-area IIIa and Adjacent Areas	North Sea and Baltic Sea	WKPLE
	Greater silver smelt (<i>Argentina silus</i>)	Greater silver smelt in ICES Subareas I, II, IV, VI, VII, VIII, IX, X, XII and XIV and Divisions IIIa and Vb	Greenland and Iceland Seas, Barents Sea, Faroes, Norwegian Sea, Celtic Sea North Sea, South European Atlantic Shelf, Baltic Sea, and Oceanic northeast Atlantic	ADGDEEP
2014	Blue whiting (<i>Micromesistius poutassou</i>)	Blue whiting in Subareas I-IX, XII, and XIV	Widely distributed and migratory stocks	WGWIDE
	Atlantic cod (<i>Gadus morhua</i>)	1) Cod in inshore waters of NAFO Subarea 1 (Greenland cod), 2) Cod in offshore waters of ICES Subarea XIV and NAFO Subarea 1 (Greenland cod)	Iceland and East Greenland	NWWG
2013	Turbot (<i>Scophthalmus maximus</i>)	ICES Subarea III d	Baltic Sea	WKFLABA
	Dab (<i>Limanda limanda</i>)	ICES Subarea III d	Baltic Sea	WKFLABA
	Brill (<i>Scophthalmus rhombus</i>)	ICES Subarea III d	Baltic Sea	WKFLABA
	Anglerfish (<i>Lophius budegassa</i>) and the white anglerfish (<i>Lophius piscatorius</i>)	1) The northern shelf stock consisting of Anglerfish in Division IIa (Norwegian Sea), Division IIIa (Kattegat and Skagerrak), Subarea IV (North Sea), and Subarea VI (West of Scotland and Rockall) 2) The northern southern shelf stock consisting of Anglerfish in Divisions VIIb-k and VIIIa,b,d 3) The southern southern shelf stock consisting of Anglerfish in Divisions VIIIc and IXa	northeast Atlantic	WKFLAT

2012	Atlantic cod (<i>Gadus morhua</i>)	ICES Subarea XIV and NAFO Sub-area 1 (Greenlandic cod)	East and West Greenland	NWWG
	Plaice (<i>Pleuronectes platessa</i>)	ICES Subarea IIIa	North Sea	WKPESTO
	Flounder (<i>Platichthys flesus</i>)	ICES Subarea IIId	Baltic Sea	WKFLABA
	Deepwater stocks:			
	Roundnose grenadier (<i>Coryphaenoides rupestris</i>)			
	Black scabbardfish (<i>Aphanopus carbo</i>)			
	Blue Ling (<i>Molva dypterygia</i>)			
	Ling (<i>Molva molva</i>)			
	Tusk (<i>Brosme brosme</i>)		Widely distributed and migratory stocks	WGDEEP
	Greater Forkbeard (<i>Phycis blennoides</i>)			
Alfonsinos (<i>Beryx splendens</i> and <i>Beryx decadactylus</i>)				
Great silver smelt (<i>Argentina silus</i>)				
Black-spot red sea bream (<i>Pagellus bogaraveo</i>)				
Beaked redfish (<i>Sebastes mentella</i>)				
2011	Beaked redfish (<i>Sebastes mentella</i>)	1) a 'Deep Pelagic' stock (ICES Vb, XII, XIV >500m), 2) a 'Shallow Pelagic' stock (ICES Vb, XII, XIV <500m), and 3) an 'Icelandic Slope' stock (ICES Va, XIV).	Iceland and Greenland Seas, Faroes	NEAFC and ACOM
	Sprat (<i>Sprattus sprattus</i>)	ICES sub-areas VI and VII	Celtic Sea	HAWG
	Haddock (<i>Melanogrammus aeglefinus</i>)	ICES area VI (west of Scotland) and IV (North Sea)	Greater North Sea, Celtic Seas	WKBENCH
2010	Beaked redfish (<i>Sebastes mentella</i>)	1) a 'Deep Pelagic' stock (ICES Vb, XII, XIV >500m), 2) a 'Shallow Pelagic' stock (ICES Vb, XII, XIV <500m), and 3) an 'Icelandic Slope' stock (ICES Va, XIV).	Iceland and Greenland Seas, Faroes	NEAFC
	Beaked redfish (<i>Sebastes mentella</i>)	1) a 'Deep Pelagic' stock (ICES Vb, XII, XIV >500m), 2) a 'Shallow Pelagic' stock (ICES Vb, XII, XIV <500m), and 3) an 'Icelandic Slope' stock (ICES Va, XIV).	Iceland and Greenland Seas, Faroes	WKREDS
2009	Blue whiting (<i>Micromesistius poutassou</i>)	ICES Subareas I-IX, XII, and XIV	Widely distributed and migratory stocks	ACOM
	Deep sea fish	General comments across ICES areas	Across ICES ecoregions	WGDEEP
	Beaked redfish (<i>Sebastes mentella</i>)	1) Western Icelandic shelf, 2) Deep Irminger Sea and Western Faroe, 3) all other localities comprised between the shallow Irminger Sea off Newfoundland all the way to the Barents Sea and the offshore Northern Norwegian waters ("shallow stock").	Iceland and Greenland Seas, Faroes, Norwegian and Barrents Seas	SGRS
2008	Herring (<i>Clupea harengus</i>)	ICES Area VIaN, VIaS, VIIc, VIIb, VIIk, VIIj, VIIg, VIIh, VIIaS	Celtic Seas	HAWG
	New MoU species (sea bass, striped red mullet, red, tun and gray gurnards, flounder, witch flounder, brill, turbot, lemon sole, dab)	General comments across ICES areas	Across ICES ecoregions	WGNEW

	Wide ranging shark species and demersal skates	General comments across ICES areas	Across ICES ecoregions	WGFE
Deepwater stocks:				
	Tusk (<i>Brosme brosme</i>)	ICES Area I,II, Va, Vb, IV, VIa, VIb		
	Blue ling (<i>Molva dypterygia</i>)	ICES Area Va, Vb, VIa		
	Ling (<i>Molva molva</i>)	ICES Area II, Va, Vb, IV, VI		
2007	Greater argentine (<i>Argentina silus</i>)	ICES Area IIIa, Va,Vb,VII	Widely distributed and migratory stocks	WGDEEP
	Roundnose grenadier (<i>Coryphaenoides rupestris</i>)	MAR, ICES Area VIb2, XIIb		
	Black scabbardfish (<i>Aphanopus carbo</i>)	ICES Area VIa, IX		
	Red seabream (<i>Pagellus bogaraveo</i>)	ICES Area IX, X		
	Beaked redfish (<i>Sebastes mentella</i>)	ICES Areas Va, Vb, and XIV, V, VI, XII, and XIV,	Iceland and East Greenland	AFWG and NWWG
2006	No species reviewed	NA	NA	NA
2005	Whiting (<i>Merlangius merlangus</i>)	ICES Subarea IV and Division VII d	North Sea	SGSIMUW
2004	No species reviewed	NA	NA	NA