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Project synthesis report

GenDC

Improving scientific knowledge to strengthen the science-basis
of management decisions under the Common Fisheries Policy



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Use of Artificial Intelligence (AI)

Parts of the text in this report have been linguistically refined using Copilot. The AI tool was used exclusively for language improvement purposes, including proofreading, grammar correction, and optimization of phrasing. All content, data, arguments, and conclusions were generated and fully verified by the authors.

1. Project Description

1.1 Background

The GenDC project (Improving stock assessment and sustainable management of marine fisheries through integrated genetic data collection) was established to support ongoing efforts to improve the scientific basis for fisheries management under the EU Common Fisheries Policy (CFP). Reliable stock assessments depend on high-quality biological data collected through the EU Data Collection Framework (DCF). However, increasing scientific evidence has shown that the distribution of biological fish populations does not always align perfectly with the geographical areas used for data collection, stock assessment, and management. As a result, additional information is often needed to better understand population structure, migration patterns, and stock mixing in support of sustainable management decisions.

In recent years, advances in genetic and genomic technologies, combined with declining cost of genetic analysis, have created new opportunities to strengthen fisheries science. Genetic methods can identify distinct biological populations and assign individual fish to their population of origin with a high degree of accuracy. Several ICES stock assessment and benchmark working groups, along with Regional Coordination Groups responsible for coordinating DCF activities, have highlighted the value of genetic data for improving the assessment of mixed-stock fisheries and understanding population dynamics. While genetic tools are increasingly available, their use within routine fisheries data collection and stock assessment remains limited and varies among countries and regions. There is therefore a need for common approaches that facilitates the collection, storage and application of genetic data within existing fisheries monitoring programs.

GenDC was developed to address this need by creating a standardized framework for integrating genetic information into fisheries data collection and assessment processes. Using Atlantic cod in the North Sea, Kattegat and Baltic Sea as a case study, the project aims to demonstrate how genetic data can complement existing fisheries information to improve stock assessments and support more informed management decisions. The project has also provided tools and procedures that can be adapted to other species and regions, contributing to more resilient and sustainable fisheries management in the future. Ultimately, GenDC provides added value to the CFP through suggested improvements to data collection under the DCF, data quality for fish stock assessments and subsequently scientific advice and fisheries management.

1.2 Objectives

Against this background, the GenDC project was initiated to address the current limitations in fisheries data collection and stock assessment by integrating genetic information into existing monitoring frameworks. A central component of the EU Data Collection Framework (DCF) is the collection of data

that supports stock assessments and provides reliable information on the status of exploited marine resources. Current stock assessment and management frameworks generally assume that biological populations correspond to the geographical management areas used for data collection. However, research has shown that the spatial distribution of fish stocks frequently does not align with these management boundaries (Reiss et al., 2009; Maggini et al., 2022).

While the DCF provides a well-established framework for standardized fisheries data collection, genetic information is not yet routinely integrated into stock assessment and advisory processes. At the same time, advances in genetic technologies have made it possible to identify biological populations with high precision and to quantify stock mixing across regions. These developments offer new opportunities to improve our understanding of population structure and dynamics, thereby strengthening stock assessments and supporting more sustainable fisheries management. By moving genetic population identification from a research tool towards operational application, GenDC contributes to improving the scientific basis for fisheries management under the Common Fisheries Policy,

To address these needs, GenDC focuses on developing harmonised sampling protocols, improving data management systems, and demonstrating how genetic information can be operationally integrated into fisheries assessment and management frameworks. The project is built around four main objectives:

- 1. Develop standardized protocols for genetic data collection**

A key objective was to create harmonized sampling strategies, protocols and procedures for collecting genetic samples through existing national and international fisheries surveys. This ensures consistent, high-quality and comparable genetic data across countries and regions. The protocols are designed to facilitate routine implementation through existing survey programmes such as the North Sea International Bottom Trawl Survey (IBTS) and Baltic International Trawl survey (BITS) and to ensure compatibility with international data collection systems within ICES.

- 2. Establish an updated genetic baseline for Atlantic cod**

GenDC has expanded and improved existing genetic reference datasets for Atlantic cod populations across the North Sea, Kattegat and Baltic Sea. These genetic baselines enable individual fish to be assigned accurately to their population of origin, providing critical information on stock structure, migration and population mixing. A metadata description of where and how these baseline samples have been collected has also been incorporated into the ICES database system.

- 3. Integrate genetic information into stock assessment models**

The project has further continued the development of how to incorporate population-level genetic data into existing multi-stock assessment models improving estimates of stock size,

population dynamics and fishing mortality, particularly in areas where fish from multiple populations mix, as is presently the case in the North Sea. By incorporating population structure into assessment frameworks, the project supports more robust scientific advice and more effective fisheries management.

4. **Develop a framework for long-term storage and use of genetic data**

GenDC has communicated with key stakeholders, including ICES, stock assessment experts and data coordinators, to establish data standards and procedures for integrating genetic information into existing fisheries databases. This work follows FAIR data principles and aims to ensure that genetic information becomes a sustainable and accessible component of future fisheries monitoring programs and advisory systems.

Collectively, these objectives support a gradual transition towards more resilient population informed fisheries management, strengthen the scientific basis for the sustainable exploitation of marine resources, and improve the ability of fisheries management systems to respond to future environmental and climate-driven changes.

1.3 Project Relevance

GenDC addresses a recognized need within European fisheries science and management to improve the integration of genetic data into fisheries monitoring, stock assessment, and advisory processes. By strengthening the evidence base for stock assessments, the project supports more effective and sustainable fisheries management. Recent reviews by the Scientific, Technical and Economic Committee for Fisheries (STECF, 2023) and several ICES assessment and benchmark processes have highlighted the increasing value of genetic and genomic tools for fisheries management, particularly for stock identification, quantifying population mixing, and defining the biological units underpinning stock assessments. The need for routine genetic sampling has been identified for a range of commercially important species, including Atlantic cod and herring, and has been repeatedly emphasized by ICES assessment working groups (ICES, 2017; ICES, 2023a; ICES, 2023b).

The relevance of GenDC is particularly evident for Atlantic cod, which serves as the project's case study. Across the Northeast Atlantic and Baltic Sea, cod populations exhibit complex population structure and mixing patterns that are not fully reflected in current assessment and management units. Recognizing this, the 2023 ICES Benchmark Workshop on Northern Shelf Cod (ICES, 2023a) redefined Northern Shelf cod as three biologically distinct sub-stock components (Northwestern, Viking, and Southern) and identified a need for improved genetic data to quantify stock distribution and mixing (ICES, 2023a). These requirements were subsequently explored through the ICES workshops WKCODSCOPE and WKCODSAMPLING, which concluded that routine genetic sampling is essential for the future assessment and management of Northern Shelf cod and should be implemented through an internationally coordinated sampling program integrated with existing data collection frameworks (ICES, 2026a; ICES, 2026b). Results generated through GenDC further demonstrate that the southern

component possesses a distinct genetic profile, providing a critical foundation for the development of operational genetic monitoring and stock assessment tools (ICES, 2026b). The importance of these developments is further reflected in the establishment of the ICES North Sea Cod Tiger Team (NSCodTT), which was tasked with reviewing available data and assessment approaches, identifying priorities for improving stock assessment and forecasting methodologies, and developing a roadmap towards the next benchmark. The Tiger Team explicitly recognizes the need for improved biological and genetic data to support more robust management advice for this complex mixed-stock fishery. Meeting this need will require a coordinated genetic sampling programme that can provide the representative and consistent data needed for future assessments.

GenDC directly addresses these priorities by providing the sampling protocols, genetic baselines, data infrastructure, and assessment methodologies required to incorporate population level information into future stock assessments. Similar needs have been identified for other cod stocks. In the Kattegat, North Sea and local cod populations mix within the assessment area, while in the Baltic Sea, genetic analyses have become an important tool for distinguishing western and eastern Baltic cod populations and quantifying stock mixing in the main mixing area (ICES, 2015; ICES, 2017; Hemmer-Hansen et al., 2019, ICES 2026c). Atlantic cod therefore provides an ideal case study for developing and testing methodologies that can subsequently be applied to other species and mixed-stock fisheries throughout European waters.

Alignment with previous projects

GenDC builds on previous European and national initiatives that have demonstrated the value of international collaboration, harmonized sampling, and centralized genetic databases for fisheries management, including the EU FP7 project *FishPopTrace*. It is also closely aligned with the conclusions of the EMFAF-funded *MED_UNITS* project, which highlighted improved coordination of data collection as a prerequisite for integrating biological population structure into stock assessment and fisheries management (Spedicato et al., 2022). GenDC has also further developed the sampling and analysis of cod samples conducted in the EMFAF-funded project FABBIO (Hussy et al., 2024). Accordingly, international coordination, standardization, and harmonization of genetic sampling, data storage, and data exchange are central elements of GenDC. Work initiated by The Second Workshop on Stock Identification and Allocation of Catches of Herring to Stocks (WKSIDAC2) to develop a genetic population data framework to support integration of genetics into the ICES advisory systems for herring has been further developed for cod under GenDC. The project has also drawn on experience from regional coordination initiatives such as Fish'NCo, fishPi2, and STOMACH, which have developed collaborative approaches to biological sampling, data management, and database implementation within existing fisheries monitoring frameworks such as scientific surveys. By building on these established networks and infrastructures, GenDC facilitates the integration of genetic monitoring into existing surveys and workflows, improving both efficiency and long-term sustainability.

In addition, GenDC capitalizes on recent advances in population genetics and stock assessment modelling generated by consortium partners and collaborators. These studies have improved understanding of cod population structure and mixing dynamics and provide a strong scientific basis

for designing efficient and targeted sampling strategies. The majority of sampling activities have been conducted within the North Sea, Skagerrak, Kattegat, and Baltic Sea, taking advantage of the established International Bottom Trawl Survey (IBTS) and Baltic International Trawl Survey (BITS) platforms, and the regional coordination mechanisms already operating under the Data Collection Framework.

Despite the recognized value of genetic data, collection efforts remain fragmented and often rely on national priorities and short-term funding. GenDC addresses this gap by developing harmonized sampling protocols, genetic baselines, assessment methods, and data integration strategies within the Data Collection Framework (DCF), providing a coordinated foundation for improved stock assessments and fisheries advice across Europe. Although focused on Atlantic cod, the approaches developed by GenDC are transferable to other species and regions. The project therefore supports the alignment of biological and management units, strengthens ecosystem-based and climate-resilient fisheries management, and contributes to the long-term objectives of the CFP, the European Green Deal, and the EU Biodiversity Strategy.

1.4 Consortium Setup

The GenDC consortium brings together complementary expertise in fisheries genetics, stock assessment, data collection and fisheries management. The project is coordinated by DTU Aqua (Denmark), which provides expertise in fisheries genetics, statistical modelling, stock assessment and advisory processes, while playing a central role in ICES assessment working groups and European Regional Coordination Groups (RCGs). This combination of competencies positions DTU Aqua (WP1, WP3 and WP5 lead) to drive the integration of genetic data into existing fisheries assessment frameworks. Key project partners include SLU Aqua (Sweden) (WP4 lead) and the Thünen Institute for Baltic Sea Fisheries (Germany) (WP2 lead), both of which are responsible for national implementation of the Data Collection Framework (DCF), actively contribute to international coordination through the RCG's, and are involved in cod stock assessments in the project's focal areas.

A central principle of GenDC is the co-development of methods with end users, including stock assessors, survey coordinators, data managers, ICES working groups and fisheries governance bodies. This ensures that project outputs are scientifically robust, operationally feasible, and compatible with existing advisory and data collection frameworks. Project partners have been actively involved in relevant ICES assessment and advisory working groups, including key roles in the assessment of Baltic cod, Kattegat cod and the Northern Shelf cod stock complex. These close links to the ICES advisory process have ensured that project outputs can be readily transferred to end-users and incorporated into future stock assessments. In addition, consortium members have extensive onboard experience with survey operations, including sample processing and workflow management. Additionally, the project is well positioned through its members' active involvement in the Regional Coordination Groups (RCGs) and associated intersessional groups, which play a central role in coordinating national data collection programmes across Europe

The project has further collaborated closely with experts from IMR (Norway), Cefas (England) and MASTS (Scotland), who have contributed to genetic sampling and strengthened links to the assessment

of Northern Shelf cod. In addition, ICES has participated as a subcontractor, supporting development of data standards and long-term solutions for the storage and accessibility of genetic information through existing fisheries databases. As an accredited data management facility hosting and managing commercial and survey sampling data across regions, the ICES Data Centre plays a fundamental role in ensuring future storage, accessibility, and long-term use of genetic data generated by the project.

The project has been governed by a Steering Committee comprising representatives from all partner institutions and chaired by the project coordinator. DTU Aqua has been the overall responsible for scientific, administrative, financial and contractual management of the project, while Work Package leaders have overseen the delivery of their respective activities and report progress to the Steering Committee. Building on extensive experience in coordinating EU-funded projects and a strong track record of collaborative initiatives that have successfully applied genetic data to fisheries stock assessment and scientific advice, the consortium has been well positioned to ensure both the successful delivery of project objectives and the long-term uptake of GenDC outputs within fisheries monitoring, assessment, and management frameworks.

1.5 CINEA meetings

During the project, a start-up meeting was held in Brussels and hosted by CINEA. Two GenDC participants attended in person and presented the objectives of the GenDC project alongside representatives from the other projects funded under the same call. This meeting provided a valuable overview of the diversity of projects and their contributions to fisheries data collection.

Further, at the end of the project period, a Workshop on Scientific Advice for Fisheries Projects from the 2023-2025 calls was held. The first part of the workshop focused on the implementation of the funding calls. Prior to the meeting, participants, including the attendees from the GenDC project, completed an EU survey, the combined results of which were presented and discussed following an overview of the 2023 and 2025 calls for proposals. During the workshop, all participating projects, including GenDC, presented their objectives, key achievements, and main outcomes. These presentations were followed by an open moderated discussion with persons from DG MARE, providing an opportunity to reflect on project impacts and their relevance to fisheries management and policymaking.

Besides these official meetings, frequent communication between the CINEA project officer and the GenDC project coordinator has ensured a successful project outcome.

1.6 Funding

The GenDC project is funded under the EMFAF-2023-PIA-FisheriesScientificAdvice call, improving scientific knowledge to strengthen the science basis of management decisions under the Common Fisheries Policy. The project has a total budget of EUR 477,202, with a 20% co-financing requirement.

A substantial part of the co-financing contribution has been provided through the collection of cod samples during scientific surveys and sampling activities conducted in cooperation with commercial

fishers. These activities were essential for securing the biological material required for the genetic analyses undertaken within the project. Overall, a large part of the funding in this project has been to ensure resources for conducting the genetic analysis needed to strengthen the stock assessment, to structure effective collaboration between the participating institutions and to support the implementation of project activities across sampling, data management, genetic analyses, and stakeholder engagement.

The project budget was allocated among the project partners as follows:

- DTU Aqua: 82%
- SLU Aqua: 12%
- Thünen Institute: 7%

ICES participated in the project as a subcontractor, with its activities financed through the budget allocated to DTU Aqua.

2. Work package 1

Project management and coordination

Lead: Marie Storr-Paulsen, DTU Aqua and Julie Olivia Davies, DTU Aqua

2.1 Steering Group meetings (D1.1- D1.5)

To support the implementation of the GenDC project, a Steering Group was established to provide strategic guidance and facilitate coordination among project partners, ICES representatives, and relevant work package leaders. The Steering Group played a central role in ensuring alignment between project activities and coordination and ensuring communication with end users, such as survey and assessment working groups, and the ICES Data Centre.

During the reporting period, Steering Group monthly meetings were held, except during holiday periods, to discuss and coordinate technical, governance, and data management aspects in connection with the project.

The following participants were invited to all Steering Group meetings.

Participants

Marie Storr-Paulsen	DTU Aqua, lead in GenDC
Cecilia Kvaavik	ICES, participating in WP2
Jakob Hemmer- Hansen	DTU Aqua, WP 3 lead in GenDC
Johan Løvgren	SLU Aqua, WP 4 lead in GenDC
Julie Olivia Davies	DTU Aqua, WGSMArt, participating in WP1, WP2
Uwe Krumme	Thünen Institute, WP 2 lead in GenDC
Patrik Börjesson	SLU Aqua, ICES chair for IBTSWG

Besides the Steering Group meetings, several meetings have been conducted with numerous ICES expert groups (assessment, survey coordination and data governance groups.) These meetings are described in more detail in sections 3.1, 3.2 and 3.3.

2.2 The two workshops conducted with ICES

In the lifetime of GenDC, two workshops were organised together with ICES where project partners actively participated and which were co-chaired by GenDC project leads from DTU Aqua alongside experts from IMR (Norway), Cefas (UK) and MASTS (Scotland). The aim being, to address a request from Norway, UK, and the EU to ICES for advice on developing a biological sampling programme, with a focus on genetic data, to support the management of the Northern Shelf cod. DTU Aqua project leads were central to formulating the workshop's resolutions, coordinating the work needed to address the Terms of Reference and delivering the final reports. Numerous meetings were attended during all steps of the process.

The first was the workshop on Scoping Data collection for Northern Shelf cod sub-stocks (WKCODSCOPE) held at ICES Headquarters, Copenhagen, Denmark (and online), 18-21 March 2025, with 47 participants, including 5 members from GenDC (Marie Storr-Paulsen, DTU Aqua as co-chair). Participants were from both the scientific community and the fishing industry, representing 11 countries and institutions. GenDC project progress was reviewed, including genetic stock definitions, a standardized genetic sampling protocol including a data format and sampling strategy.

The second was the Workshop on Sampling Data for Northern Shelf cod sub-stocks (WKCODSAMPLING) held at ICES Headquarters, Copenhagen, Denmark (and online), 10-14 November 2025, with 41 participants, including 6 members from GenDC (Jakob Hemmer-Hansen, DTU Aqua as co-chair). Again the participants represented both the scientific community and the fishing industry. Genetic results based on data collected following internationally coordinated sampling protocols and analysed under GenDC, formed the basis for much of the discussions and decision making during the workshop.

A more detailed description of the outcomes of the workshops can be found under WP5 section 6.1.

3. Work package 2

The intention of WP 2 was to ensure collection, harmonization and storage of genetic data through the design and implementation of sampling plans and protocols for genetic data collection. In addition, the WP has discussed data compatibility with database hosts to secure effective long-term storage of genetic data and lasting impacts of the GenDC project.

*Lead: Uwe Krumme, Thünen Institute and Julie Olivia Davies DTU Aqua
ICES is involved*

3.1 Communication with survey data providers (WGBIFS and WGIBTS)

The Baltic Sea

International Fish Survey Working Group (WGBIFS) recommended in 2023 that genetic samples of cod should be collected during the Baltic International Trawl Survey (BITS) in the first and fourth quarters. The objective was to distinguish between Western Baltic cod and Eastern Baltic cod in ICES Subdivisions (SDs) 24–26. The recommendation targeted cod already sampled for biological data, including age, length, and stomach content analyses. Based on this recommendation, Denmark and Germany started collecting tissue samples for genetic analysis, however neither country had dedicated funding available at the time to analyse the genetic material.

At the 2024 WGBIFS meeting, representatives from the GenDC project participated and presented the project's objectives. This initiated discussions on establishing a more systematic and standardized approach to genetic sampling across Member States participating in the BITS surveys conducted during the first and fourth quarters in the Baltic Sea.

As an outcome of these discussions, WGBIFS agreed to implement a coordinated sampling scheme during the fourth-quarter survey in 2024 and the first quarter in 2025 (Figure 3.1.1). All participating Member States collected one genetic sample per station and 5-cm length class (e.g. 0–5 cm, 6–10 cm, 11–15 cm, 16–20 cm, etc.). The results from this pilot study were intended to inform future decisions on the geographical scope and intensity of genetic sampling, particularly regarding its application outside SD 24 (ICES, 2024a).

At the 2025 WGBIFS meeting, GenDC project representatives again participated in the survey meeting. Based on the initial findings and feedback from the 2024 sampling exercise, the group agreed to continue genetic sampling of cod and extend the sampling area into SD 25 (Figure 3.1.2). The aim was to investigate whether Western Baltic cod migrate into areas typically inhabited by Eastern Baltic cod and, if so, to estimate the proportion of genetically identified Western Baltic cod within the sampled population.

As of 2026, it was decided that the sampling scheme comprises of two individuals per 5-cm length class and ICES statistical rectangle (ICES 2025).

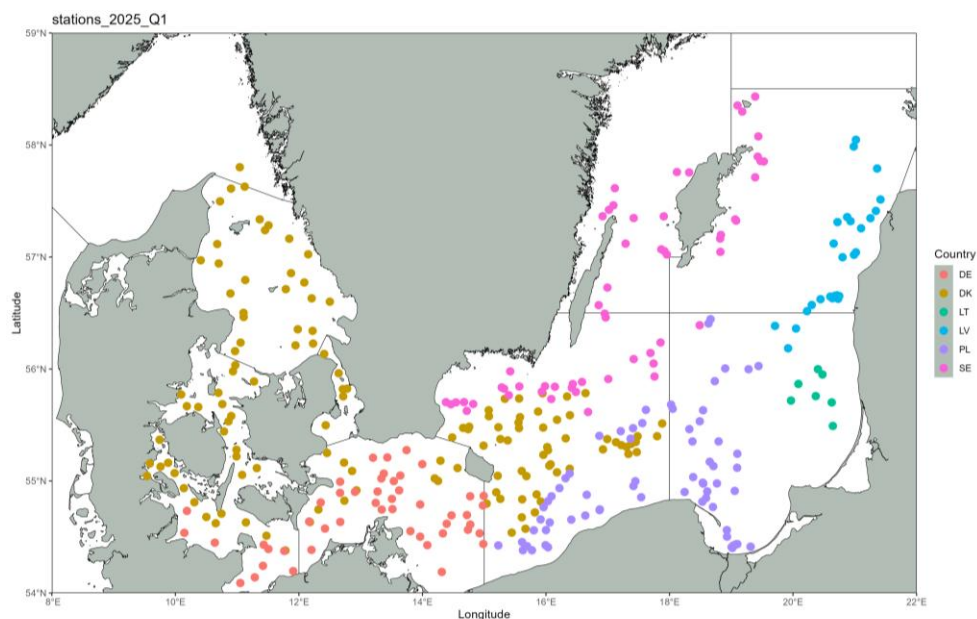


Figure 3.1.1. Station map from the 2025 quarter 1. BITS survey. The first priority sampling area was between 12- and 15-degree longitude. From ICES 2025.

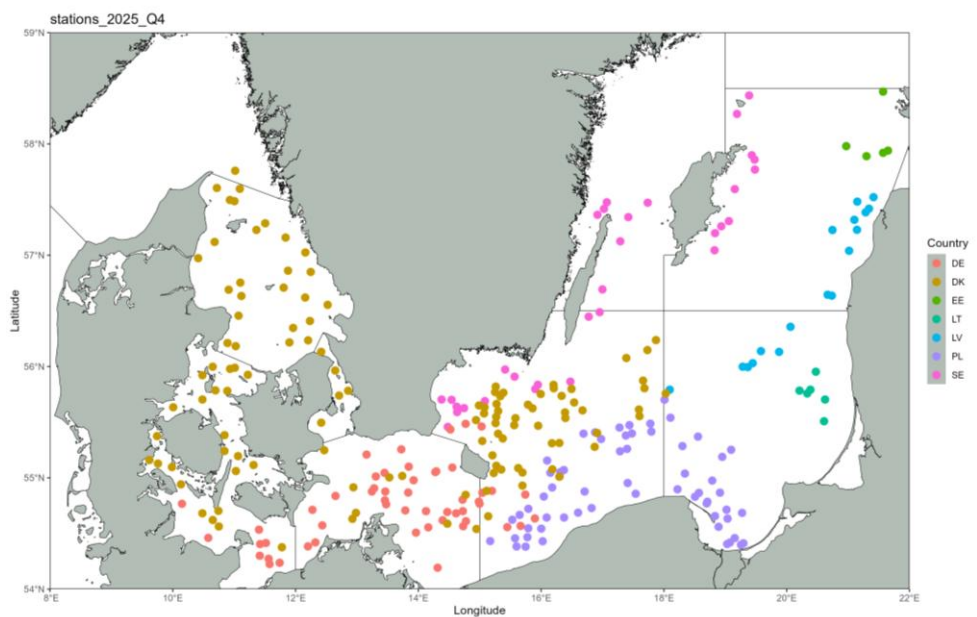


Figure 3.1.2. Station map from the 2025 quarter 4. BITS survey. In the second priority sampling area was extended to 18-degree longitude. From ICES 2025.

The North Sea

The GenDC project was also presented at the 2024 meeting of the International Bottom Trawl Survey Working Group (IBTSWG), where the need for samples from actively spawning cod was highlighted to strengthen the genetic baselines for the proposed northern shelf cod subunits (Northwestern, Viking, and Southern) was highlighted. In response to this call, several IBTS Q1 participants collected tissue samples from actively spawning cod in these subunits during the 2025 and 2026 Q1 surveys as well as 2024 Q3 survey, following the sampling protocol developed within the project (ICES 2026d, ICES 2026e). In addition, several countries had initiated genetic sampling programmes prior to GenDC but lacked funding for genetic analyses. These previously collected samples were therefore also requested and analysed within the project, providing additional data to strengthen the genetic baselines and the robustness of the project results (Figure 3.1.3).

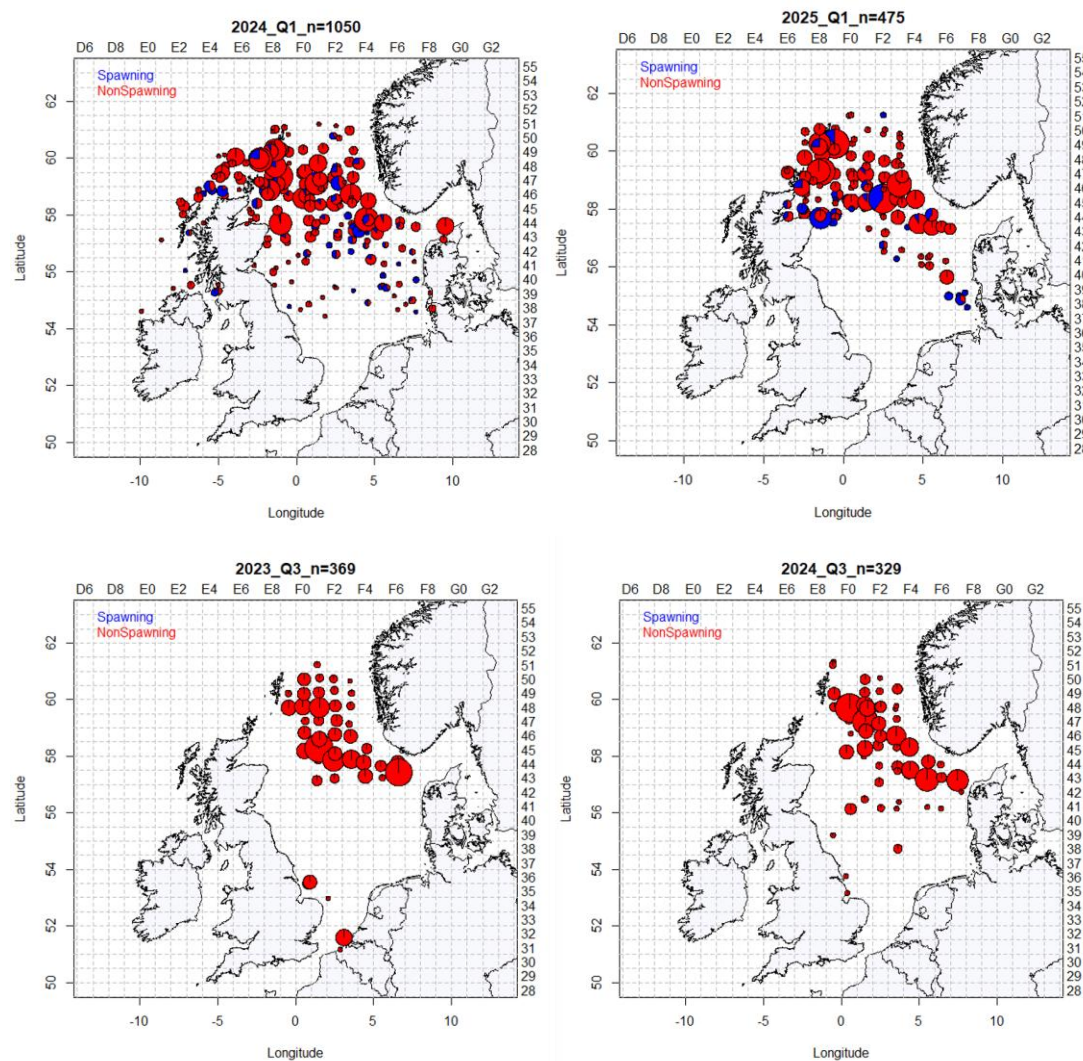


Figure 3.1.3. Samples collected during the IBTS first and third quarter from 2023-2025. Blue indicates if the cod are spawning and red are non-spawning.

3.2 Communication with the assessment groups on end user needs

To ensure that the genetic data collected and analysed aligned with end-user needs, meetings were held with the ICES assessment working group for the Greater North Sea (WGNSSK) and the Baltic Sea (WGBFAS).

The assessment working group for the Greater North Sea (WGNSSK)

The first meeting consisted of an online presentation during the WGNSSK assessment meeting, where the project objectives were presented and feedback was sought on how to secure the most relevant and comprehensive dataset within the available time of the project.

Based on the discussions from the first meeting, a second meeting was organised, inviting all WGNSSK participants with an interest in the cod stock complex. During this meeting, a prioritisation of sampling needs was established, and alternative sources of genetic samples for the highest-priority group, the southern spawning component, were discussed (Figure 3.2.1).

Prioritisation of sampling activities:

1. Spawning cod from the southern component

Collection of all spawning cod encountered during the IBTS survey first quarter survey, within the ICES sub divisions 4c or 7d, was identified as the highest priority. It was further discussed that alternative sources of data, e.g. other surveys or observer programmes could be used as sampling sources.

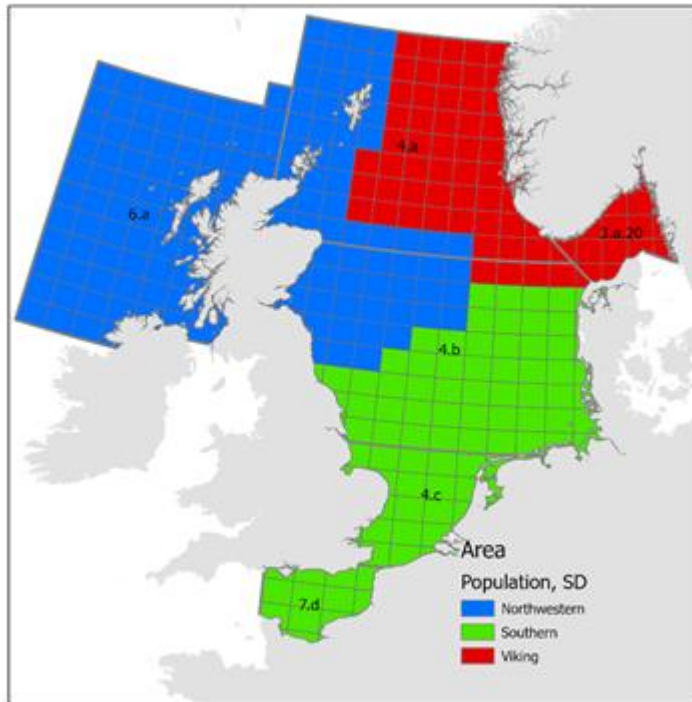


Figure 3.2.1. Northern Shelf cod sub-stock areas. From ICES 2026c.

2. Spawning cod from the Viking and Northwestern components

Sampling of 50 to 100 spawning individuals per area (approximately one fish per cm class per station) was prioritised to strengthen the existing genetic baseline.

Participants discussed whether sufficient numbers of spawning ("running") cod could be sampled during the quarter one IBTS survey. Since baseline development requires samples from spawning fish, it was emphasised that maturity stage information should be recorded for all sampled cod.

In the shorter term, the updated baseline would support mapping the spatial distribution of stock components, for example identifying areas dominated by Viking cod and areas where Viking cod are absent or occur at low proportions in adjacent areas (Northwestern and Southern area).

3. Commercial catches all year round

The third priority was to investigate the distribution and mixing of the three cod subpopulations within commercial catches. This would involve targeted sampling from areas where commercial fishing activity is concentrated. However, during the meeting it was recognised that this objective represents a longer-term priority because it depends on an updated genetic baseline and would require broader sampling to quantify mixing among populations across the entire distribution area, extending beyond the scope of GenDC. It was therefore agreed that work on commercial catch composition should follow the completion of the baseline update and initial distribution mapping.

The assessment working group for the Baltic Sea (WGBFAS)

Cod in the Baltic Sea is assessed and managed as two separate stocks: Eastern Baltic cod and Western Baltic cod. The management areas for the two stocks are ICES subdivisions (SDs) 25–32 for Eastern Baltic cod and SDs 22–24 for Western Baltic cod. However, the assessment areas overlap in SD 24, as there is clear evidence that individuals from both stocks regularly occur in this subdivision (Hemmer-Hansen et al., 2019). Given the differences in biological characteristics between the two stocks, it is important to distinguish Eastern and Western Baltic cod in areas where they co-occur to ensure that catches are assigned to the correct stock for assessment purposes.

Since 2015, the stock assessments for both the Western and Eastern Baltic cod have accounted for this stock mixing in SD 24. Initially, stock assignment was based solely on otolith shape. Since 2019, this approach has been further developed and validated using genetically assigned Baltic cod (Hemmer-Hansen et al., 2019). Stock-specific proportions are estimated separately for different parts of SD 24 to account for the east–west gradient in the relative occurrence of the two stocks (Hüssy et al., 2016).

In recent years, results from the Baltic International Trawl Survey (BITS) have indicated that Western Baltic cod may occur increasingly further east, including in SD 25 and 26. This potential eastward shift is currently not accounted for in the stock assessment, which assumes that stock mixing relevant to the separation of Eastern and Western Baltic cod occurs only within SD 24.

As part of the GenDC project, it was therefore agreed, in consultation with the Baltic assessment working group (WGBFAS), stock assessors, and coordinators, to include genetic sampling of cod during the Baltic International Trawl Survey in SDs 25 and 26. The purpose of this sampling is to test the hypothesis that Western Baltic cod occur further east than currently assumed, and to quantify their contribution to catches in these areas. The results will provide a basis for evaluating whether the current spatial approach to stock separation remains appropriate or should be extended to account for mixing east of SD 24.

3.3 Inclusion in the ICES databases

A key component of the GenDC project has been the collaboration with ICES to develop sustainable long-term solutions for storage and accessibility of genetic information within ICES databases.

By integrating genetic information into existing ICES data flows and databases, such as DATRAS and RDBES, the project supports the needs of stock assessment working groups and the future development of population-informed and multi-stock assessment approaches. The ICES Data Centre hosts and manages commercial and survey sampling data across regions and is therefore fundamental for ensuring the long-term storage and accessibility of the project data, thereby supporting the sustainability of the project beyond its lifetime.

During the early phase of the project, a meeting was organised by the GenDC team with participants from the ICES Data Centre and several ICES governance groups responsible for fisheries databases and data standards, where the aim was to explore how genetic information could be incorporated into existing ICES databases, while ensuring consistency with established data structures, reference vocabularies, and principles for open and accessible data. As the ICES Vocabulary Server already contains the controlled vocabulary GeneticPopulation it was agreed to use this vocabulary across other relevant ICES databases, including DATRAS, SmartDots, RDBES and the Egg and Larvae Database. It was also agreed that a numerical measure of assignment certainty should be recorded alongside the population assignment to reflect the probability of an individual belonging to a particular population or stock. To support the linking of genetic information and biological observations across ICES databases, a unique fish identifier (FishID) is required, with responsibility for maintaining its uniqueness resting with the data provider.

In addition to storing genetic population assignments, it is important to document how these assignments were produced. GenDC built on work initiated by the ICES Second Workshop on the Allocation of Catches of Herring Stocks (WKSIDAC2), which developed a framework for describing genetically identified herring populations. This framework includes a unique population code (i.e. GeneticPopulation), a description of each genetic population, and information on the samples used to establish the genetic baseline (ICES, 2024b). GenDC adapted this approach for Atlantic cod and compiled corresponding descriptions for cod populations, including information on the location and timing of baseline sampling, as well as references to the genetic methods and genomic resources used. Information on where to find the genotype method/panel and the whole-genome resources are also included. These population descriptions (Table 3.3.1) will support the integration of cod populations into the ICES GeneticPopulation vocabulary (<https://vocab.ices.dk/?codetypeguid=a350e6dc-b5c3-41db-91bc-db0736eb743d>) and help ensure transparency and consistency in the use of genetic information. The full table including temporal and spatial information on the baseline sampling, references to the genetic methods and genomic resources used, can be found in Annex 1 (Table 1.1).

Table 3.3.1 Cod genetic populations described.

Genetic Description	GeneticCode	Location baseline samples
Genetic analysis was performed but results were inconclusive	cod_000	
Viking Cod (Gadus Morhua) in the Northern North Sea and Skagerrak	cod-001	Northern North Sea and Skagerrak
Southern Cod (Gadus Morhua) in the Southern North Sea and English Channel	cod-002	Southern North Sea and English Channel
Northwestern Cod (Gadus Morhua) in the Central North Sea and West of Scotland	cod-003	Central North Sea and West of Scotland
Cod (Gadus Morhua) in ICES SD 21-24	cod-004	Kattegat to Western Baltic Sea
Eastern Baltic Cod (Gadus Morhua) in the Eastern Baltic Sea	cod-005	Eastern Baltic Sea

3.4 Drafting the sampling plan (D2.1)

Genetic baseline

A genetic baseline must be established prior to any routine sampling aimed at investigating stock mixing proportions within specific management areas. The baseline serves as a reference dataset that characterizes the genetic signatures of the source populations to which future tissue samples from fish of unknown origin can be compared.

The baseline samples should be collected from spawning individuals (ICES maturity codes C, Ca and Cb (ICES, 2018) within the core area of each stock component during the spawning season. This approach is based on the assumption that many fish species exhibit pronounced natal homing or spawning site fidelity, meaning that a substantial proportion of individuals return to their area of origin to reproduce. Such behaviour has been documented, for example, in Atlantic cod (Skjæraasen et al., 2011, Zemeckis et al., 2014) and Western Baltic spring spawning herring (Moll et al., 2025).

Consequently, tissue sampling for the establishment of a genetic baseline should target the spatial and temporal window in which a specific stock component is known to reproduce. Samples should be representative of the respective sub-population. A minimum of 50 individuals is recommended, and to reduce sampling bias, the baseline should be as balanced as possible in terms of sex, size or length classes, and geographic coverage within the spawning area. Ideally, sampling should extend over more than one year and the temporal stability of the baseline should be evaluated at regular intervals.

Additional considerations and current challenges associated with establishing a genetic baseline for the three North Sea cod stock components are summarized in ICES, 2026a.

One objective of this project was the establishment of a genetic baseline for the Southern component of the Atlantic cod in the North Sea. Samples were collected in ICES Divisions 4b and 4c, as well as Division 7d (eastern English Channel), during Quarter 1 through the International Bottom Trawl Survey (IBTS) and other relevant scientific survey programmes. Where feasible, additional samples were obtained through fisheries observer programmes.

Cruise leaders participating in the surveys were instructed to prioritize the sampling of spawning (“ripe-and-running”) individuals across all survey areas in order to ensure representative coverage of the Southern, Viking, and Northwestern cod stock components and to support the establishment of a robust genetic baseline for reliable stock assignment. This prioritization reflected the urgent need to establish a genetic baseline for reliable assignment of individuals to the three cod stock components. This guidance was distributed together with a standardized sampling protocol (Section 3.6). Following completion of the surveys, cruise leaders submitted the tissue samples together with associated biological information and metadata, including capture location and sampling date. Where national sampling capacities allowed, additional non-spawning individuals were also collected to establish supplementary material for future analyses and potential baseline refinement.

In the Baltic Sea, baseline sampling for Western and Eastern Baltic cod had already been conducted prior to the GenDC project (Hemmer-Hansen et al., 2019, Weist et al., 2019), allowing stock assignments to be performed using these existing baseline datasets. However, further genetic sampling was conducted as described in section 3.2.

Sampling strategies for stock mixing analyses

To determine the mixing proportions of sub-stocks within a management area, dedicated sampling strategies are required for both (a) scientific surveys covering the management area and (b) catches originating from commercial fisheries operating within that area.

Surveys

In many stock assessments, data from both the scientific surveys and the commercial fishery are available and used. Depending on the type of assessment, it may therefore be important to include samples from only one source or both.

However, it is not always appropriate to assume that patterns observed in survey data are representative of the commercial fishery. Scientific surveys are typically conducted during a limited time window – for example, in the first quarter for the IBTS survey – when fish are at or migrating to their spawning grounds. This period may not accurately reflect the timing or composition of the commercial fishery throughout the year.

The international, fishery-independent surveys are coordinated through working groups of the International Council for the Exploration of the Sea (ICES). In the Baltic Sea, the Baltic International Fish Survey Working Group (WGBIFS) is responsible for the planning, coordination, and implementation of demersal trawl and hydroacoustic surveys. The equivalent body for demersal surveys in the North Sea is the International Bottom Trawl Survey Working Group (IBTSWG).

Within the GenDC project, genetic samples (fin clips) were collected during the North Sea International Bottom Trawl Survey (IBTS) as well as during other relevant North Sea survey programmes (ICES 2026a). Sampling included both tissue samples (fin clips) for genetic analyses and otoliths (for complementary stock identification analyses using otolith shape analysis).

Data sampled in quarter 3 on the IBTS survey can be used in the North Sea cod stock assessment model to test the mixing proportion outside the spawning period.

In the Baltic Sea, fin-clip samples of cod have been collected since 2019. As of 2026, the sampling scheme comprises two individuals per 5-cm length class and ICES statistical rectangle (ICES 2025).

Commercial catches

Sampling commercial catches is generally more complex than sampling during scientific surveys. In scientific surveys, hauls typically represent the primary sampling unit, and sampling locations are predetermined to provide representative spatial coverage of the entire area of interest. In contrast, commercial catch sampling is constrained by fishing operations and fleet dynamics. In this context, fishing vessels or fishing trips usually constitute the primary sampling units, while hauls are nested within trips and trips are nested within vessels. Consequently, the resulting sampling design is hierarchical, and estimation procedures should account for this multi-stage sampling structure.

A key requirement for sampling commercial catches is to ensure adequate temporal and spatial coverage of the fisheries operating within the management area. The sampling design should therefore

account for variation among seasons, fishing grounds, fleets, and métiers in order to produce representative estimates of sub-stock composition. In particular, sampling effort should be distributed to ensure sufficient coverage of the time-area strata in which the main part of the fishery is conducted.

When establishing a new sampling scheme, it is essential to clearly define the objectives of the programme and identify the parameters of interest. A short-term objective, directly relevant for fisheries management and advisory processes, could be the partitioning of national and international catch weight among sub-stocks. A longer-term objective would be the estimation of catch numbers-at-age by sub-stock for incorporation into analytical stock assessments. The latter objective requires substantially more detailed biological sampling and, consequently, larger sample sizes to achieve comparable levels of precision.

As is standard practice in the development of new sampling programmes, an initial pilot survey should be conducted to test sampling protocols, evaluate logistical feasibility, and generate preliminary estimates of the parameters of interest. These pilot data can subsequently be used to evaluate sampling variance and determine the sample sizes required for a statistically robust operational sampling scheme.

Following the pilot phase, the preferred long-term approach would be the implementation of a coordinated regional sampling programme involving the principal nations exploiting cod within the management area. Such a programme should be based on standardized ICES sampling protocols to ensure comparability among datasets, while still allowing sufficient flexibility to accommodate national sampling frameworks and logistical constraints. Further methodological and organizational work is required to develop and implement such a coordinated scheme. In particular, national data submitters need to be closely involved in the estimation procedures for catch numbers-at-age by sub-stock and linked directly to the relevant experts from the stock assessment working groups.

Practical considerations

An efficient and logistically straightforward approach for obtaining genetic samples is the collection of tissue from commercial landings at fish markets or landing sites. However, a major limitation of this method is the relatively low spatial resolution of the associated catch information. In most cases, the fishing location can only be resolved to the level of an ICES statistical rectangle, resulting in the loss of detailed positional information on where individual cod were actually caught.

An alternative approach is the collection of samples directly onboard commercial fishing vessels, either by scientific observers or by trained industry personnel, such as vessel crew members. Onboard sampling offers several important advantages. First, samples can be obtained from the entire catch rather than only from the landed fraction, thereby reducing potential sampling bias arising from discarding or sorting practices. Second, detailed spatial and temporal information on fishing operations can be recorded, including haul positions, fishing depth, and timing.

Many sampling programmes, whether conducted from the landings (e.g., harbours or fish auctions) or directly onboard fishing vessels through observer programmes, already apply protocols specifying the collection, e.g., of 1 fish per length group and haul, box, or trip. Such approaches help ensure that sampling is distributed across both time and space and remains representative of the fishery. In addition, because these individuals are often already sampled for biological data such as length, weight and otoliths, the additional effort required for genetic sampling is minimized.

In some cases, however, these protocols may result in a larger number of genetic samples than necessary, particularly given the still relatively high cost of genetic analyses. To optimize sampling efficiency, the intensity may be reduced, for example, to 1 fish per 5 cm length class. In general, it is preferable to collect a smaller number of fish from a larger number of trips as this improves the representativeness of the dataset, rather than many fish from the same haul or sampling cluster. The deployment of scientific observers specifically for genetic sampling would likely be costly if implemented through a dedicated programme. However, integration into existing observer schemes could provide a cost-efficient solution. An additional advantage of observer-based sampling is that the genetic information could be directly linked to biological sampling data collected on the same trips, thereby enabling the partitioning of catch-at-age data by sub-stock within stock assessments. Industry-based sampling programmes may provide substantially larger sample sizes and broader fleet coverage. Nevertheless, such programmes require clear training procedures, quality assurance measures, and regular monitoring to ensure consistency and reliability of the collected samples and associated metadata. In addition, direct integration with catch-at-age estimation procedures is generally more difficult compared to observer-based sampling.

Regardless of whether samples are collected by scientific observers or vessel crew members, standardized and unambiguous sampling protocols are essential. These protocols should specify, among other aspects, the type and preparation of sampling tubes (e.g., pre-filled with ethanol or other preservatives), the required size and type of tissue sample, labelling conventions, metadata recording procedures, and appropriate sample storage and transport conditions to ensure sample integrity for subsequent genetic analyses.

In the Baltic Sea, ICES Subdivision 24 (Arkona Sea) is recognized as an important mixing area for Western and Eastern Baltic cod stocks. During the meeting of the Baltic International Fish Survey Working Group (WGBIFS) in March 2024, it was agreed to systematically investigate the extent to which mixing between the two Baltic cod populations also occurs outside Subdivision 24.

As part of this initiative, all participating member states collected genetic samples of cod during the Baltic International Trawl Survey (BITS) in Quarter 4 of 2024. The agreed sampling protocol required the collection of at least one genetic sample per station and per 5-cm length class (e.g., 0–5 cm, 6–10 cm, 11–15 cm, 16–20 cm, etc.) (ICES 2025). This sampling design was intended to provide representative spatial and size-specific coverage across the survey area.

The results of this study will be used to evaluate the spatial extent of stock mixing and to determine whether routine genetic sampling should also be implemented in Baltic Sea areas outside ICES Subdivision 24.

The most recent version of the sampling protocol is provided in the next section.

3.5 Drafting the sampling protocol and the feedback loop (D2.2)

A key objective of GenDC was the development of a standardized genetic sampling protocol to support the routine collection of genetic material within existing fisheries data collection programmes. The protocol was designed to harmonize procedures for tissue collection, preservation, labelling, storage, and metadata recording, thereby ensuring consistent data quality and supporting future integration of genetic information into fisheries stock assessment and management frameworks.

The protocol was developed through a stepwise and collaborative process. An initial draft was prepared based on established sampling procedures from DTU Aqua and the Thünen Institute of Baltic Sea Fisheries, supplemented by experience and documentation from international initiatives including TABACOD and AquaGen. In parallel, a simplified standardized data format based on DATRAS was developed to facilitate future integration of genetic information into ICES databases and workflows.

Stakeholder engagement formed a central part of the protocol development process. The draft protocol was distributed to national DCF correspondents, survey coordinators, and relevant partner institutions involved in the IBTS and BITS surveys. Practical implementation during the IBTS Q1 2025 survey provided an opportunity to evaluate the protocol under operational survey conditions and establish a feedback loop with end users. Comments and recommendations received from sampling personnel were used to refine the protocol and improve its clarity and usability. Updates included expanded guidance on the collection of different tissue types (Figure 3.5.1), additional options for sample storage and labelling, and the inclusion of more detailed visual material illustrating sampling, handling, and preservation procedures.



Figure 3.5.1. Procedure to follow when taking a tail fin clip ([Protocol for genetic sampling. GenDC project](#)).

The protocol subsequently underwent review by two dedicated ICES workshops, WKCODSCOPE and WKCODSAMPLING. Both workshops emphasized that standardized sampling procedures are essential if genetic samples collected by different countries, surveys, observers, and fleets are to be comparable and suitable for assessment purposes. Particular importance was placed on maintaining adequate tissue sample size, appropriate storage conditions, robust labelling systems (Figure 3.5.2), and procedures that minimize contamination risk.

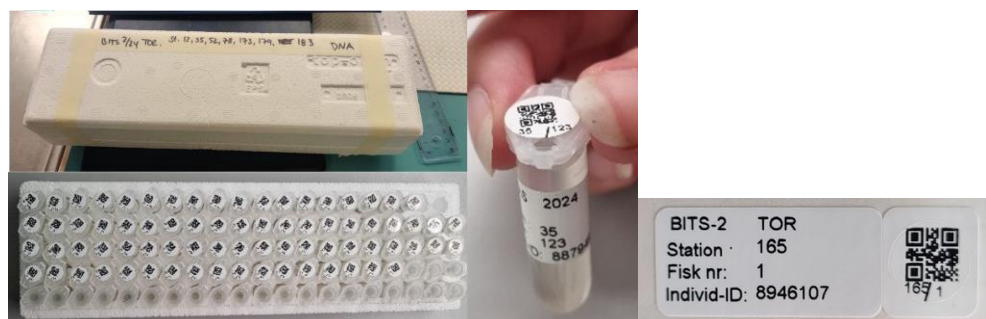


Figure 3.5.2. Labelled sample tube with QR code for reliable identification and data linkage ([Protocol for genetic sampling, GenDC project](#)).

Importantly, both workshops identified the protocol as a robust, flexible, and scalable framework for genetic data collection. While originally developed for fisheries-independent surveys, the protocol was considered readily transferable to pilot studies and commercial sampling programmes.

WKCODSAMPLING specifically concluded that the protocol can serve as a common foundation for coordinated genetic sampling across countries and sampling platforms, while remaining sufficiently flexible to accommodate national priorities, existing data collection systems, and operational requirements in commercial fisheries. The workshop further recommended continued use of the protocol in research surveys and recognized its value as the basis for future fisheries-dependent sampling initiatives.

Through this iterative process of development, testing, stakeholder consultation, and independent review, the GenDC sampling protocol ([GENDC](#)) has evolved into a standardized and widely endorsed framework that supports both current genetic baseline development and the longer-term implementation of coordinated genetic monitoring programmes across Europe

3.6 Data management plan (D2.3)

A Data Management Plan was developed for GenDC to ensure that research data generated and used within the project are well documented, standardized, discoverable, accessible, interoperable, and reusable, in line with FAIR data principles. The plan covers all data collected, processed, used, or stored within GenDC and defines procedures for data documentation, quality assurance, access, licensing, long-term preservation, and compliance with the General Data Protection Regulation (GDPR).

Three main types of research outputs are covered by the plan: (1) Update of the genetic baseline data for cod populations, including the new genetic baseline for the southern component of the Northern shelf cod; (2) individual genetic assignment results for cod sampled during scientific surveys and commercial fisheries, including information on population origin and assignment certainty; and (3) software developed to incorporate genetic stock-composition information into the multi-stock State-space Assessment Model (SAM).

A central objective of GenDC was to ensure that genetic information could be integrated into existing fisheries data infrastructures rather than being maintained in stand-alone project databases. In collaboration with ICES, data structures and terminology were therefore developed to accommodate genetic information within established ICES systems. The aim was that genetic population and quantitative assignment certainty could be incorporated alongside existing biological and fisheries information. Genetic results from scientific surveys are made available through ICES DATRAS, while corresponding information from commercial fisheries is stored in the Regional Database and Estimation System (RDBES), subject to ICES access policies. The genetic baseline is documented

through appropriate metadata describing, among other information, sampling location and period, population, species, genetic methodology, contact institution, and whole-genome resources.

GenDC follows an open access data approach wherever legally and technically possible. Individual assignment results from surveys are made publicly accessible through DATRAS and can be downloaded in standard formats such as CSV. Whole genome data are not deposited directly in ICES databases because these infrastructures are currently not designed for storage of whole genome datasets, these data can instead be made available to researchers upon request. Software developed within the project is openly available as R code through the project's multi-stock SAM GitHub repository. Project outputs are licensed under CC BY 4.0, where applicable.

https://github.com/calbertsen/multi_SAM/tree/F_TAC.

Interoperability and data quality were addressed throughout the project. GenDC worked with end users and ICES to align terminology and data structures with existing ICES vocabularies and database standards. Standardized sampling protocols were developed to ensure consistent collection, processing, documentation, and storage of genetic samples and associated biological information. These protocols, together with documentation of the genetic methodology and assignment procedures, support both reproducibility and future application of the approach to other stocks, species, and DCF sampling programmes.

Long-term accessibility is supported by storing project results within established ICES data infrastructures, which provide professional data management, curation, backup, and recovery procedures. Data stored in these systems are expected to remain accessible and reusable for at least 10 years. ICES was subcontracted within GenDC for data management activities, including development of standardized formats compatible with existing ICES systems. The genetic fisheries data generated by GenDC are not considered sensitive personal data.

Overall, the data management approach developed in GenDC provides a pathway for moving genetic information from individual research projects into routine European fisheries data collection and stock assessment workflows, thereby supporting both the immediate use of GenDC results and their continued reuse beyond the lifetime of the project.

4. Work package 3

Genetic analyses to determine population of origin and distribution of populations.

Lead: Jakob Hemmer-Hansen, DTU Aqua

4.1 Detailed description of the baseline (D.3.1)

The genetic baseline in GenDC is split into two separate cases: one for the Northern shelf cod stock and one for the combined analyses of samples from the Kattegat, Western Baltic Sea and Eastern Baltic Sea. The Northern shelf cod baseline was updated with extensive collection and genome sequencing of spawning cod from the North Sea and neighbouring areas, as described in (ICES 2026b), while the existing baseline for Kattegat to the eastern Baltic cod presented in (Hemmer-Hansen et al., 2020) was deemed sufficiently powerful for the purpose of providing information for stock assessments in these areas. Consequently, while the existing baseline data file for Kattegat to the Baltic Sea consists of only 187 genetic markers, the new data for the Northern shelf complex has 2.970.268 genetic markers and is hence not reported in detail in D3.1.

Northern shelf baseline (see ICES 2026b for additional details)

Tissue samples of cod in spawning condition (maturity stage “running”) were collected in quarter 1, primarily on the IBTS in 2024 and 2025 and supplemented with additional samples collected by GenDC participants and external collaborators from previous years to increase sample sizes. The supplementation was needed because early status of GenDC sample collection revealed challenges with obtaining sufficiently large sample sizes, particularly in the southern parts of the North Sea. The samples sequenced within GenDC were supplemented with publicly available whole-genome sequencing data from Barth et al., (2019) and unpublished sequence data available at DTU Aqua to both increase sample sizes within the North Sea and to include additional reference populations to facilitate Northern shelf area genetic patterns. The data source and geographical origin of sequenced samples are shown in Table 4.1.1.

Table 4.1.1. Available samples with genome sequencing data (from ICES 2026b).

Area	Sample size	Sample/data source
Baltic Sea	32	Barth et al., 2019; DTU Aqua unpublished data
Celtic Sea	6	GenDC (Marine Institute, Ireland)
English Channel	6	GenDC (DTU Aqua samples/unpublished data)
Fjord (Skagerrak)	27	Barth et al., 2019
Irish Sea	10	GenDC (Marine Institute, Ireland)
Kattegat	66	GenDC (DTU Aqua samples); Barth et al., 2019; DTU Aqua unpublished data
Northwestern total	51	
- “Historical”	10	DTU Aqua samples/unpublished data (2002/2003)
- “Contemporary”	41	GenDC (IBTS/SCOWCGFS samples from GER, NL, SCT; 2024/2025)
Norway	20	Barth et al., 2019

Area	Sample size	Sample/data source
Southern total	105	
- “Historical”	24	Barth et al., 2019 (2002)
- “Contemporary”	81	GenDC (IBTS samples from GER, NL, DK. BE samples; 2014-2025)
Viking total	40	
- “Historical 2002”	11	DTU Aqua samples/unpublished data (2002/2003)
- “Historical 2007”	14	Institute of Marine Research, Norway (2007)
- “Contemporary”	15	GenDC (IBTS samples from NO; 2024/2025)
Total	363	

With the extension of the project, it was possible to organise the collection of further samples from monitoring cruises in quarter 1, 2026 (Table 4.1.2). These will be used to further strengthen the baseline genomic information through additional sequence data.

Table 4.1.2. Tissue samples collected in quarter 1, 2026, for further strengthening of the Northern Shelf genetic baseline.

Country	Number of tissue samples
Norway	152
Denmark	59
Germany	180
France	51
Netherlands	33
Scotland	122
Belgium	12
Total	610

All samples collected and sequenced within GenDC were genome re-sequenced at medium to high depth (average 30X after data filtering) using Illumina PE150 sequencing. These data were merged with publicly available data from Barth et al., (2019) where samples were on average sequenced at lower depth (app. 10X, compared to app. 30X in the GenDC samples). We used a genotype imputation approach to merge the two data sets. After data filtering, 2.970.268 genetic markers were used for assessing population structure while a data set with 7.396.258 genetic markers was used for a denser

marker set for estimating local differentiation across the genome (see ICES 2026b for details on methodology and data filtering).

Kattegat, western Baltic and eastern Baltic baseline (see Hemmer-Hansen et al., 2020 for additional details)

The baseline used in the transition zone between the North Sea and eastern Baltic consists of three genetic “reporting groups”: “North Sea”, “Kattegat” and “Eastern Baltic”. With this baseline, it is not possible to differentiate between the three Northern shelf sub-stocks. Likewise, spawning individuals from ICES SD21-SD24 (spring) are pooled into the “Kattegat” reporting group, since genome sequencing data has found that spawning cod in these areas are genetically similar (Hüssy et al., 2024). The number of individuals included in the baseline are shown in Table 4.1.3. Consequently, the baseline represents the three main genetic groups known to occur in the geographic area from the Kattegat to the eastern Baltic Sea.

Table 4.1.3. from Hemmer-Hansen et al., 2020.

Table 1. Baseline individuals collected for genetic analyses

Sample	Sample size
<i>North Sea</i>	213
2002 North Sea "Viking"	98
2003 North Sea "Dogger"	45
2014 Q01 North Sea "Dogger" (DK IBTS)	18
2016 Q01 North Sea "Viking" (DE IBTS)	3
2016 Q01 North Sea "Viking" (NO IBTS)	49
<i>Kattegat/transition zone</i>	293
2004 Kattegat (SE)	48
2015 Kattegat (DK)	75
1997 Oresund (DK)	45
2003 Oresund (DK)	45
1996 Western Baltic (DK)	45
2012 Western Baltic (DK)	35
<i>Eastern Baltic</i>	80
1997 Eastern Baltic (DK)	40
2007 Eastern Baltic (DK)	40

4.2 Kattegat to the eastern Baltic

Within GenDC we compiled the genetic data time series of cod samples from different ages and time points, to estimate mixing in the Kattegat area for use in an updated stock assessment taking stock mixing into account (see WP4). The available time series was supplemented with genetic analyses of new samples to cover data gaps identified by needs from stock assessments (Table 4.2.1).

Table 4.2.1. Samples of cod with genetic information compiled and provided as input to improved stock assessments of cod in the Kattegat. GenDC analysed samples were selected for genetic assignment (D 3.2).

Year	Type of sample	Number of available and analysed genetic samples	GenDC analysed samples
1986	Otolith	68	
1992	Otolith	59	
1996	Tissue	47	
1998	Otolith/tissue	61/78	
1999	Otolith	85	
2001	Otolith	53	
2002	Otolith	90	
2005	Otolith	107	
2006	Otolith	106	
2008	Tissue	92	
2010	Otolith	59	
2011	Otolith	165	
2012	Otolith	79	
2013	Otolith/tissue	54/251	
2014	Otolith/tissue	80/93	
2015	Otolith/tissue	92/604	
2016	Tissue	679	24
2017	Tissue	383	
2018	Tissue	260	66
2019	Tissue	316	47
2020	Tissue	328	34
2021	Tissue	179	23
2022	Tissue	120	15
2023	Tissue	174	34
Total		4762	243

In addition, we analysed cod samples collected across the full transition zone from SD21 to SD25, including an examination in 2925 of population mixing outside of the main expected mixing zones in SD21 and SD24 (Table 4.2.2 and Figure 4.2.1). These samples were sub-selected for genetic analyses, using the Kattegat, western Baltic and eastern Baltic baseline described in section 4.1.

Table 4.2.2. Samples from 2023 used to estimate mixing in the full transition zone from the Kattegat to the western Baltic Sea. A total of 433 of these samples were selected for genetic assignment (D 3.2).

Area	Samples collected in 2023
SD21	174
SD22	173

SD23	164
SD24	157
Total	668

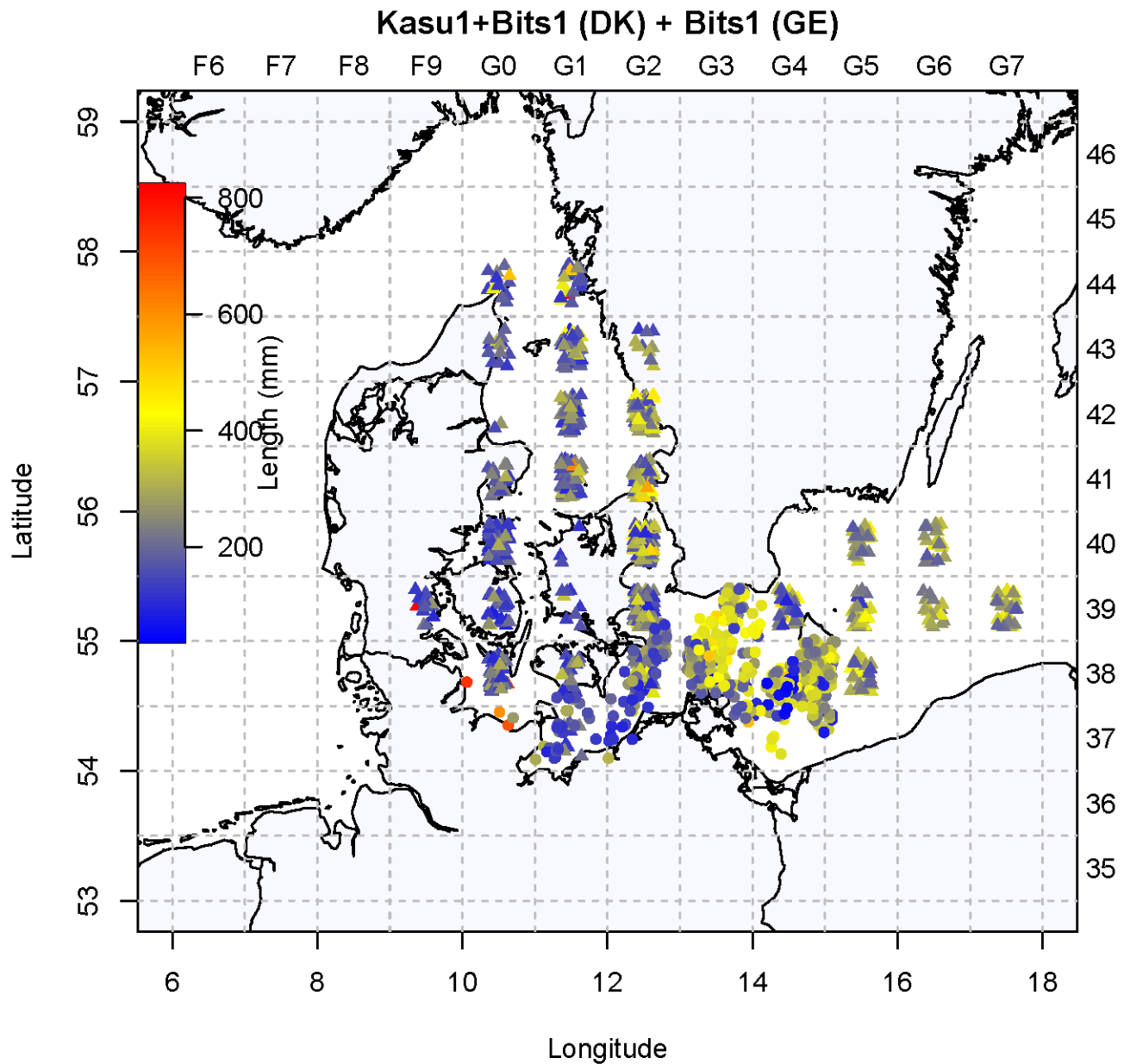


Figure 4.2.1. Samples (total of 1493 samples) collected in 2025 across the transition zone. Samples collected by Denmark and Germany are shown as triangles and circles, respectively. A total of 345 of these samples were selected for genetic assignment (D 3.2).

Genetic assignment methodology followed (Hemmer-Hansen et al., 2020), where individual fish were assigned to the most likely baseline population based on genotype likelihoods, following the method in Rannala and Mountain (1997) through the programme GeneClass2 (Piry et al., 2004; see Hemmer-Hansen et al., 2020 for further details on the assignment method, including assessment of marker panel assignment power).

The results from the genetic assignment analyses showed mixing in ICES SDs 21 (Kattegat) and SD24 (Arkona basin) in particular, while mixing was limited outside these regions (SD 22 and SD 25) (Figures 4.2.2 and 4.2.3). This follows earlier findings [Hüssy et al., 2024] but extends the geographical focus from earlier work into the eastern Baltic Sea.

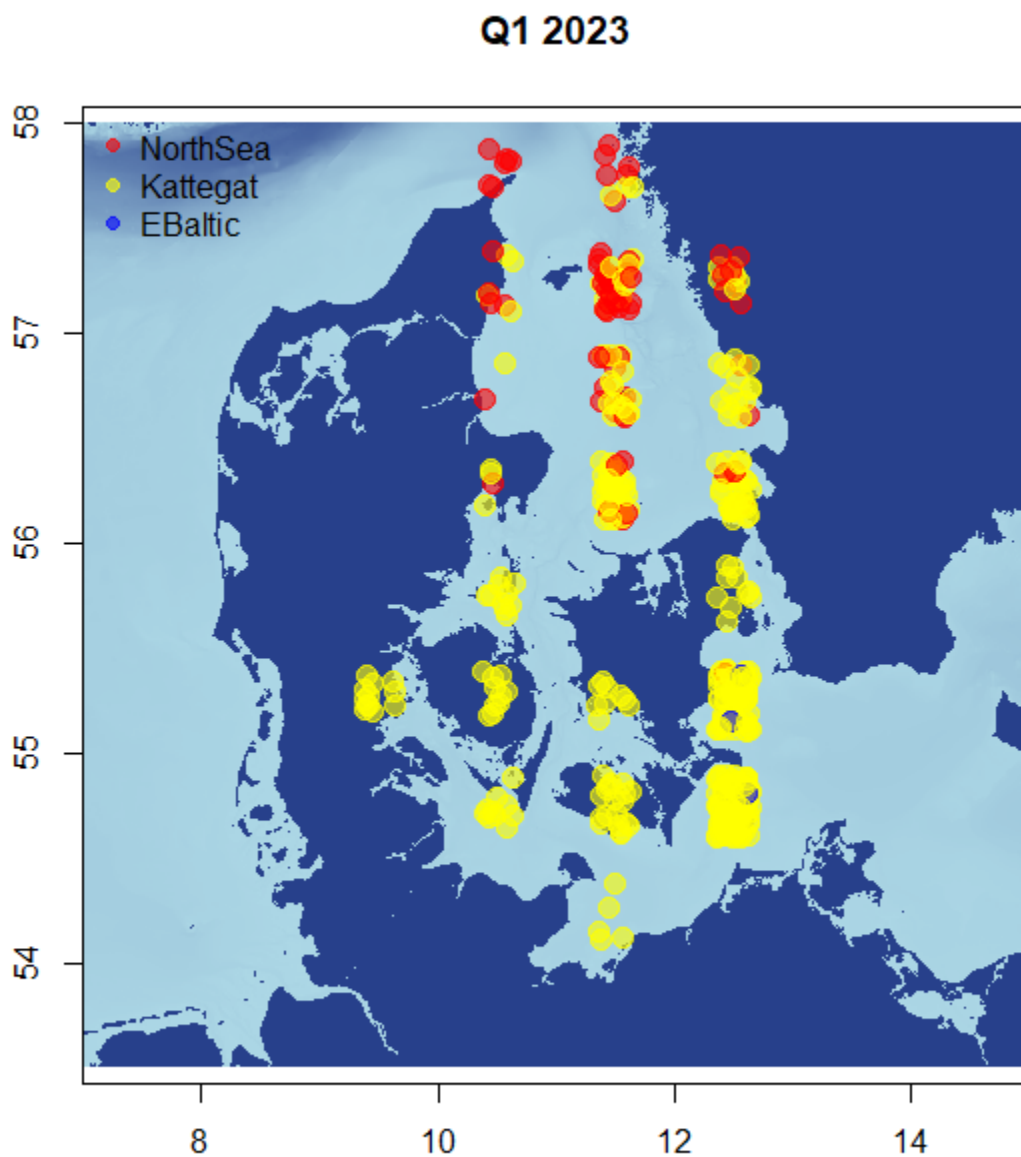


Figure 4.2.2. Genetic assignment of cod collected in the transition zone in 2023. One circle corresponds to one fish, and the colour corresponds to the most likely baseline population based on the individual genetic profiles. (D3.2).

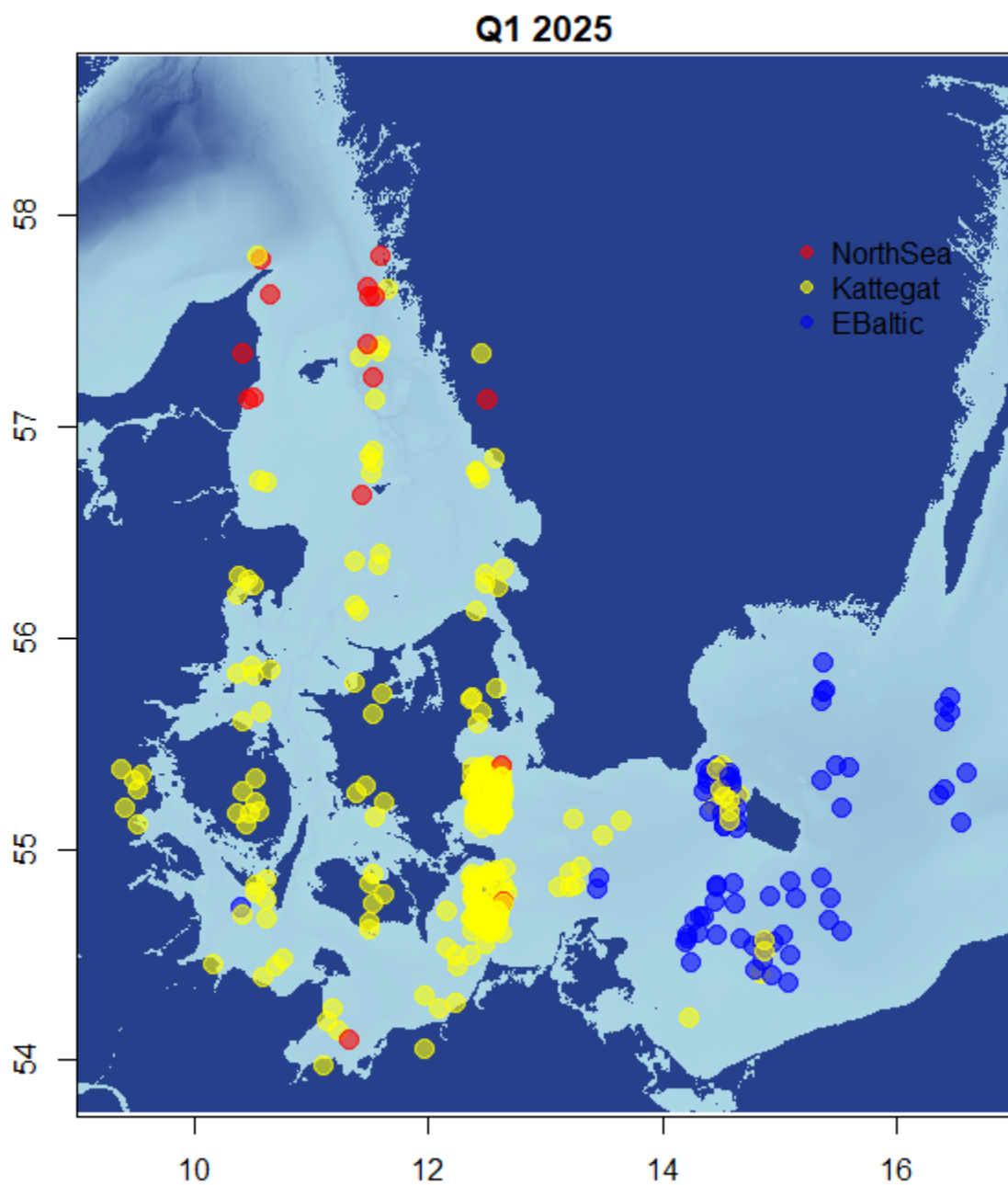


Figure 4.2.3. Genetic assignment of cod collected in the transition zone in 2025. One circle corresponds to one fish, and the colour corresponds to the most likely baseline population based on the individual genetic profiles. (D3.2).

4.3 Northern shelf stock complex

Results from the genome sequencing demonstrated genetic differences between the three areas within the Northern Shelf stock complex. Differences were evident across the genome as well as in localized genomic regions known as inversions (Figure 4.3.1 and ICES, 2026b). Importantly, the results demonstrated a unique genetic profile in the Southern North Sea (Figure 4.3.2), an essential prerequisite for further development of a genetics-based tool to support stock assessment and advice in the Northern shelf stock complex.

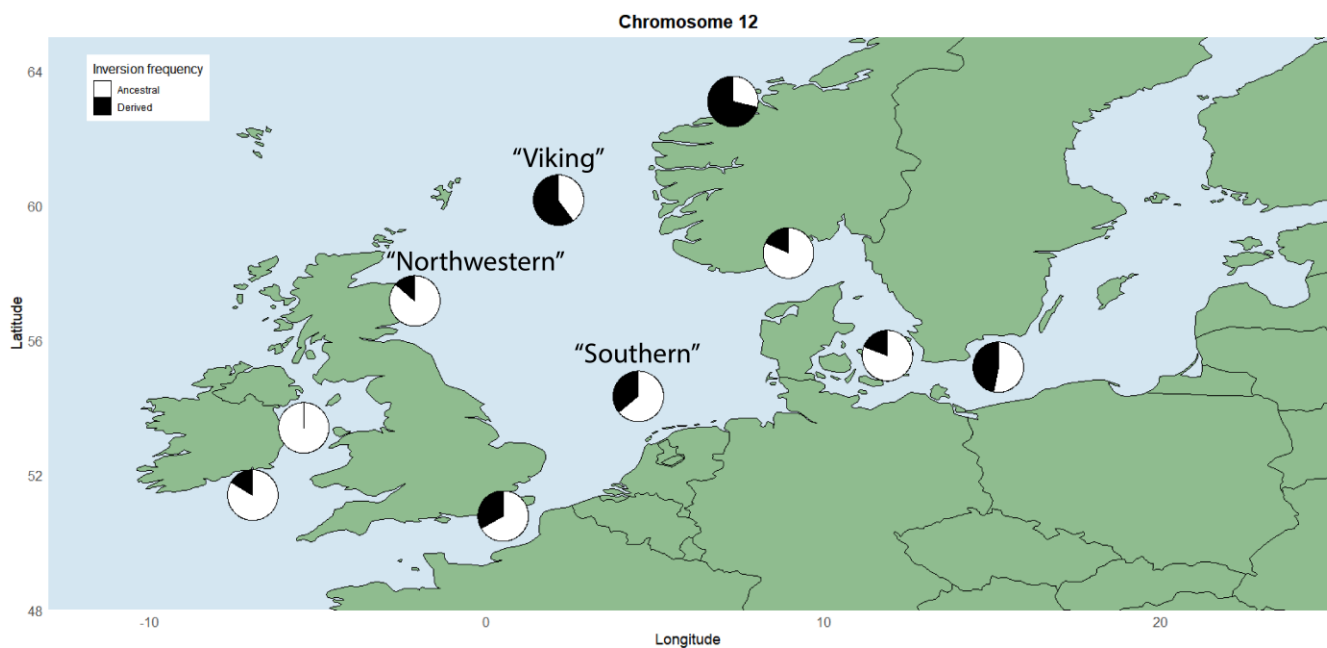


Figure 4.3.1. Inversion allele frequencies in chromosomes 12. Southern, North-western, and Viking are represented as approximate geographical locations on the map. (D3.2).

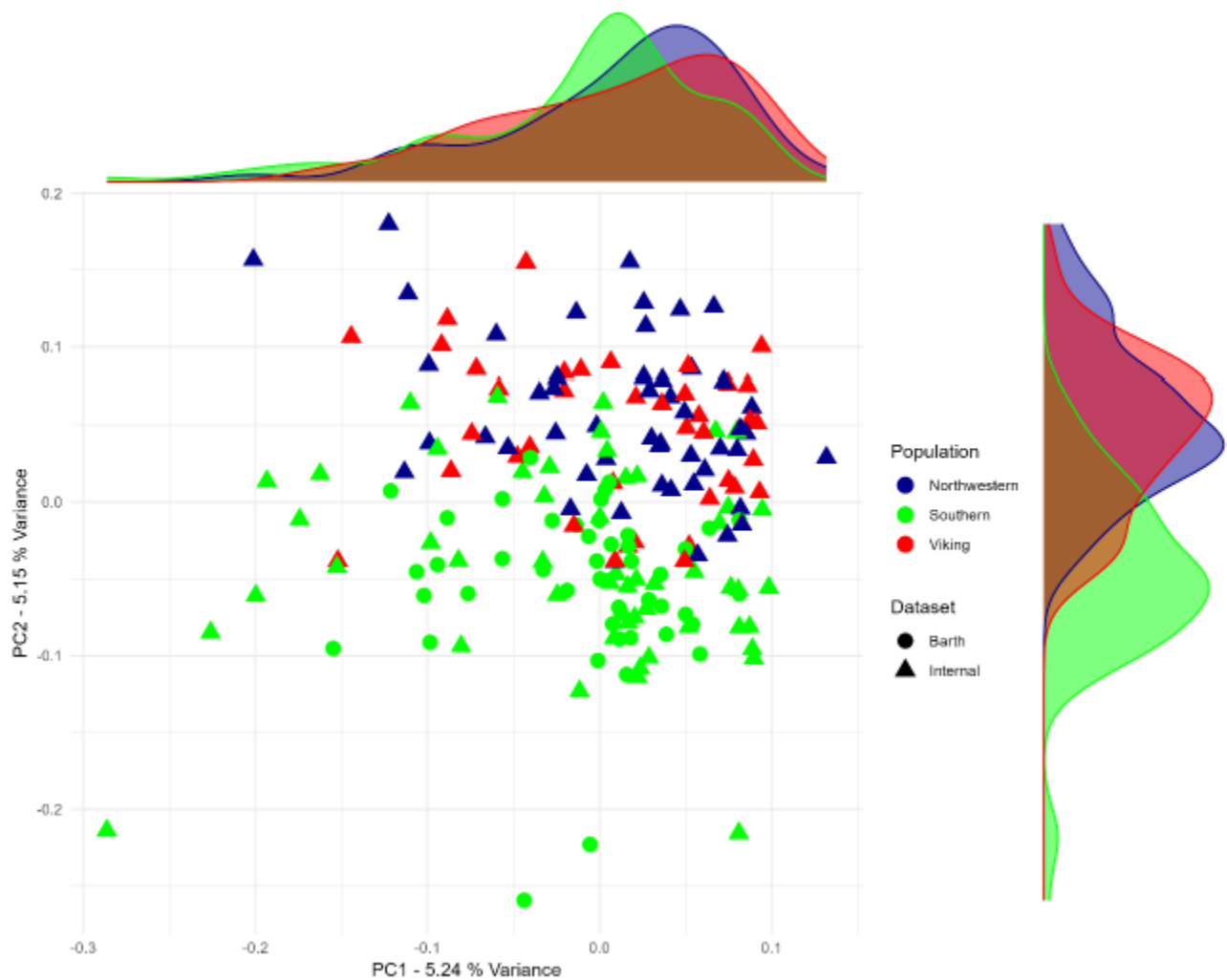


Figure 4.3.2. PCA of North Sea samples. Individuals from Barth et al., (2019) are shown as circles and individuals from GenDC/DTU Aqua as triangles. Density curves for PC coordinates are included to illustrate area differences.

4.4 Future sampling recommendation on cod

It is recommended that further sampling for genetic analyses in some areas is conducted to follow up on the results in the current project.

Northern shelf stock complex

- Genetic sampling should be conducted in the main cod fisheries and cover the main fishing periods. The GenDC project has demonstrated that the southern cod stock component can be genetically distinguished from the Viking and Northwestern components. The next step is therefore to determine the extent to which these stock components mix within the fishery. It is recommended that genetic samples are collected from commercial catches, preferably through

observer trips where possible. This would provide accurate information on the location of catches and enable sampling of both the landed and discarded components of the catch.

- Genetic sampling during scientific surveys outside quarter one, complemented by sampling from commercial fisheries throughout the year, will be important for determining how the three stock components mix across geographical areas and seasons. Sampling should be continued over multiple years to quantify interannual variation and assess the temporal stability of observed mixing patterns.
- Further sampling of spawning fish during quarter 1 is recommended to strengthen the genetic baseline even further. This should include increasing sample sizes across the different stock components and evaluating the temporal stability of genetic differences among them. Such sampling could most efficiently be incorporated into existing scientific surveys conducted during the spawning period.

Baltic Sea (SD 22-25)

- Preliminary GenDC results suggest that mixing between western and eastern Baltic cod is concentrated in the Arkona Basin (SD 24), with limited mixing observed in SD 22 and SD 25. While several years of genetic data are available from the main mixing area in the Arkona Basin, and for some years in SD 22, analyses for the eastern Baltic Sea (SD 25) currently include only samples from 2025. Within GenDC, however, samples have been collected in SD 25 over three years (2024, 2025 and 2026). If analyses of the additional years confirm the preliminary finding of limited mixing in SD 22 and SD 25, annual genetic sampling and analysis of stock mixing in these areas may not be necessary. In contrast, given the mixing between western and eastern Baltic cod in SD 24, continued genetic sampling in this area is recommended if stock abundance recovers to levels that allow fishing opportunities to reopen.

Kattegat and transition zone

- Substantial mixing between cod stock components has been observed in the Kattegat, particularly in the northern part of the area. This mixing is primarily driven by younger cod from the Northern Shelf stock complex entering the Kattegat to feed and subsequently leaving the area as they approach first spawning. Genetic sampling should therefore focus primarily on younger cod (below age 3). As these younger age groups are the main target for genetic analysis, sampling could be conducted most cost-effectively through existing scientific surveys, where individuals can be sampled systematically across relevant areas and age groups

5. Work package 4

Integration of genetic data with stock assessment and existing advisory frameworks.

Lead: Johan Lövgren, SLU Aqua with support from Christoffer Albertsen, DTU Aqua

5.1 Introduction to stock assessment

Several assessments within the ICES area rely on information on stock identity and mixing (mainly cod and herring stocks), although the extent to which genetic data are incorporated varies among assessments. The need to distinguish between stocks or stock components can arise for several reasons, particularly when biologically distinct populations overlap spatially but differ in stock status, productivity, or management requirements. In such cases, reliable estimates of stock composition are important to correctly assign catches and survey observations to the relevant stock components and to ensure that depleted or vulnerable components are adequately protected.

The western and eastern Baltic stocks provide an example where stock separation has been particularly important. The two stocks differ in their biological characteristics and historical stock status, while substantial mixing occurs in part of the distribution area. The main mixing area is the Arkona Sea, corresponding largely to ICES subdivisions (SD) 24 (Hemmer-Hansen *et al.* 2019, Weist *et al.* 2019). Otolith shape analysis, based on genetically assigned baseline material, has been used since 2015 to determine mixing ratios of the commercial data; and a model approach is used for the BITS data.

Stock mixing has also complicated the assessment of Kattegat cod (SD 21). For several years, ICES has been unable to conduct a full analytical assessment of the Kattegat cod stock. One of the key challenges is the occurrence of cod of North Sea origin in the Kattegat. These fish may enter the Kattegat and subsequently leave the area, for example in connection with spawning migrations. Such movements complicate the interpretation of changes in abundance because declines in the number of fish observed within the assessment area cannot necessarily be attributed solely to fishing mortality and natural mortality. The assessment working group (WGBFAS) therefore identified improved information on the contribution of North Sea-origin cod in the Kattegat as important for progressing from the present data limited approach towards a fully analytical assessment (ICES, 2017). This could only be estimated with genetic data with a high spatio-temporal resolution.

This has led to the GenDC project initiating sampling of Kattegat cod to investigate the extent and temporal dynamics of mixing and to evaluate whether genetic information could contribute to the future development of a fully analytical assessment

The main priority in the GenDC project has been to support the ongoing benchmark of the Northern shelf cod complex and the further development of the multi-stock model. The multi-stock model currently used for the Northern Shelf cod stock complex incorporates both stock-wise and mixed-stock data sources to assess sub-populations. Under the current data limitations, surveys from quarter one

are assumed to be representative of sub-stocks based on geographical position, while surveys from quarter three and commercial catches are treated as mixed-stock data. Incorporating genetic information will improve the estimated allocation to sub-stocks and, in turn, the assessment of stock status and fishing opportunities

By incorporating all data sources in an integrated assessment model, as opposed to several ad hoc procedures, sampling and model uncertainty will be accounted for; thereby, improving both the estimates and uncertainty evaluations of stock status and fishing opportunities, which are central to sustainable and precautionary fisheries management.

The main focus of the GenDC project has been to provide a genetic tool that can separate the different substocks present in the Northern Shelf cod stock complex. By providing this tool it would be possible in the near future to look into the assumptions of mixing that are present in the model.

The long going benchmark of the Northern Shelf cod stock complex that started 2023 has recently been closed (September 2026). It has been agreed that the multistock model will be the model that will be used in the next coming years. How this decision will affect future sampling and data analyses remains to be decided.

5.2 Description of the genetic split conducted in SD 24 (D4.1)

Updated code for stock assessment model

The Baltic cod stock complex consists of two populations, which are mixing in ICES subdivision 24. The GenDC project has supported the continued estimation of the stock composition in catches, used to split catches to the correct populations for use in ICES assessment and advice. The estimation of stock compositions is based on a combination of otolith shapes and genetic classifications. Further, developments were made to the fishpopmix R package to secure continued efficient and accurate deliveries of stock composition estimates.

The estimation of stock composition in cod catches from ICES subdivision 24 combines otolith shape analysis with genetic classifications in a statistical model (Fig. 5.2.1). Otolith shape is described by normalized Fourier descriptors, which encodes the contour as a harmonic series. In turn, the distribution of descriptors per stock is modelled by a multivariate normal, where the mean depends on the fish length, time of year, and year of capture. The length effect is modelled by a spline, while the time of year effect is modelled by a periodic spline to ensure that the effect at the beginning of the year is close to the effect at the end of the year. The effect of capture year is modelled as a categorical variable. The otolith shape in cod is strongly affected by both fish length, time of year and year. Based on a cross validation analysis, the model includes the normalized Fourier descriptors A10, C8, A3, A9, D9, A4, D5, and A11. As the fish grows, the otolith becomes relatively wider. Likewise, when the cod grows faster during spring and summer, lobes are formed on the contour, which becomes less pronounced after periods of slower growth. Finally, the capture year effect reflects environmental differences experienced by the fish over time.

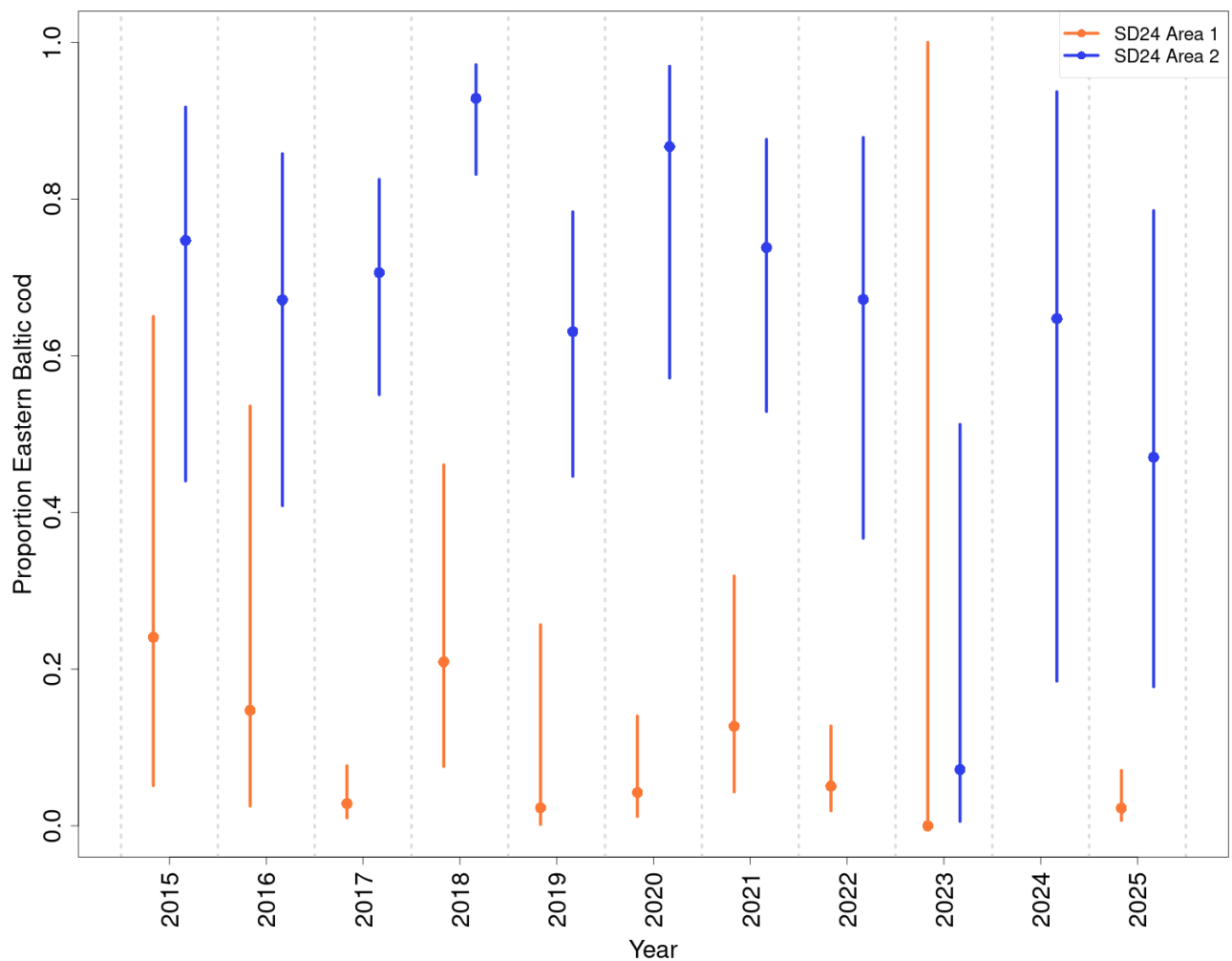


Figure 5.2.1. Estimated proportion of Eastern Baltic cod in Danish commercial catches from otolith shapes and genetic classifications.

Accounting for length and temporal effects in the otolith shape is a necessity for accurately estimating stock compositions based on population differences in the shape. If the exogenous effects are not accounted for, they will be confounded with population effects, resulting in misclassifications, incorrect composition estimates and thereby uncertain scientific advice.

The yearly estimation of stock compositions for assessment and advice has been conducted using the R package “otoclass” (available on GitHub: <https://github.com/calbertsen/otoclass>). The package implements a flexible statistical model, which can combine different data sources and external classifications for estimation of stock compositions and individual population origin classification of fish. The model is implemented using TMB. Developments have been made on a replacement package, implemented using RTMB, called fishpopmix. The fishpopmix package is implemented in a modular fashion with the primary focus on modern genetic data, which will be the predominant source of population origin information in the future. However, the package will be further developed to handle historically important data sources and fully replace the otoclass package.

The work has contributed to the ICES assessments of western Baltic cod (cod.27.22-24) and eastern Baltic cod (cod.27.24-32) by the Baltic Fisheries Assessment Working Group (WGBFAS).

5.3 Description of the work conducted on Kattegat cod (D4.1)

Updated code for stock assessment model

In the Kattegat, local populations are mixing with juvenile cod from the Northern shelf populations. However, the current assessment of Kattegat cod (cod.27.21) does not account for this juvenile migration from the North Sea into the Kattegat area.

The GenDC project has supported the developments of a statistical model to incorporate genetic samples into the Kattegat assessment. The model incorporates ‘contaminating’ populations that can be filtered out of catch and survey observations based on genotype data. Besides the assessment model, the model developments combines two parts: a random process for the exploitable biomass of contaminating populations, and a statistical description of genotype data.

In a simulation study, several approaches were examined and compared. The study simulated population dynamics of a Northern Self cod stock and a Kattegat population including migration of juvenile North Sea individuals to the Kattegat area. In turn, the data was modelled using: area-based data, similar to the current assessment; genetically pure Kattegat data, representing a utopian scenario; area-based data combined with genotype data to filter out the contaminating stock using the novel model developments; data from both the North Sea and Kattegat combined with genotype data in a multi-stock model; data from the Kattegat area combined with genotype data in a multi-stock model. Further, the impact of only having genotype data every other year was explored.

As expected, the Kattegat area-based model overestimated the abundance of juveniles and, in turn, total stock biomass, while spawning stock biomass was close to the true simulated Kattegat population values. When used for assessment and advice, such an approach would overestimate productivity and result in biased reference points, possibly with a too low Blim, since a large part of the perceived recruitment does not depend on the actual Kattegat spawners. In contrast, it was possible to get unbiased estimates of both spawning stock and total stock biomass when using the genotype data to remove stock contamination (Fig. 5.2.2).

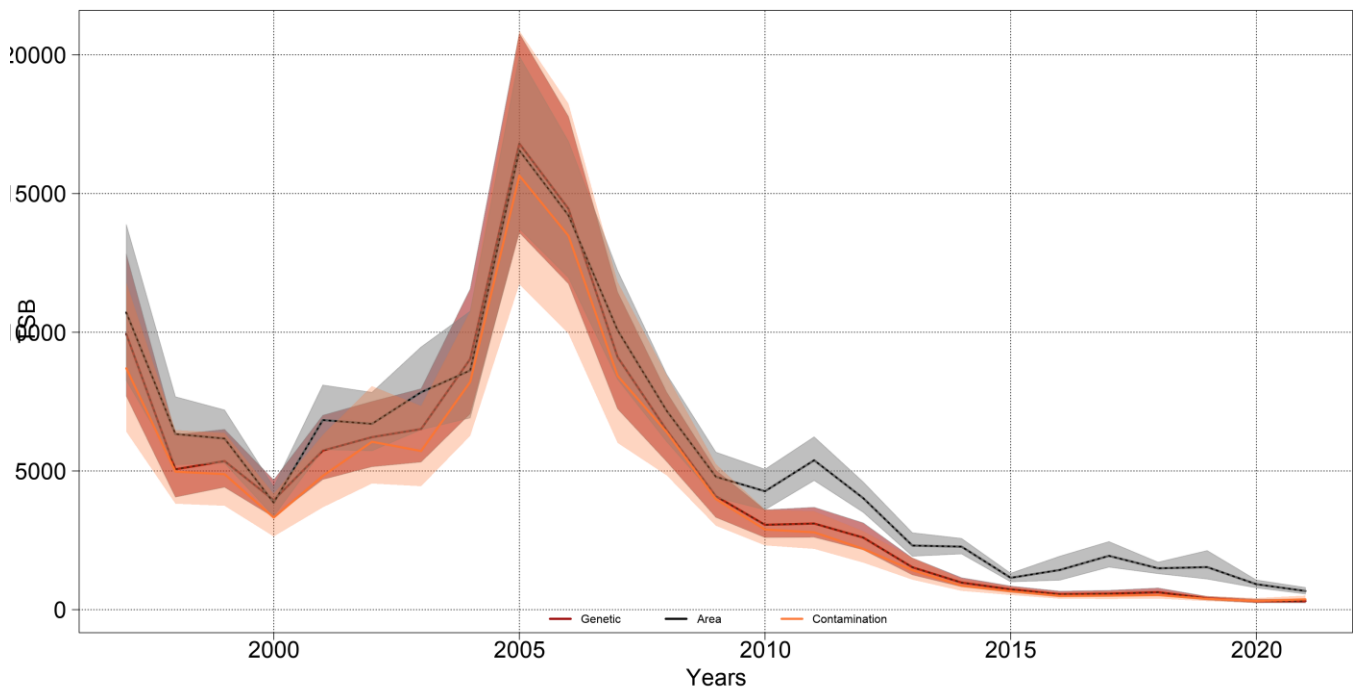


Figure 5.2.2. Illustrative example of estimated total stock biomass trajectories from a single simulation of the Kattegat scenario assuming a unit stock (black), with genetic samples to remove the contaminating stock (orange) compared to a perfect genetic information assessment (red). Copied from the WKCODSAMPLING report.

While incorporating genotype data allows accurate assessment of true populations, it increases computational complexity, and more care is needed to ensure robust and fail safe procedures for advice. Genotype data can also be used to pre-split data, similar to the Baltic population complex. This has the practical advantage of reducing computational complexity and the possibility of dividing the workload of the two-step procedure. On the other hand, incorporating genotype data directly in the assessment model has theoretical advantages of correctly accounting for sampling uncertainty, accounting for the risk of misclassifications, as well as the possibility of using the estimated population dynamics to interpolate between sampling events. Thereby, having a statistically sound procedure for years without genotype samples. Code developments to the assessment model are available on GitHub (https://github.com/fishfollower/SAM/tree/F_TAC/ and https://github.com/calbertsen/multi_SAM/tree/F_TAC/)

The work has contributed to the ICES Workshop on Sampling Data for Northern Shelf cod sub-stocks (WKCODSAMPLING). The model and simulations are fully documented in the workshop report.

5.4 Description of the multi stock model in the North Sea (D4.1)

Updated code for stock assessment model

The Northern Shelf cod stock complex primarily consists of three reproductively isolated populations. Since benchmark workshop in 2023, the populations have been assessed separately in an integrated multi-stock state-space assessment model. The model accounts for unknown mixing patterns outside of the spawning season, as well as a lack of stock composition data, which means that catch data and

survey indices for the second half of the year cannot be pre-allocated to populations. That is, where, for example, the Baltic cod stock complex assessment uses a two-step procedure with a splitting model followed by separate assessments, the Northern Shelf cod assessment uses an integrated approach with splitting and three assessments in the same model.

Following precautionary principles, and since mixing patterns are currently unknown, ICES headline advice follows the weakest population. If MSY advice suggests a reduction in fishing mortality rates for any stock, the largest advised reduction is applied to all three stocks. Similar principles have been suggested for mixed-species fisheries.

In 2025, the ICES procedure resulted in a zero-catch advice for 2026 for all three Northern Shelf cod populations to protect the South population, although the Northwest and Viking populations were slightly above, respectively, slightly below the MSY Btrigger reference point. Following the zero-catch advice, concerns were raised about the ability of the multi-stock SAM model to assess the separate populations. In particular because (i) there is no stock composition data, (ii) the average fishing mortality trajectories are similar and (iii) the recruitment trajectories are similar between the three populations. To investigate the potential issue and possible solutions, ICES began a review level benchmark process through the Northern Shelf cod “Tiger Team”.

The GenDC project has supported work on the multi-stock assessment of Northern Shelf cod through the Tiger Team and investigations on incorporation of genetic data presented at the WKCODSAMPLING workshop. Both are briefly described below and in detail in the ICES reports.

Related to the Northern Shelf cod multi-stock assessment, the ICES Tiger Team review-level benchmark reconfigured the assessment model and conducted several sensitivity analyses and simulation studies to investigate the performance of the model (ICES 2025-2026).

The reconfiguration resulted in a substantial improvement in model fit with good model diagnostics. In particular, the model was improved in terms of fit to the available landing data by spawning area in the first quarter of the year. The reconfiguration resulted in a slight rescaling of spawning stock biomass between the three populations (Fig. 5.2.3). However, relative to ICES biological reference points, the perceptions of the stocks and their status remained largely unchanged.

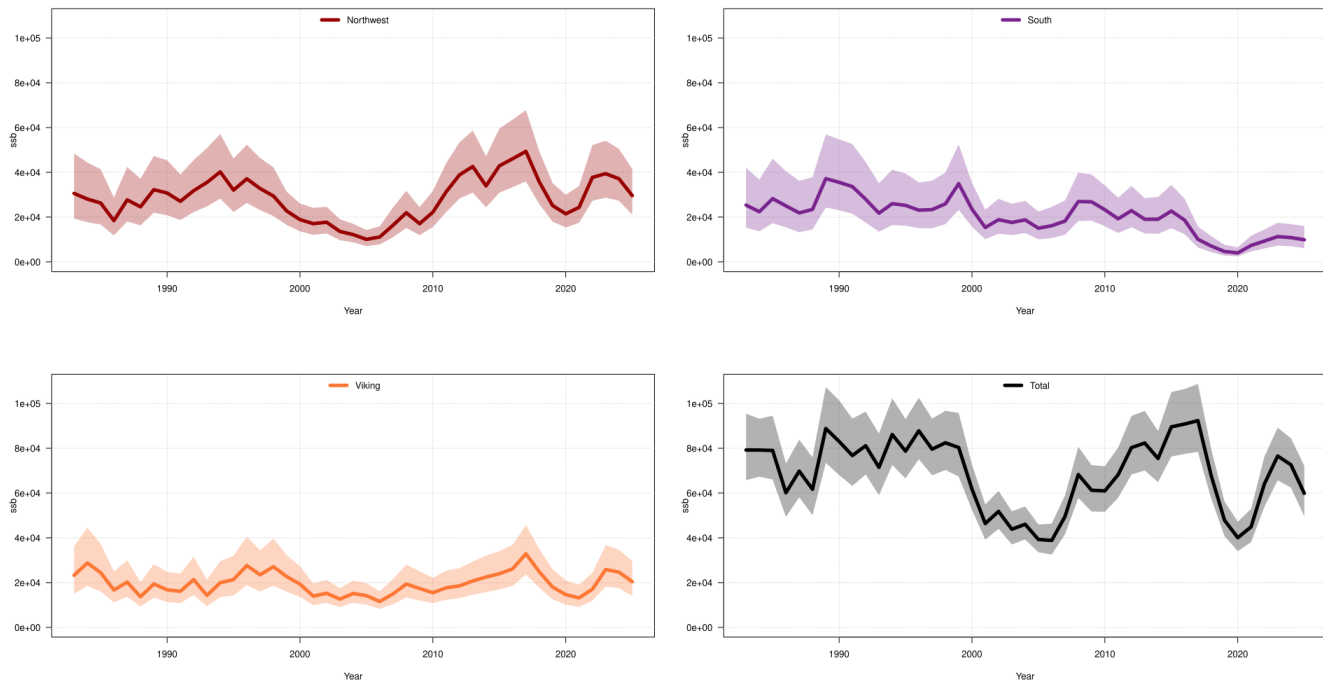


Figure 5.2.3. Estimated spawning stock biomass for the Northwest (red), South (purple), Viking (orange), and aggregate (black) populations.

Besides the reconfiguration, several sensitivity analysis and simulation studies were conducted to evaluate the performance and suitability of the model and modelling framework. The studies concluded that the multi-stock model - with the currently available data, knowledge and assumptions - can give accurate and precise estimates of historical stock status for all three populations under different scenarios for historical fishing patterns. Further, the simulations showed that treating the stock complex as a homogeneous population resulted in biased estimates of abundance, fishing pressure and productivity, which can lead to unsustainable fisheries management (Fig. 5.2.4).

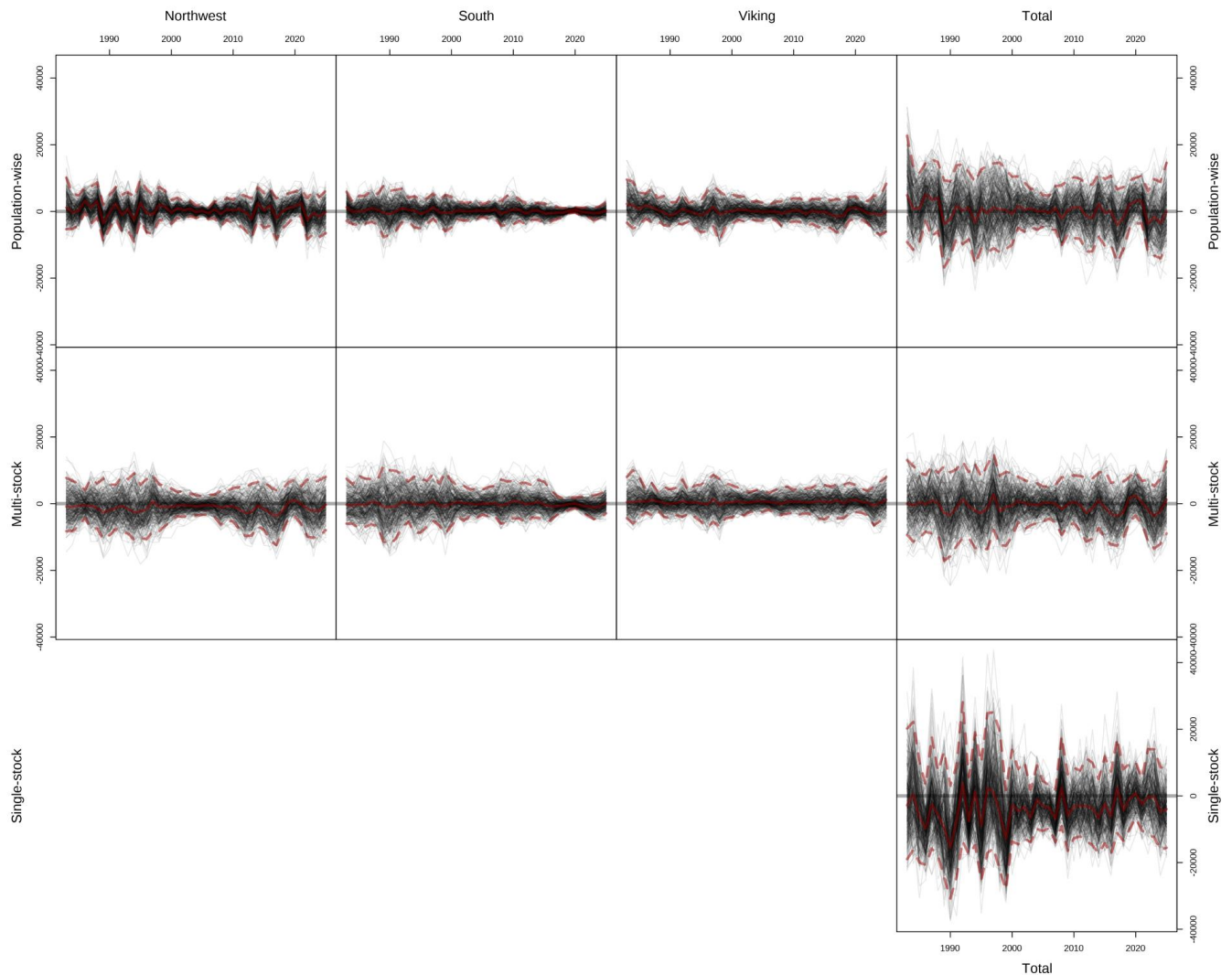


Figure 5.2.4. Difference between estimated and true simulated spawning stock biomass in the first simulation study, based on the reconfigured assessment.

The alternative configurations investigated through sensitivity analyses did not improve the model or assessment, with the exception of utilizing the historical area-based catches from the west of Scotland (FAO 27.6.a) area and Greater North Sea (FAO 27.4, 27.7.d, and 27.3.a.20) separately. Without any identifying information, the model estimated west of Scotland catches to be almost exclusively from the Northwestern population, which has a spawning area that covers the west of Scotland area. However, incorporating multiple fleets in the assessment can greatly increase the complexity of assessment, short term forecasts, and advice. The work was fully documented in working documents and reviewed by the working group (WGNSSK), two external reviewers, the ICES Benchmark Oversight Group (BOG), and the ICES advisory committee (ACOM), and subsequently adopted for use in the 2026 advice on Northern Shelf cod fishing opportunities in 2027.

The work of the ICES Tiger Team showed that the multi-stock model can provide accurate and precise assessments of the three Northern Shelf populations with the currently available population-specific

data. However, this especially relies on a model configuration and assumption that the relative difference in fishery selectivity between stocks is constant over time. The multi-stock SAM model has been developed to be able to incorporate genotype data to internally split catch and survey data to populations. As part of the WKCODSAMPLING, these developments were simulation tested. Based on the current assumptions, the primary advantage of incorporating genetics is that it can reduce uncertainty in model estimates and be used to weaken assumptions and model structure. Further, it is possible to reduce the number of assumptions needed in the model, such as the assumptions on fishing selectivity. While the impact is limited if the assumptions are good, the assessment and advice will be better equipped to handle changes in fishing patterns in the future. Moreover, genetic samples may supplement the assessment model in the short term to provide possible mitigation strategies that protects vulnerable populations.

The work has contributed to the ICES review-level benchmark Tiger Team on Northern Shelf cod, the ICES Workshop on Sampling Data for Northern Shelf cod sub-stocks (WKCODSAMPLING), and the ICES advice on Northern Shelf cod through the Working Group on the Assessment of Demersal Stocks in the North Sea and Skagerrak (WGNSSK) in 2026.

6. Work package 5

Project dissemination and communication.

Lead: Marie Storr-Paulsen, DTU Aqua

6.1 Scoping and Implementation Workshops (D5.2)

GenDC was central to two ICES workshops which we set up to answer a special request from Norway, UK, and the European Commission to ICES. The workshops should advise on developing a biological sampling programme with a focus on genetic data, to enhance understanding of sub-stock mixing and spatial dynamics and to support the development of area-specific management advice for Northern Shelf cod. The workshops took place in spring and autumn 2025 at ICES HQ, following a hybrid meeting format to allow for a wider participation from research institutes, fishing industries and management authorities.

The Workshop on Scoping Data collection for Northern Shelf cod sub-stocks (WKCODSCOPE), held in March 2025 was the first step in this two-workshop process. It was established to explore data needs for Northern Shelf cod sub-stocks, including genetic information, sampling strategies, and methods for distinguishing between sub-stock components. The majority of this work being carried out under GenDC. In 2023, ICES redefined the Northern Shelf cod stock, merging North Sea and West of Scotland cod into a single stock assessment unit consisting of three biological sub-stocks: Northwestern, Viking and Southern. The stock assessment at the time could estimate stock dynamics for these sub-stocks but could not reliably determine which sub-stock the individual fish belong to outside of the spawning season. Thus, ICES could only provide advice for the combined stock rather than area-specific catch advice. WKCODSCOPE was tasked with identifying the data and sampling approaches needed to quantify stock mixing and eventually support spatially explicit management. The relevance of the following data types was investigated; genetics, historical tagging studies, otolith chemistry, otolith morphology, growth and maturity characteristics and larval drift modelling.

Specifically related to genetics the workshop reviewed previous genetic studies and ongoing work within the GenDC project. Previous studies demonstrated two major genetic populations, "Viking" and "Dogger" but studies were limited due to limited geographic coverage and numbers of genetic markers plus a poor representation of southern spawning cod. WKCODSCOPE identified resolving the status of the Southern cod component as the highest priority. To address this, plans for further sampling and analysis included the sampling of spawning cod across the southern North Sea, the collection of additional baseline samples from Viking and Northwestern spawning areas and that whole genome sequencing be undertaken. The GenDC project has coordinated the collection of spawning cod samples from the Southern North Sea and additional spawning samples from Viking and Northwestern areas. The WKCODSCOPE report highlights the substantial international sampling effort conducted by GenDC where spawning samples from the southern North Sea were obtained via collaboration with IBTS (International Bottom Trawl Survey) networks, through the Regional Coordination Group (RCG NANSEA) and coordinated observer programs by engaging in countries actively fishing in the southern

North Sea. At the time of the workshop GenDC had already collected 1,289 samples in 2024 and 484 in 2025. WKCODSCOPE reviewed new genome data generated under GenDC and found evidence for additional highly differentiated genomic regions that were not captured by the former SNP panel. The improved genetic baselines can now show that Southern cod can be genetically separated from Northwestern cod. WKCODSCOPE endorsed GenDC's plans for additional sampling and sequencing of spawning cod from the southern North Sea, plus further improvements to assignment panels by identifying new diagnostic genetic markers.

A major output from WKCODSCOPE was the outline of a coordinated regional sampling framework. Here the GenDC standardized genetic sampling protocol will underpin the sampling program. The workshop considered this a crucial step toward international harmonisation and future operational monitoring. GenDC distributed the protocol to national survey coordinators and observer programs operating across the greater North Sea region. The protocol specifies details related to equipment, handling and storage procedures, labelling requirements and storage methods. The data recording format was developed in line with the ICES DATRAS data formats to allow for future integration into ICES databases. The protocol can be adapted and refined to fit commercial fishery routines but is ready to be applied on scientific surveys. WKCODSCOPE agreed that for international scientific surveys, genetic sampling should continue consistent with the application of the protocol and that otolith collection should occur alongside genetic sampling. For commercial fisheries multiple approaches were considered depending on whether sampling took place onboard where entire catches could be sampled with exact sample location data but would be more costly, or at market where costs would be lower but limited on detailed spatial data. A suggested sampling plan was discussed during the workshop, and it was agreed to conduct pilot sampling programmes during 2025-2026 to test protocols, estimate required sample sizes and aid the design of a long-term coordinated regional sampling programme across nations.

The workshop concluded that the path toward area-specific advice requires several stages and consistently positions GenDC as the project that will provide the key evidence needed to make that transition possible. The top priorities highlighted were to complete genetic analyses and determine whether Southern cod represent a distinct genetic unit, to continue collecting survey samples and launch pilot commercial sampling programmes. Additionally, mixing rates among sub-stocks should be quantified, robust population assignment tools created and simulation studies conducted to assess how genetic information can improve assessments. GenDC has focussed its efforts on these activities with the longer term view on developing the stock assessment framework to assign catches to biological sub-stocks and quantify mixing explicitly, ultimately supporting spatially explicit management and area-based catch advice for Northern Shelf cod.

The ICES Workshop on Sampling Data for Northern Shelf cod sub-stocks (WKCODSAMPLING) was the second workshop in the ICES process, took place from 10th-14th November 2025 at ICES HQ. The workshop built directly on WKCODSCOPE, moving from "scoping" to "implementation" and focussed on whether genetic data can be operationally used to identify sub-stocks, estimate mixing, support assessments, and guide future management. The workshop reviewed progress in genetics, otolith

shape analysis, tagging studies, assessment modelling, genetic data management, and sampling programme design. Its overall conclusion was that the evidence is now sufficiently strong to proceed with the development of a coordinated genetic sampling programme for Northern Shelf cod.

The central finding of the workshop came from the GenDC project. At WKCODSCOPE, a major uncertainty was whether the Southern cod component was genetically distinct. Without that evidence, a genetics-based monitoring programme could not be justified. GenDC addressed this directly through extensive genome sequencing of spawning cod collected across the Northern Shelf stock complex. The projects outputs presented at the workshop concluded that genetic differences are evident among all three sub-stock areas (Northwestern, Viking, and Southern) and that genetic markers have strong potential for assigning fish to sub-stock origin. These outcomes being fundamental critical prerequisites for implementing a genetic monitoring programme.

GenDC delivered the first comprehensive Northern Shelf cod genetic baseline, WKCODSAMPLING describing the dataset as "the most comprehensive available to date" for Northern Shelf cod genetic structure. GenDC analysed 363 spawning cod from Northern Shelf sub-stocks and adjacent populations using whole-genome resequencing and millions of SNP markers. The baseline included contemporary and historical samples from Northwestern, Viking, and Southern areas and now underpins future stock assignment work.

One of the key questions raised at WKCODSCOPE was whether Southern cod form a distinguishable genetic cluster. GenDC showed evidence that this is the case and reported strong indications that Southern spawning cod possess a unique genetic signature not solely driven by the well-known inversion regions in the cod genome. This finding substantially strengthens the case for area-specific management and future stock-assignment tools.

Based on GenDC results, WKCODSAMPLING recommended proceeding with a coordinated sampling programme incorporating both genetic samples from surveys and from commercial catches. The workshop recommended that all future survey sampling follow the GenDC sampling protocol which specifies tissue sampling procedures, sample preservation methods, labelling systems and storage requirements. In addition, specific metadata are required to support the integration of data with international survey databases at ICES. Otolith extraction and storage from all samples collected, to allow for complementary microchemical and/or shape analysis.

GenDC has embedded genetic sampling within key international ICES-coordinated bottom trawl surveys which provide fishery-independent biological samples and abundance data used in stock assessments and monitoring of Northern Shelf cod sub-stocks. The workshop recommended continuing and expanding this network because it provides the most cost-effective route for long-term monitoring. The following were listed as surveys that could contribute samples for estimating Northern Shelf cod sub-stock mixing; NS IBTS Q1 (North Sea International Bottom Trawl Survey Quarter 1), NS IBTS Q3 (North Sea International Bottom Trawl Survey Quarter 3) and SCOWCGFS (Scottish West Coast Groundfish Survey). The coverage of these seasonal surveys can help quantify movement and mixing

patterns throughout the year and provide access to cod samples from the northwestern sub-stock area and provides the opportunity to collect both tissue samples and otoliths

In relation to genetics data integration into ICES data systems, a major practical contribution from GenDC is the work with the ICES Data Centre to create a mechanism for storing genetic information in DATRAS and the RBDES. The standardized data format developed and based on DATRAS, using common ICES vocabularies simplifies future upload to other databases. GenDC contributes to the operational integration of genetics into the ICES advisory systems by building on the genetic population data framework developed through WKSIDAC2 (The Second Workshop on Stock Identification and Allocation of Catches of Herring to Stocks). By following the format agreed upon by WKSIDAC2, GenDC supports interoperability across systems and enables population assignments and associated probabilities to be stored within ICES databases and linked directly to fisheries monitoring and assessment workflows.

In relation to stock assessments, WKCODSCOPE concluded that genetic assignment methods developed through GenDC could provide stock-specific information that would allow assessment inputs to be split by biological sub-stock rather than inferred from geographic area alone. The workshop concluded that genetic stock-identification data have the potential to substantially improve the Northern Shelf cod assessment by providing direct estimates of sub-stock composition in catches and surveys. The multi-stock SAM assessment relies on assumptions about spawning distributions and seasonal mixing because individual fish cannot routinely be assigned to the Northwestern, Viking, or Southern sub-stocks. The workshop recommended further intersessional modelling and simulation studies to evaluate how genetic information could be used to improve data allocation, estimate mixing rates, test assessment performance, and determine the requirements for future assessment frameworks that explicitly incorporate stock identity and movement among sub-stocks. The workshop positioned simulation studies as a critical next step as the benefits and readiness of genetics-based assessment approaches still need to be demonstrated through simulation testing.

6.2 Meetings with policy makers and end users

GenDC has contributed with supporting information to EU DG Mare and the trilateral parties (Norway, United Kingdom) in connection with trilateral negotiations on Northern shelf cod management. Early in the project (June and November 2024), we provided an update on project aims and data flows, with a particular focus on the joint special request submitted to ICES in early 2024 regarding advice on a genetics-based sampling programme to support management of the Northern shelf stock complex. This was followed up in April 2026 by three presentations of project findings as background to the ICES advice at the technical DG Mare meeting, the trilateral group and the national contact points and external experts. Further, additional meeting after the project ending has been arranged.

6.3 Home page (D5.4)

The project website <https://aqua.dtu.dk/gendc/> was launched in summer 2024 and provides information on the project's background, objectives, expected impact, funding, organizational structure, and partners (Figure 6.3.1). The genetic sampling protocol developed as part of the project is available on the website, where the final project report will also be made publicly available. In the time period the homepage has been active 252 persons has visited the page, 43% from Denmark, 15% from Spain, 11% from UK, 4% from France and 4% from Sweden.

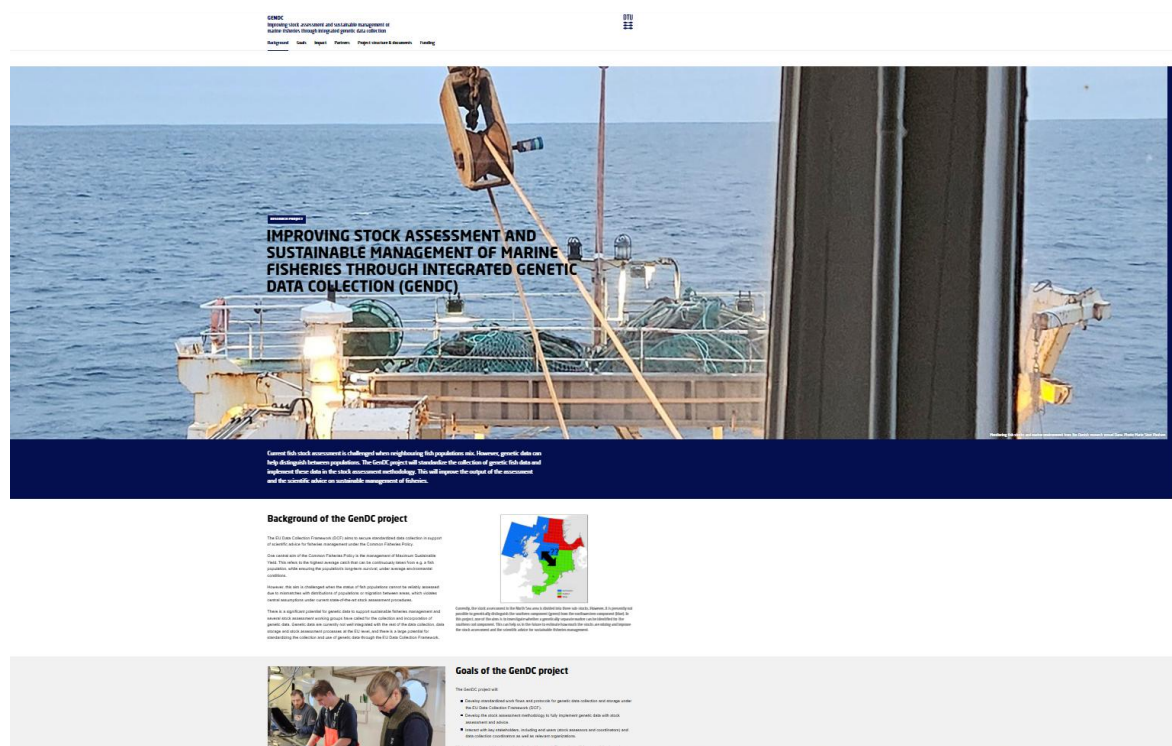


Figure. 6.3.1 Picture of homepage for the GenDC project.

6.4 Policy brief (D5.3 and D5.5)

As part of GenDC, a policy brief was developed to translate the project's scientific results into key messages and recommendations for fisheries management and policy. The brief highlights the potential for integrating genetic information into routine fisheries data collection, stock assessment, and in the end, scientific advice, and outlines the institutional and funding conditions needed to support its long-term implementation. Drawing on the project's work with Atlantic cod, it demonstrates how genetic data can improve understanding of stock structure and support more targeted and sustainable management of mixed and vulnerable stock components.



Fisheries research vessels such as the Danish Dana IV play a central role in at-sea data collection. Photo: Bastian Huwer.

GenDC POLICY BRIEF

Improving stock assessment and sustainable management of marine fisheries through integrated genetic data collection

Sustainable fisheries management is essential for supporting economic development, food security, and livelihoods in European coastal communities while securing the protection of biodiversity and resilience of marine ecosystems.

The GenDC project contributes to more precise, resilient, and sustainable management of fish stocks by addressing critical information gaps and developing advanced methods for data collection, stock assessment, and thereby scientific advice.

Effective management depends on reliable information about the status, structure, and distribution of fish stocks. However, conventional monitoring and assessment approaches are not always aligned with the biological complexity within managed stocks, particularly where distinct stock components mix within the same fishing and management areas.

Using Atlantic cod in the North Sea, Kattegat, and Baltic Sea as a model, GenDC has demonstrated the full pathway from standardized and cost effective genetic sampling and analysis to stock assessment and scientific advice.

The protocols, analytical approaches, and data-storage solutions developed through the project are designed to be transferable to other species and marine regions, including the Mediterranean Sea.

Key Messages

- The biodiversity and climate crises require more targeted and innovative approaches to fisheries data collection and advice.
- Understanding the composition and distribution of fish stock components is essential for accurate stock assessments, the protection of vulnerable stock components, and supporting sustainable fisheries.
- Genetics is a powerful tool for supporting the assessment and management of fisheries resources, contributing to the objectives of the Common Fisheries Policy, biodiversity conservation, and nature restoration goals.
- Coordinated sampling programmes and standardized protocols for data collection and analysis are required to ensure high-quality and comparable genetic data across regions.
- To comply with FAIR (Findable, Accessible, Interoperable and Reusable) data management principles, genetic data used in fisheries stock assessments should be stored in international databases with open and standardized access.

Project partners



THÜNEN



Subcontractor



ICES
CIEM



Co-funded by
the European Union

From Sampling to Data

GenDC provides a harmonized pathway from coordinated sampling to ICES interoperable genetic data.



International Coordination

- Coordination through ICES survey and assessment networks.
- Alignment with national Data Collection Framework (DCF) programmes.
- Harmonized sampling plans developed through GenDC lead ICES workshops and stakeholder engagement.



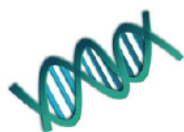
Sample Selection

- Priority areas identified with end-users.
- Cost-effective sampling by integration into existing surveys (IBTS, BITS) and fisheries sampling.
- Representative coverage across areas, seasons and length classes.



Standardized Tissue Sampling

- Common GenDC sampling protocol.
- Fin clips collected alongside routine biological sampling.
- Standard labelling, metadata recording and preservation procedures.
- Unique ID to link samples with biological observations.



Genetic Analysis & Population Assignment

- DNA analysis using validated genomic markers of baseline spawning individuals.
- Assignment of individuals to biological populations.
- Possibility of quantification of stock mixing and population distribution.



Data Standardization & Integration

- Use of agreed ICES vocabularies and data formats ensuring interoperability with ICES data systems including RDBES and DATRAS.
- Documentation of genetic baselines and analytical methods.
- Inclusion of genetic origin and assignment probability.
- Genetic data sharing following the FAIR principles.
- Long-term storage and accessibility through the ICES Data Centre.



Improved Stock Assessment & Management Advice

- Population-informed fisheries assessments.
- Better estimates of stock mixing and population dynamics.
- Stronger scientific evidence for sustainable and climate resilient fisheries management.

Protocol for genetic sampling

GenDC has developed a protocol for data collection to ensure high-quality and comparable data across regions.

The protocol is available on aqua.dtu.dk/gendc



How Results are used in Stock Assessment and Advice

GenDC enhances the accuracy of stock assessment models.

A key achievement of GenDC is its direct contribution to the stock assessment of Northern Shelf Cod, which consists of three distinct stock components.

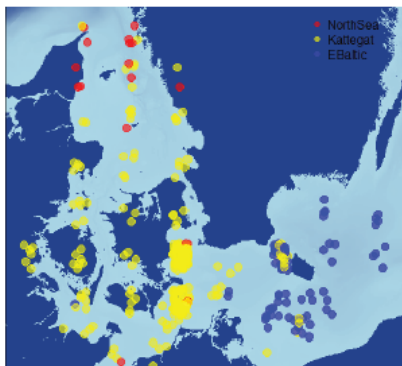
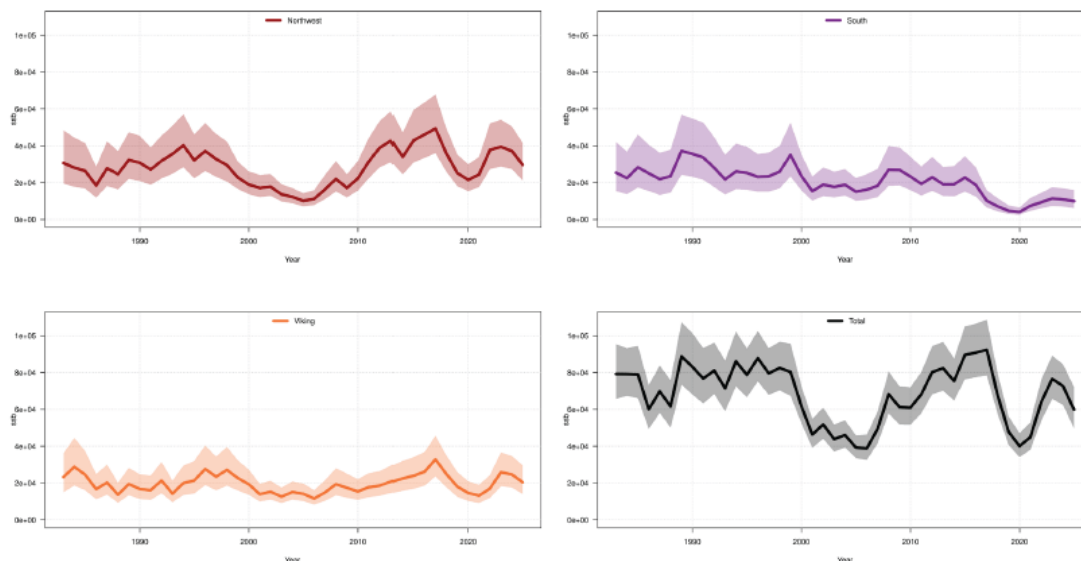
The southern component (purple plot below) is currently at a critically low level, creating an urgent need to understand and quantify its distribution and its degree of mixing in with the two northern components (red and orange plot below).

The results of GenDC will support more targeted management measures, helping to protect the vulnerable southern

stock while allowing sustainable fishing activities where risks of overexploitation are lower.

GenDC has also contributed to the development and validation of assessment models that can integrate individual level genetic data, enabling different stock components to be accounted for in stock assessment and advice.

Close collaboration with ICES stock assessment groups, data center, and advisory experts has ensured that the outputs of GenDC are readily adopted within existing assessment and advice frameworks.



Example genetic assignment data set of cod sampled across three stock assessment and management areas (Kattegat, Western Baltic Sea and Eastern Baltic Sea). Colors correspond to individual fish assignments to each of the three reporting groups in the baseline.

Illustrative example of estimated total stock biomass trajectories from a simulation of the three sub stocks in the Northern Shelf cod (red: Northwest, orange: Viking, and purple: Southern sub stock. A combined stock biomass is shown in black). Ref: EMFAF-2023-PIA-FisheriesScientificAdvice-101156887.

Recommendations

Recommendations for the EU

- Genetic data collection should be fully integrated with the Data Collection Framework (DCF). This will support the objectives of the Common Fisheries Policy and contribute to future policy developments aimed at addressing broader ecosystem, climate change, and biodiversity challenges.
- Future revisions of the Data Collection Framework (DCF) should allocate funding for genetic sampling and analysis to support evidence-based fisheries management and biodiversity assessments.
- Future EU funding mechanisms should facilitate the participation of key partners from countries such as Norway and the United Kingdom, ensuring comprehensive data collection and coordinated management of shared marine resources. Many European fish stocks are shared with neighbouring non-EU countries and effective data collection and management require cross-border collaboration.

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Project title: GenDC: Improving stock assessment and sustainable management of marine fisheries through integrated genetic data collection.

Duration: 1 May 2024 - 30 Sep 2026.

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Disclaimer: The contents of this policy brief are the sole responsibility of the GenDC partners and do not necessarily reflect the opinion of the European Union.



7. Summary

7.1 Achievements and impacts

GenDC has coordinated the sampling of large quantities of tissue samples for genetic analyses, covering three different stock assessment and management areas in Atlantic cod: the Northern shelf stock complex, the Kattegat and the Baltic Sea.

The genetic data from GenDC have been directly applied to support an urgent need for genetic data in support of management in the Northern shelf cod and to refine a population specific stock assessment methodology. In addition, they have provided important time series estimates of mixing in the Kattegat and an overview of the extent of potential mixing in the eastern Baltic Sea.

The main achievements from GenDC include the development of standardized workflows and protocols for the collection of samples for genetic analyses and the standardization of data storage of genetic assignment results within existing database structures at ICES. Thus, GenDC has provided the foundations needed to move towards fully integrated genetic data collection as part of the Data Collection Framework.

7.2 Future prospects and recommendations from the project

Genetics is emerging as a critical tool to support ambitious developments towards ecosystem-based fisheries management, and to support increasing focus on broader biodiversity conservation and nature restoration goals under climate change. To fully capitalize on the operational potential of this tool, it will be important to formalize and standardize data collection and indicator reporting in future policy implementation. In the future, genomic data also has strong potential to contribute to fisheries and climate change vulnerability assessments to support both short-term and longer-term management, conservation and restoration goals.

Recommendations from the project

- Genetic data collection should be fully integrated with the Data Collection Framework (DCF). This will support the objectives of the Common Fisheries Policy (CPF) and contribute to future policy developments aimed at addressing broader ecosystem, climate change, and biodiversity challenges.
- Future revisions of the Data Collection Framework (DCF) should allocate funding for genetic sampling and analysis to support evidence-based fisheries management and biodiversity assessments.
- Future EU funding mechanisms should facilitate the participation of key partners from countries such as Norway and the United Kingdom, ensuring comprehensive data collection and coordinated management of shared marine resources. Many European fish stocks are shared

with neighbouring non-EU countries and effective data collection and management require cross-border collaboration.

- More detailed recommendations on how to conduct future sampling on the different cod stocks analysed within the GenDC project can be found in Section 4.4.

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Annexes

Annex 1

Table 1.1 List of Cod genetic populations, including a description, code (cod_000 to cod_005), temporal and spatial information on the baseline sampling and references to the genotype methods and genomic resources used. The later two fields are shown on the following page.

Genetic Description	GeneticCode	Location baseline samples	GeneticType Code	Species code	Latitude	Longitude	3a27	3a26	3a25	3a24	3a23	3a22	3a21	3a20	4a	4b	4c	7d	6aN	Quarter	Year range	Contact person	Contact Institute
Genetic analysis was performed but results were inconclusive	cod_000		Genetic population																				
Viking Cod (Gadus Morhua) in the Northern North Sea and Skagerrak	cod-001	Northern North Sea and Skagerrak	Genetic population	COD										x	x	(x)				1	2002-2025	Jakob Hemmer-Hansen	DTU Aqua
Southern Cod (Gadus Morhua) in the Southern North Sea and English Channel	cod-002	Southern North Sea and English Channel	Genetic population	COD												x	x	x		1	2002-2025	Jakob Hemmer-Hansen	DTU Aqua
Northwestern Cod (Gadus Morhua) in the Central North Sea and West of Scotland	cod-003	Central North Sea and West of Scotland	Genetic population	COD											(x)				x	1	2002-2025	Jakob Hemmer-Hansen	DTU Aqua
Cod (Gadus Morhua) in ICES SD 21-24	cod-004	Kattegat to Western Baltic Sea	Genetic population	COD							x	x	x							1	1996-2015	Jakob Hemmer-Hansen	DTU Aqua
Eastern Baltic Cod (Gadus Morhua) in the Eastern Baltic Sea	cod-005	Eastern Baltic Sea	Genetic population	COD			x	x	x											2	1997-2007	Jakob Hemmer-Hansen	DTU Aqua

Genetic Description	Genotype method/panel	Whole-genome resources in
Gentic analysis was performed but results were inconclusive		
Viking Cod (<i>Gadus Morhua</i>) in the Northern North Sea and Skagerrak	ICES. 2026. Workshop on Sampling Data for Northern Shelf cod sub-stocks (WKCODSAMPLING; Outputs from 2025 Meeting). ICES Scientific Reports. 8:12. 112 pp. https://doi.org/10.17895/ices.pub.31205980	ICES. 2026. Workshop on Sampling Data for Northern Shelf cod sub-stocks (WKCODSAMPLING; Outputs from 2025 Meeting). ICES Scientific Reports. 8:12. 112 pp. https://doi.org/10.17895/ices.pub.31205980
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Cod (<i>Gadus Morhua</i>) in ICES SD 21-24	ICES. 2017. Report of the Benchmark Workshop on Baltic Stocks (WKBALT), 7–10 February 2017, Copenhagen, Denmark. ICES CM 2017/ACOM:30. 108 pp.	ICES. 2026. Workshop on Sampling Data for Northern Shelf cod sub-stocks (WKCODSAMPLING; Outputs from 2025 Meeting). ICES Scientific Reports. 8:12. 112 pp. https://doi.org/10.17895/ices.pub.31205980
Eastern Baltic Cod (<i>Gadus Morhua</i>) in the Eastern Baltic Sea	ICES. 2017. Report of the Benchmark Workshop on Baltic Stocks (WKBALT), 7–10 February 2017, Copenhagen, Denmark. ICES CM 2017/ACOM:30. 108 pp.	ICES. 2026. Workshop on Sampling Data for Northern Shelf cod sub-stocks (WKCODSAMPLING; Outputs from 2025 Meeting). ICES Scientific Reports. 8:12. 112 pp. https://doi.org/10.17895/ices.pub.31205980

