

WORKSHOP ON SCOPING DATA COLLECTION FOR NORTHERN SHELF COD SUB-STOCKS (WKCODSCOPE; OUTPUTS FROM 2025 MEETING)

VOLUME 8 | ISSUE 11

ICES SCIENTIFIC REPORTS

RAPPORTS
SCIENTIFIQUES DU CIEM



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ISSN number: 2618-1371

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ICES Scientific Reports

Volume 8 | Issue 11

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Recommended format for purpose of citation:

ICES. 2026. Workshop on Scoping Data collection for Northern Shelf cod sub-stocks (WKCODSCOPE; outputs from 2025 meeting).
ICES Scientific Reports. 8:11. 51 pp. <https://doi.org/10.17895/ices.pub.30693761>

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i Executive summary

The WKCODSCOPE workshop brought together representatives from 11 countries and institutions, including participants from both the scientific community and the fishing industry. In total, 47 individuals attended. The workshop was chaired by Côme Denechaud (Norway), Liz Clarke (UK), Marie Storr-Paulsen (Denmark), and Nicola Walker (UK).

In 2023, ICES redefined the Northern Shelf cod stock by merging West of Scotland and North Sea cod into a single assessment unit with three sub-stocks: northwestern, Viking, and southern. To enable area-specific advice, more routine genetic sampling from fisheries and surveys is needed. Norway, the UK, and the EU have requested ICES to develop a comprehensive genetic sampling design to better understand sub-stock dynamics and stock mixing. ICES initiated a two-workshop process, with WKCODSCOPE being the first.

During the workshop genetic studies were presented that confirmed genetic differentiation of North Sea cod into two main populations “Viking” and “Dogger.” However, earlier research was limited by few genetic markers and restricted sampling. A new project, GenDC aims to resolve these limitations and has collected and will finalize sequencing of spawning cod from the southern North Sea to determine whether a distinct sub-population exists there. These genetic results will be compared with data from Viking and northwestern areas to strengthen the baseline for population assignment. Results from southern spawning cod will be analyzed before the next WKCODSCOPE meeting to guide future sampling and stock assessments.

During the workshop tag-recapture data (1961–2015) were reanalyzed and showed limited mixing among the three sub-stocks, Northwestern, Southern, and Viking, though some border movement exists, especially between Viking and Northwestern regions. New tagging programs are recommended to update movement data and validate genetic findings.

During the workshop complementary approaches such as otolith morphology and chemistry were being presented to explore if this could be used to identify population structure and mixing. Otolith shape analysis offers a simple, cost-effective tool for distinguishing sub-stocks, though it can be influenced by environmental variation. Otolith chemistry provides insights into natal origin, life-history migrations, and mixing patterns, potentially serving as a powerful alternative or complement to genetics, especially where genetic differentiation is weak.

Further, a suggested sampling plan was discussed during the workshop and for commercial fisheries, future work should focus on designing and piloting sampling schemes that combine genetic and otolith data from market landings or onboard collections. Multi-stage sampling designs will account for variability among vessels, trips, and hauls. Pilot surveys planned for 2025–2026 will test protocols and determine required sample sizes, with the goal of developing a coordinated regional sampling scheme across nations.

A standardized onboard genetic sampling protocol has been developed under GenDC, detailing equipment, procedures, and storage methods. It aligns with DATRAS data formats for streamlined integration into ICES databases. Consistent application of this protocol, alongside further refinement for commercial settings, will be key to achieving reliable, comparable data for cod stock assessment and management across the Northern Shelf.

ii Expert group information

Expert group name	Workshop on Scoping Data collection for Northern Shelf cod sub-stocks (WKCODSCOPE)
Expert group cycle	Annual
Year cycle started	2025
Reporting year in cycle	1/1
Chairs	Nicola Walker, UK
	Liz Clarke, UK
	Côme Denechaud, Norway
	Marie Storr-Paulsen, Denmark
Meeting venues and dates	18-21 March 2025, Copenhagen, Denmark (and online), 47 participants

1 Introduction

The request for advice from Norway, UK and the European Commission (DGMARE)

The Northern shelf cod advice from ICES (ICES, 2023a) establishes a new stock definition merging the West of Scotland cod with the North Sea cod and making a single assessment unit with three sub-stocks: northwestern, Viking and southern. The ICES advice allocates catches by sub-stock but advises that it should not be taken as area-specific advice. Additional genetic data sampled routinely from both commercial fisheries and scientific surveys is required for ICES to provide area-specific catch advice.

Consequently, the Norwegian, UK and EU Delegations approach ICES for guidance in the management of these stocks that include additional sampling of genetic material and the exchange of information regarding ongoing relevant research on the topic.

ICES, as the coordinating body, is requested to suggest a comprehensive experimental design including a detailed sampling protocol and methodological specifications, for the genetic analysis of the Northern Shelf cod stock complex. This sampling design will aim to enhance the understanding of sub-stock dynamics, especially stock-mixing throughout the year, aligning with the broader goal of guiding area-specific catch advice.

After consultation with the ACOM leadership and expert network, ICES accepted the request and suggested a planning towards an operational (area-based) advice for Northern Shelf cod consisting of:

A scoping workshop (WKCODSCOPE, 18-21 March 2025) focusing on the understanding of sub-stock dynamics, evaluating existing sampling data and outlining the genetic data and alternative data types needed to inform the stock assessment.

A second workshop in continuation of WKCODSCOPE (WKCODSCAMPLING, 10-14 November 2025) to further work on the use of genetic data and alternative data types, implications for the assessment, develop procedures for integrating genetic data in ICES databases and ultimately design a coordinated sampling scheme for the Northern Shelf cod complex.

2 Current Stock Assessment and Advice

2.1 Substock definition and basis

Prior to 2023, the North Sea (Subarea 4, Division 7.d and Subdivision 3.a.20) and West of Scotland cod (Division 6.a) were assessed as separate stocks. However, benchmarks for both stocks identified stock structure as an issue. While stock ID was not a main focus of the 2015 benchmark for North Sea cod (ICES, 2015), subarea boundaries were proposed based on areas of low mixing and monitored going forwards. The 2019 benchmark for West of Scotland cod (ICES, 2020b) suggested the existence of sub-stocks in 6.a and connectivity of the 6.a cod with the North Sea cod.

Two stock ID workshops were conducted for North Sea (ICES, 2020c) and West of Scotland cod (ICES, 2022), respectively. Each workshop conducted an extensive review of the literature (~200 papers in the case of WKNSCodID; ICES, 2020c) to make conclusions on stock ID based on distribution (tagging, surveys, commercial landings and distribution models), genetics, otolith microchemistry, morphometrics and meristics, life history and parasites.

The North Sea workshop rejected the hypothesis of a unit stock in Subarea 4, Division 7.d and Subdivision 3.a.20, concluding that:

- Viking cod (red) is a separate genetic population that is reproductively isolated from Dogger cod (green and blue), with some mixing near the Shetlands and continuous distribution with southern areas and a nursery area in the Skagerrak (Swedish & Danish coasts). This conclusion was based primarily on genetics, but supported by tagging, larval dispersal, size/age at maturity, otolith chemistry, otolith shape and different recent trends in biomass than the southern North Sea.
- Dogger cod does not appear to have clear genetic heterogeneity, but the population appears to have some spatial structure, with different rates of growth and maturity (faster in the south, <50m) and different recent biomass trends (no recovery in the south). There also appeared to be more extensive mixing between 4b-4c than between 4a-4bc.
- The 'northern offshore component' of cod in 6.a is part of the 'Dogger cod' population, based genetics, tagging and trends in abundance. The other adjacent management units (Faroe Plateau, Norwegian coastal cod, Kattegat and Western English Channel and southern Celtic Sea) are genetically distinct despite some mixing of different life stages.

The workshop for West of Scotland cod concluded multiple overlapping sub-populations (inshore and offshore) related to dogger stocks between 6.a and 4.a and a separate Clyde subpopulation. This was based on genetics, otoliths and tagging. However, it was considered problematic to treat the Clyde separately and therefore included as part of the inshore population. Furthermore, the most recent data compilation workshop (ICES, 2023b) concluded that there was not enough data to treat the inshore northwestern cod separately from the offshore cod. Based on these conclusions, the sub-stock definition shown in Figure 2.1 was taken forward to benchmark (ICES, 2023b). This benchmark combined the former North Sea and West of Scotland cod in a multi-stock framework that models the dynamics of the individual sub-stocks.

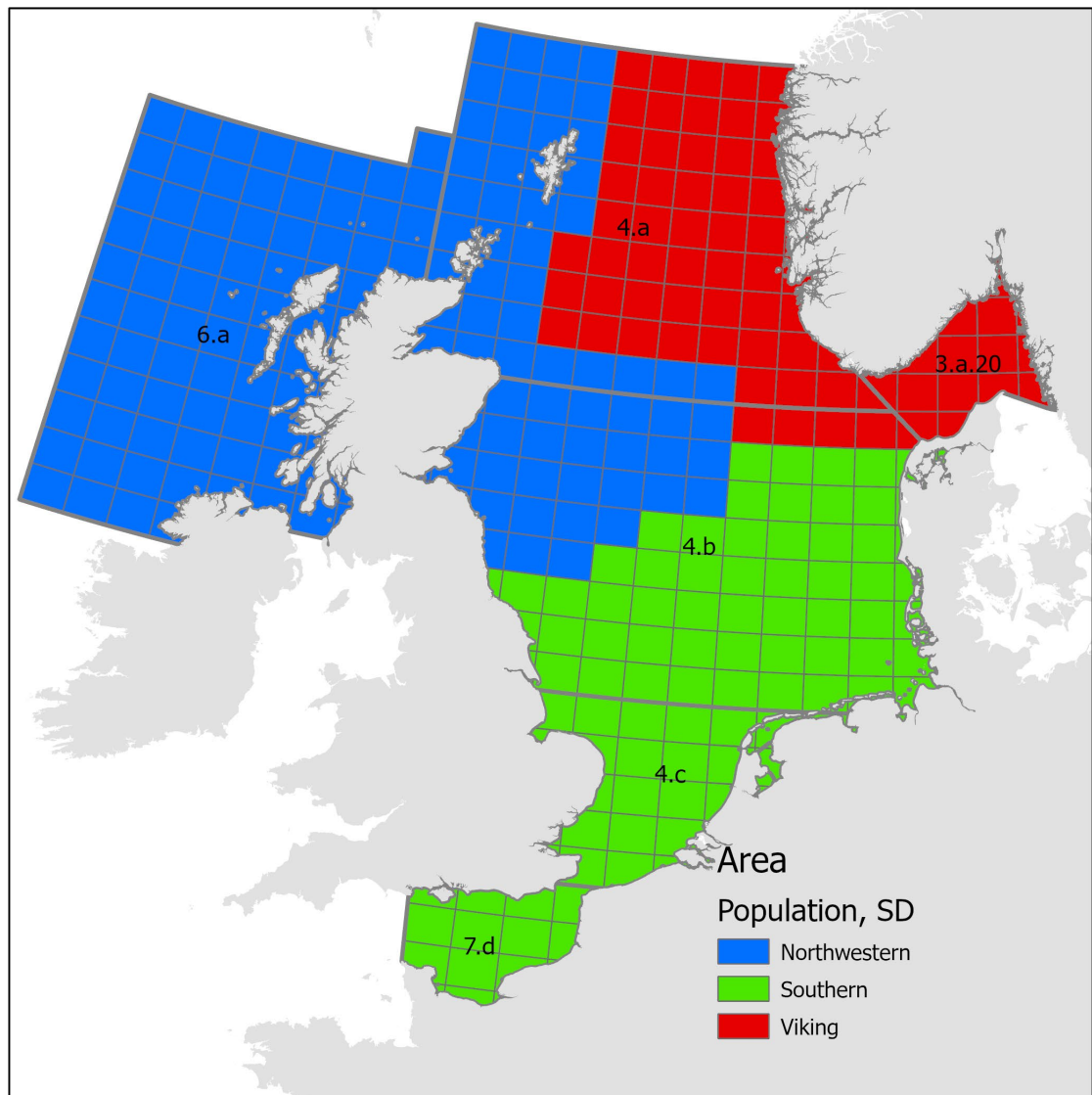


Figure 2.1. Assumed distribution of the sub-stocks of Northern Shelf cod at spawning time.

2.2 Current Assessment

The Northern Shelf cod stock is assessed with a multi-stock SAM model that uses shared observations (Albertsen *et al.*, 2018). Multi-stock SAM models the population dynamics of the biological sub-stocks (Viking, Northwestern and Southern; Figure 2.1) but does not explicitly model movement or the stock distribution, i.e., it quantifies the size of sub-stocks over time but does not say anything about where they are.

While the assessment model itself does not track the movement of fish, assumptions are made to provide multi-stock SAM with observations relating to each of the sub-stocks, thereby facilitating a multi-stock assessment. These assumptions are:

- Any mixing during Q1 is small / negligible, such that mature fish can be assumed to assemble in their own areas to spawn. This assumption does not apply to the juvenile

fish represented by the recruitment indices, which are not expected to perform seasonal migrations.

- Some unknown level of mixing is expected during the other quarters.

These assumptions are based on the conclusions of the North Sea stock ID workshop (ICES, 2020c): Tagged cod that were recaptured during the spawning season were typically caught within their release area, whereas recapture outside of their release area was much more common during the summer foraging season. Adults were found to disperse further than juveniles.

Based on these assumptions, assessment input data that are derived from the Q1 surveys are split to sub-stock, such that each sub-stock has its own Q1 index, annually varying maturity ogive and stock weights. The only exception is that the recruitment indices derived from the Q3 and Q4 surveys are also split to sub-stock, given the assumed limited movement of juveniles. Data that are annual (catches) or from a different time of year (the Q34 index) are treated as shared observations that represent the whole stock. In this case, multi-stock SAM sums the expected catch or index values (using the standard equations) from each sub-stock and compares the total expected value to the observations from the shared data. Additionally, landings proportions by sub-stock in Q1 and landings proportions by quarter (independent of sub-stock) are included as auxiliary data. A fleet-to-stock key (Table 2.1) is used to specify the vulnerability of each sub-stock to a catch, survey or auxiliary fleet in the observations.

Table 2.1. Fleet-to-stock key. A '1' means that a sub-stock is fully vulnerable to a fleet's observation while a '0' means that a sub-stock is not vulnerable to a fleet's observation.

	Northwest	South	Viking
Catch	1	1	1
Survey_Q34	1	1	1
Survey_Q1_NW	1	0	0
Survey_Q1_SO	0	1	0
Survey_Q1_VI	0	0	1
Survey_Rec_NW	1	0	0
Survey_Rec_SO	0	0.75	0
Survey_Rec_VI	0	0.25	1
AUX_SeasonProp	1	1	1
AUX_SubNew	1	1	1

Multi-stock SAM produces sub-stock-wise estimates of SSB, F and recruitment and is used to produce sub-stock specific forecasts.

2.3 Advice

Although forecasts are run at the sub-stock level, it is stated that “catches by sub-stock should not be taken as area-specific advice”, and a total catch value is advised for the entire stock. This is because, outside of Q1, specific sub-stocks cannot be identified without additional data (genetics or otherwise), i.e., there is no way of knowing that a cod caught in the northwestern sub-

stock area is in fact a northwestern cod or from another sub-stock that has migrated into the area. Landings proportions by biological sub-stock estimated in the assessment are significantly different to the annual landings proportions observed in the sub-stock areas, particularly for the Viking and Northwestern sub-stocks. For example, in recent years, the assessment estimates the Viking sub-stock to account for 20–30% of landings while 50–65% of Northern Shelf cod landings have been observed in the Viking area. This suggests that catches from the Viking area include fish belonging to other sub-stocks. Furthermore, the limitations of the data mean that the assessment's ability to resolve the dynamics of the different sub-stocks cannot be validated.

Given the data limitations, strong correlations in fishing mortality and current poor state of the southern sub-stock ($SSB < B_{lim}$), advice for the Northern Shelf cod is based on the MSY approach for the southern sub-stock and precautionary considerations to protect the southern sub-stock for the northwestern and Viking sub-stocks. Under this approach, the same reduction in F is applied to all three sub-stocks, in line with the mortality reduction for the southern sub-stock in the MSY approach scenario.

2.4 Other mixing stocks within ICES

The following sections detail how mixing is dealt with in the assessments of some other ICES stocks.

2.4.1 Greenland cod

Prior to the 2023 WKGRENCOD (ICES, 2023b) the Atlantic cod stocks in Greenland waters were assessed based on geographical boundaries. At the benchmark this was changed and is now based on genetic analysis, such that the Greenlandic cod stocks are assessed as separate genetic stocks. The three main genetic populations of cod in Greenland waters are West Greenland Offshore Spawning Cod (WOSC), West Greenland Inshore Spawning Cod (WISC), and East Greenland – Iceland offshore spawning cod (EGIOSC).

Extensive mixing of genetically different cod stocks occurs in West Greenland especially in the inshore area. Genetic and tagging data combined with survey data show that the EGIOSC stock typically migrate eastwards out of West Greenland waters at onset of spawning at age 5-6 yrs. The WOSC stock has its spawning sites on the offshore banks in West Greenland but do migrate inshore both as juveniles and adults. The WISC stock will primarily stay inshore. The inshore area is therefore a mixing area of all three stocks whereas the offshore area is primarily a mixing site for the WOSC and the EGIOSC stocks. Substantial isolation between major fjords along the coast appears likely, as this is indicated by tagging experiments, age distributions, recruitment patterns as well as trend in survey indices and commercial catches. The inshore stock is split into a northern (N-WISC) and southern (S-WISC) component.

Commercial catches, weight at age, and survey data are split into stocks are split into stocks using a GAM model. The model includes parameters for age, latitude, longitude, inshore /offshore, and cohort group. Due to gaps in the genetic data for the early part of the assessment period it was not possible to fit the model to individual cohorts. Each cohort is therefore assigned to a cohort group based on a range of criteria related to genetic composition and cohort distribution. It was found that assigning a cohort to the correct cohort group is important, therefore the genetic dataset is updated each year with app. 1200 samples from the survey and commercial fisheries. The model is fitted each year to the full genetic dataset (app. 12000 samples in 2024) and applied to split the data timeseries into stocks. For each of the stocks WOSC, N-WISC, and

S-WISC a SAM assessment is used to provide advice. For the EGIOSC stock it has not been possible to conduct an analytical assessment, the stock is currently a category 5 stock.

2.4.2 Western Baltic cod

Cod in the Baltic Sea is assessed and managed as two separate stocks, i.e. eastern and western Baltic cod, located in ICES Subdivisions (SD) 24–32 and 22–24, respectively. There is clear evidence that eastern Baltic cod regularly occur in SD 24 (Hemmer-Hansen et al., 2019). Given the apparent difference in biological parameters between the two stocks, eastern cod needs to be separated from the western stock, for stock assessment purpose. In later years there is also indication the Western Baltic cod is migration into SD 25, this is however presently not included in the assessment.

Stock splitting is based on otolith shape in combination with genetics or spawning cod sampled during the respective spawning time in SD 22 or SD 25. Stock-specific otolith shape description based on Elliptic Fourier Analysis provides a means for classifying individuals caught in a mixed-stock area to their respective natal stocks. For Baltic cod, this approach has been documented to separate individuals belonging to the eastern and western stock (Paul et al., 2013). This approach has been further developed and tested using genetically validated Baltic cod (Hemmer et al., 2019). Stock splitting proportions are calculated separately for subareas 1 and 2 (Figure 2.2), due to an east-west gradient in stock mixing proportions (Hüssy et al., 2016).

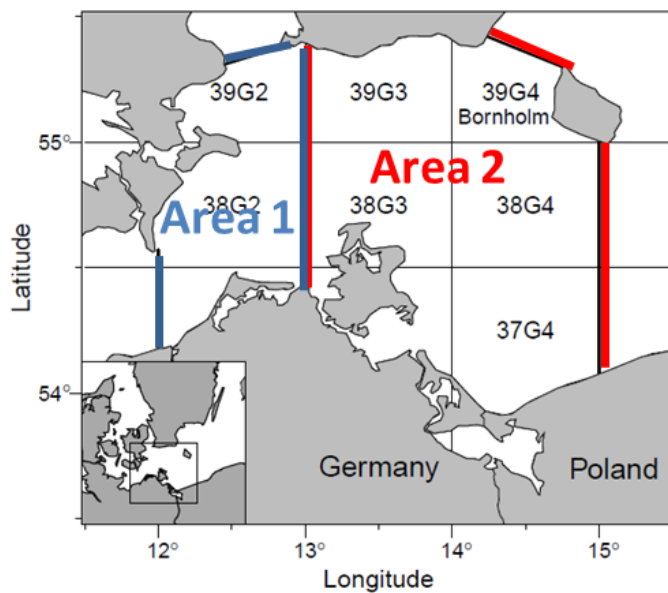


Figure 2.2. The mixing area in the western Baltic management area where the cod stock is split.

The time-series of estimated proportions of eastern and western Baltic cod within SD 24 are available for the years shown in Figure 2.3, based on otolith shape analyses and genetics from Germany and Denmark. Systematic differences in the proportion of mixing were found by subareas within SD 24, with a larger proportion of eastern cod closer to SD 25. The proportions of mixing in the easternmost rectangles in SD 24 and those in the middle of SD 24 were relatively similar. Therefore, these data were merged. The final proportions for splitting populations in SD 24 were estimated separately for two subareas, marked as Area 1 and Area 2 in Figure 2.2. To prolong the commercial data series of stock mixing proportions back in time, historical survey data from 1985–1995 were used. From 1996 until 2022, only commercial mixing proportions were used. However, there were several years without splitting data (1987–1991, 1997, 1999, 2001, 2004, 2009,

and 2012). The missing information for single years, when the data for adjacent years were available, was filled by averaging the data from neighboring years. In later years the commercial catches in SD 24 have been very low and therefore genetics samples derived from surveys have been used together with commercial samples to conduct the split. The resulting proportions of western cod in SD 24, by years and subarea for 1977–2023 are shown in Figure 2.3 (ICES 2019)

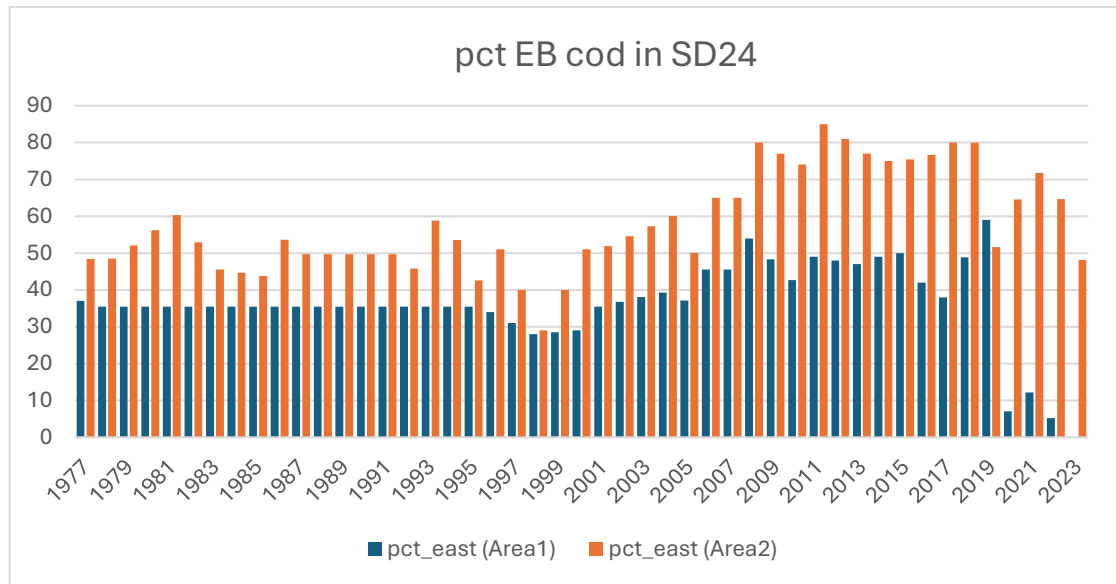


Figure 2.3. Final proportions for splitting populations in SD 24 were estimated separately for two subareas, marked as Area 1 and Area 2, based on a combination of genetics and otoliths.

Total landings in SD 24 are adjusted to include only those representing the WB cod population. For each country, annual landings of cod by ICES rectangles in subareas 1 and 2 within SD24 is submitted. These average proportions of landings between Areas 1 and 2 were then used as weighting factors to derive an average splitting key for landings in SD 24.

To translate the assessment into a management advice a template was developed for management that can be found in the 2019 and 2020 advice for the stock (ICES 2020).

To derive a management area-based total commercial cod catch for the western and eastern Baltic areas (subdivisions 22–24 and 25–32) in line with ICES advice for the two cod stocks, ICES considers that the following issues could be taken into account:

1. The distribution area of the WB cod stock is subdivisions 22–24. The proportions of the WB cod stock commercial catch taken in subdivisions 22–23 and Subdivision 24 have been quite stable since 1994, amounting to 76% and 24%, respectively, on average in the most recent three years.
2. The distribution area of the EB cod stock is subdivisions 24 and 25–32.
3. Commercial fishing in subdivisions 22–23 will provide a catch of the WB cod stock only.
4. Commercial fishing in subdivisions 25–32 will provide a catch of the EB cod stock only.
5. Commercial fishing in Subdivision 24 will provide a mixed catch of the EB and WB cod stocks. In the most recent three years, the ratio EB cod / WB cod commercial catch in Subdivision 24 has been 2.90.
6. In an area that includes two stocks of a species, the species TAC should be set such that the risk of overexploitation of the weakest stock is minimized.

The European Commission has requested ICES to provide information on catch opportunities by management area consistent with the stock advice, assuming a status quo distribution of the fisheries on subareas and stocks (option A in Table 2.2).

As an example (Option A in Table 2.2) assuming the geographical distribution of the commercial catch in 2020 remains as outlined in point 1 above and with average recreational catch in 2020, the distribution of a commercial catch of 5 105 t of WB cod will be 3 880 t in subdivisions 22–23 and 1 225 t in subdivision 24. However, catches in subdivision 24 should be zero in order to comply with the zero-catch advised for EB cod. With a status quo effort in 22-23, this would result in a TAC of 3 880 t for the western management area which can only be fished in 22-23. Alternatively, the implied commercial catch (5 105 t) could be taken entirely in 22-23. This would represent an increase of effort in this area which is considered the main spawning grounds for WB cod. This may negatively affect the spawning success of WB cod due to disturbance (though the effects on recruitment cannot be quantified). Given this circumstance the reintroduction of a temporal fishery closure during spawning time could be considered.

(Option B in Table 2.2), assuming the geographical distribution of the commercial catch in 2020 remains as outlined in point 1 above and with average recreational catch in 2020, the distribution of a commercial catch of 5 105 t of WB cod will be 3 880 t in subdivisions 22–23 and 1 225 t in Subdivision 24. Under this circumstance the additional amount of EB cod fished in Subdivision 24 is estimated to be 3 555 t, assuming the same ratio between EB cod and WB cod as observed on average during 2016–2018 in the commercial catches (i.e. 2.90, see point 5 above). This would result in a TAC of 8 660 t for the western management area which could be taken across the entire western Baltic management area. This option is not in line with the catch advice for EB cod.

Table 2.2 Cod in subdivisions 22–24, western Baltic stock. Scenarios illustrating the implications of zero catch advice for Eastern Baltic cod on the commercial catch by management area. Assuming a recreational catch of 2140 tonnes in 2020. Weights are in tonnes.

	Commercial catch WB cod stock			Commercial catch EB cod stock			Commercial catch of cod by management area (TAC)			
	A	B	C	D	E	F	G	H		
Area	Ad-vice Total	SDs 22–23	SD 24	Total	SD 24	SDs 25–32	SDs22–24	% TAC change (SDs 22–24)*	SDs 25–32	% TAC change (SDs 25–32)**
<i>a. Status quo distribution No catch of EB cod in Western Baltic management area</i>										
Calcu-lation		= A × 0.76 [^]	= A × 0.24 [^]		= C × 2.90 ^{^^}	= D – E	= B + C + E		= F	
EU MAP: F _{MSY}	5105	3880	0	0	0	0	3880	-59	0	-100
F=MA P F _{MSY} lower	3065	2329	0	0	0	0	2329	-76	0	-100
<i>b. Status quo distribution with catch of EB cod in Western Baltic management area</i>										
Calcu-lation		= A × 0.76 [^]	= A × 0.24 [^]		= C × 2.90 ^{^^}	= D – E	= B + C + E		= F	
EU MAP:	5105	3880	1225	-	3555	-	8660	-9	-	-

	Commercial catch WB cod stock			Commercial catch EB cod stock			Commercial catch of cod by management area (TAC)			
	A	B	C	D	E	F	G	H		
F=MA	3065	2329	736	-	2134	-	5199	-45	-	-
P _{FMSY}										

* Compared to the 2019 TAC for subdivisions 22–24 (9515 tonnes).

** Compared to the 2019 TAC for subdivisions 25–32 (29912 tonnes).

^ Average proportions of the WB cod stock commercial catch that has been caught in subdivisions 22–23 and Subdivision 24 in the most recent three years (2016–2018).

^^ The EB cod catch / WB cod commercial catch ratio observed in Subdivision 24 in the most recent three years (2016–2018).

2.4.3 Northeast Arctic cod and Norwegian coastal cod

Atlantic cod in subareas 1 and 2 is divided into multiple ecotypes with overlapping distributions but different life histories and populations dynamics. The northeast arctic cod (formerly ICES stock cod.27.1-2 and now assessed bilaterally between Norway and Russia) primarily inhabits the Barents Sea but is found along the northern Norwegian coast in particular during spawning season in March-April, where it migrates to its main spawning grounds in the Lofoten. It is a category 1 stock with age-based full assessment (ICES, 2021). The Norwegian coastal cod is mostly distributed along the coast but can be occasionally caught more offshore and is since 2021 managed as two different stocks respectively called northern coastal (cod.27.1-2coastN) and southern coastal (cod.27.2coastS) cod. Northern coastal cod is also a category 1 stock with age-based full assessment (ICES, 2024a), southern coastal cod started as a data-poor category 3 with trends-based assessment but was in 2024 benchmarked to a category 2 stock with SPiCT assessment (ICES, 2024b).

These ecotypes can be genetically separated but are primarily identified using otolith inner morphology during age reading, so their assessment does not account for mixing: each stock is assessed in isolation, where all input data is split into its respective stock based on otolith type. The associated surveys essentially cover one stock each (NEA cod for the winter & Lofoten surveys; coastal cod for the autumn coastal survey). The percentage of coastal cod in the winter and Lofoten surveys is calculated every year but is usually negligible (<5 % for 2024 data). That percentage of coastal cod is subtracted only from the Lofoten survey when developing NEA cod indices for the assessment. Likewise for the autumn coastal survey, the proportion of NEA cod is split out and not included in the index used in the coastal cod assessment. For commercial data, otolith type alone is used to assign catches to their respective populations.

Genetic analysis conducted in parallel shows that otolith type is generally fitting to discriminate between the two ecotypes, but also highlights higher uncertainties and misidentification rates for specific areas or for local coastal sub-populations whose life history and environmental conditions lead to inner morphologies closer to those of NEA cod. This issue is highlighted in the assessments and is a main factor of uncertainty for northern Norwegian coastal cod. In addition, both Norwegian coastal cod stocks likely encompass a complex structure of local substocks whose diversity could be vulnerable to local depletion. Because it is taken as part of a mixed fishery with NEA cod from which it cannot be visually distinguished, the advice is not associated to a separate TAC and the stock is managed through targeted technical measures such as increased minimum landing sizes within the baseline, and specific area closures.

2.4.4 North Sea and channel plaice stocks

Plaice in the North Sea and Channel are assessed as three separate stocks: Plaice in the North Sea and Skagerrak (Subarea 4 and Subdivision 20), Plaice in the eastern English Channel (Division 7.d) and Plaice in the western English Channel (Division 7.e). The Q1 migrations of mature plaice into Division 7.d are accounted for in all three assessments by allocating 50% and 15% of the plaice caught in the eastern English Channel to the North Sea and western English Channel stocks respectively. These percentages were estimated during WKFLAT in 2010 (ICES, 2010) based on published tagging results and previous studies (Hunter et al., 2004; Kell et al., 2004). However, migration likely fluctuates from year-to-year and the migration of each stock into Division 7.d remains uncertain. To address this issue, further research is needed on plaice migration and stock identity in the Greater North Sea Ecoregion and maybe in adjacent seas. Furthermore, a stock identification workshop and a benchmark focusing on plaice stocks will be required to account for changes in migration between the plaice stocks.

3 Investigation of relevance and use of different data types

The discussions on evaluating and monitoring sub-stock mixing that led to this workshop have mostly focused on the incorporation of genetics, which is a commonly used method for discriminating between populations. This focus was also driven by the current developments of the GenDC project whose goal is to investigate genetic differences between the different cod sub-stocks, and their potential integration into stock assessment and advisory frameworks. However, ahead of the workshop it was not yet fully clear to which extent genetics may be able to evaluate sub-stock mixing, and a dedicated effort was put into scoping different data types. A thorough evaluation of multiple North Sea cod biological traits and studies was conducted during both cod ID workshops (WKNSCodID & WK6aCodID) and eventually led to the current stock definition following the 2023 benchmark (ICES, 2023c). During the workshop these different data types were therefore discussed and compared again considering the now agreed sub-stock structure, with the purpose of evaluating their potential for discriminating between the northern shelf cod sub-stocks and quantify mixing.

Discussions for each data type are developed in the following sections, but their general relevance and applicability is summarized in the following table:

Table 3.1: summary of relevance and applicability as a tool to investigate sub-stock mixing for each data type

Method	Relevance to stock structure	Applicability to quantify mixing	Specific costs	Limits
<i>Morphology</i>	No support	None	None beyond routine laboratory	Redundant with genetic
<i>Life history</i>	Highly relevant to sub-stock dynamics	Limited to a diagnostic tool	None beyond routine laboratory	Individuals can't be ID from population signals
<i>Drift simulation</i>	Supports limited mixing	Good for hypothesis testing	Expensive data collection. Significant modelling effort.	Not observed data. Strong assumptions.
<i>Tagging</i>	Fundamental to current stock borders	New knowledge of movement (Viking and Southern); limited routine applicability	High upfront costs (survey effort and tagging). Recapture more passive.	Time-lagged and variable output
<i>Otolith morphology</i>	Supports some population signals	Good for finding population differences and complement other types	None beyond digitalization (but higher for 3D)	Requires cross-validation (genetics); affected by environment
<i>Otolith chemistry</i>	Supports population-specific spawning grounds and natal origins with low movement	Elucidates population ID with natal origin and movement; usable on historical archives	Time-consuming and high lab costs	Depends on environmental gradients strength and variability

3.1 Genetic

3.1.1 Review of methodology

From a sustainability and biodiversity perspective, a primary concern is accurately assessing and managing the stocks so that biological diversity is also maintained (Kerr *et al.* 2017). Furthermore, not accounting for complex population structures and mixing within stock units can lead to misrepresentation of fish productivity metrics and sub-optimal use of resources (Kerr *et al.* 2017).

For the purpose of this section, the term “sub-stock” should not be confused with the term “population”. “Stock” or “sub-stock” is a management term whereby individuals are aggregated based on a number of variables, including biological, economic and sociopolitical (Reiss *et al.* 2009; Kerr *et al.* 2017). “Population” is used to describe a self-sustaining group of individuals whose dynamics are biologically connected (Cadrin *et al.* 2014), in this case identified using genetics. Consequently, stocks or sub-stocks can contain either a single or multiple populations, each of which may display their own unique biological characteristics. In the sections below, we refer to the “Dogger” and “Viking” populations as the genetically unique units described in Heath *et al.* (2014). In this study, there was no genetic difference between “Dogger” fish collected from ICES Division 4.a-c, 7.d and the northern parts of Division 6.a.

3.1.1.1 Tissue sampling for genetic analyses

Tissue sampling for DNA extraction can be performed in several ways. Historically gill or fin-clip have been collected and stored in ethanol and some countries still do that. The GenDC project has developed a sampling protocol based on tissue sampling on board research vessels. This protocol specifies sampling procedures as well as optimal storage and labelling of samples after collection. The protocol was distributed to IBTS sampling coordinators for use during the Q1 survey in 2025. GenDC will collect feedback from the users to improve clarity of the protocol in a revised version

Several types of commercially available sampling kits are now also available for a safer and faster, although also more expensive, way of collecting tissue samples. Cefas and the Marine Institute’s genetic studies on sole (*Solea solea*), plaice (*Pleuronectes platessa*) and pollack (*Pollachius pollachius*) have utilised these systems to successfully obtain high quality whole genome sequencing reads. The kits typically include 2D-coded tubes for straightforward identification and sample tracking, as well as a genetic sampling tool incorporated into the screwcap of the tubes. The sampling tool is designed to pierce fish using the pointed tip while the rear facing cutting edge enables the collection of ~30mg of muscle tissue. These systems are optimised to help avoid contamination issues and have been successfully incorporated into sample collection pipelines onboard both scientific survey and commercial vessels. Muscle tissue typically yields lower quantities of DNA per sample compared to e.g. gill tissue and fin clips. Training is crucial if this equipment is to be used correctly onboard commercial vessels as ~30mg is the minimum tissue size required for successful whole genome sequencing. If smaller tissue sizes are collected there is a risk that sequencing may not have sufficient DNA to fully identify diagnostic loci. Routine application of genetic marker genotyping typically requires lower quantities of DNA and may hence not suffer from these restrictions.

3.1.1.2 DNA sequencing and genetic marker genotyping

Whole Genome Sequencing (usually referred to as “high coverage WGS”) is the gold standard approach for accurate estimation of genetic population structure. It can be used on individuals or pools of individuals within spawning locations and with the corresponding maturity characteristics. For these initial steps it is important to sample sufficiently large numbers of individuals from the spawning populations (Andersson *et al.* 2024). This information is then used to identify

genetic markers that can specifically distinguish genetic populations as needed (Andersson *et al.* 2024). These genetic markers can subsequently be analyzed on cost effective platforms to facilitate routine applications on large numbers of individuals. WGS allows identification of diagnostic SNPs with confidence due to the high coverage (typically 20-30x: this means that specific positions in the genome have been sequenced 20 or 30 times, with high quality sequences). The downside of WGS are the elevated cost and the relatively high effort that is needed for data analysis.

On the other hand, low coverage whole genome sequencing (lcWGS), is an increasingly used protocol. This approach is different from the previous one in the sequencing coverage achieved (as the name suggests, usually about 5x or below) meaning that diagnostic SNPs, such as outlier loci could be potentially missed. The main advantage of this technique, which has contributed to its high uptake, is the cost efficiency (Therkildsen and Palumbi 2017). In comparison to the relative high cost of high coverage WGS, the lower cost of lcWGS allows for sequencing of a larger number of individuals, which are also needed for accurate estimation of allele frequencies with this sequencing strategy (Lou *et al.* 2021).

Genotyping arrays (often called “SNP-chips” or “panels”) may include only the diagnostic loci identified using WGS, allowing for routine screening of an even larger number of individuals, and for this reason they are very useful tools when identification of genetic populations are required for fisheries assessments and management. They are produced with a substantial - initial - financial and scientific investment, and are usually then made commercially available. Examples of the application of genetic marker panels include genetic evidence that resulted in the realignment of horse mackerel stock units (ICES 2024) and routine genetically based monitoring of population mixing in Atlantic cod and herring.

3.1.1.3 Individual assignment methods

The baseline (spawning) individuals are used to train assignment models, and to choose the best fitting one amongst those available: this is crucial for high accuracy in the assignment (Chen *et al.* 2018). When baselines associated with specific genetic populations are artificially removed from analysis, individuals previously assigned to those populations are reassigned to the next most likely population. This highlights the need for a comprehensive collection of all unique spawning components to ensure that, for assessment purposes, individuals are not incorrectly assigned to populations outwith their sub-stock units. The output from assignment models are based on % likelihood calculations. Previous studies have set thresholds from >70 - >90% likelihood assignment as confirmation that individuals have been assigned to correct populations (Seljestad *et al.* 2024). As part of method validation and documentation, assignment power with the implemented set of baselines, genetic markers and assignment thresholds could be evaluated (see e.g. Ogden and Linacre 2015). Finally, for reproducibility and accessibility purposes, the underlying statistical approaches implemented in the assignment procedures should be clearly described. These analyses could be carried out using a single open source program which is reviewed periodically to ensure it continues to provide the best available science for the assessment. R- and python-based packages, such as assignPOP (Chen *et al.* 2018) and popfinder (Birchard *et al.* 2025) are two such open-source options.

3.1.2 Definitions of baseline

As reviewed above and in several ICES workshops, previous genetic studies of cod in the North Sea have found evidence for the presence of two populations (termed “Viking” and “Dogger” by Heath *et al.* 2024). In these previous studies, cod from the southern and parts of the north-western sub-stocks showed similar genetic profiles. However, since previous work was limited by the use of relatively few genetic markers and/or limited sampling, a first aim of the GenDC

project will be to collect spawning cod from the southern North Sea to investigate if there is evidence for the presence of a unique population in this area. The samples will be analyzed through full genome sequencing (see above) and related to similar data from cod collected in other parts of the North Sea, including cod from the “Viking” population and spawning cod collected from the northwestern North Sea.

The genetic marker panel currently implemented for population assignment in the GenDC project has been developed to identify the population of origin of cod in the transition zone from the North Sea to the Baltic Sea (described in ICES 2015 and ICES 2017). Consequently, the panel has high power for identifying these populations. ICES (2015) examined the power for identifying “Viking” and “Dogger” fish with the existing panel (Table 3.2). These analyses showed that the panel was able to differentiate between the two populations, in particular with the application of a more strict assignment threshold of >95%, although some level of mis-assignment should be expected. The baseline has since been updated with additional samples from the Kattegat, which has improved the diagnostic power with respect to this population.

Table 3.2. Assignment to three baseline populations with the existing assignment panel of 187 SNP markers (adapted from ICES (2015)).

	No threshold			95% threshold		
	N. North Sea ("Viking")	S. North Sea ("Dogger")	Kattegat	N. North Sea ("Viking")	S. North Sea ("Dogger")	Kattegat
N. North Sea ("Viking")	63%	24%	12%	77%	9%	
S. North Sea ("Dogger")	32%	67%	24%	23%	86%	7%
Kattegat	4%	9%	64%		5%	93%

New low coverage genome sequencing data from Viking (Viking Bank) and Dogger (Moray Firth) populations have been analyzed to identify highly differentiated genomic regions (Figure 3.1). The results show the existence of several potential candidate genomic regions of high differentiation that are not included in the current genetic marker panel. Consequently, the results indicate the potential for increasing the statistical power for identifying Viking and Dogger populations. The analyses will be updated with the inclusion of additional sequencing data from new baseline individuals collected during the GenDC project.

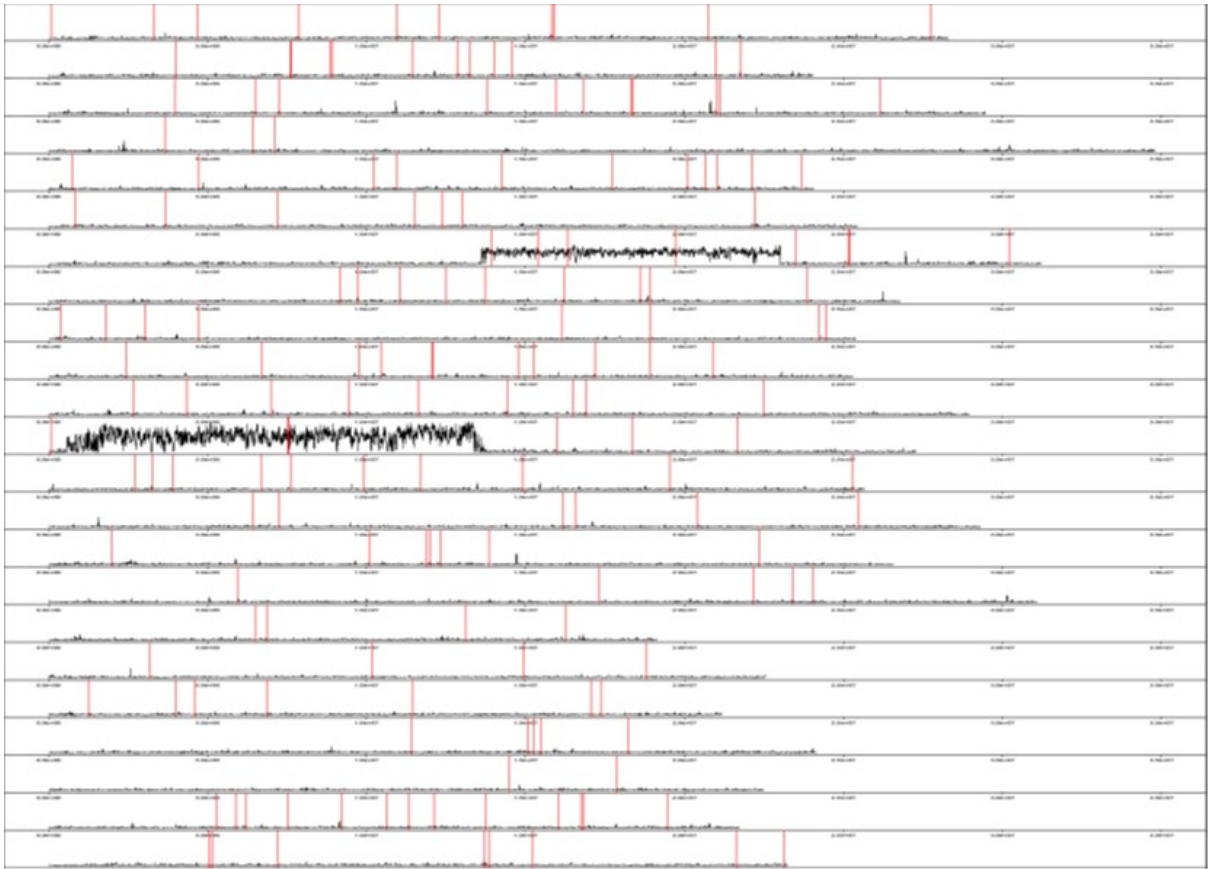


Figure 3.1. Genetic differentiation (F_{ST}) between Viking Bank and Moray Firth estimated from low coverage genome sequencing data. Each line represents a chromosome in the cod genome and values on the y-axis represent estimates of genetic differentiation. Red lines indicate the genomic location of the genetic markers in the current assignment panel.

3.1.3 Future directions

For decades, genetic methods have identified mismatches between biological populations and stock units (Reiss *et al.* 2009; Kerr *et al.* 2017). For cod, genetic evidence suggests that there may be multiple populations within the existing management areas in the North Sea as in several North Atlantic regions (Health *et al.* 2014; Wright *et al.* 2021). For the North Sea, Wright *et al.* (2021) found indications of genetic differentiation between the Minch (ICES Division 6.a) and the east of Shetland (ICES Division 4.a), which are currently assessed as a single sub-stock unit. These results may indicate mixing of two populations across the “Viking” and “Northwestern” areas, and hence that genetically based monitoring may be useful for future monitoring applications in this area. Additionally, these substock areas are not closed systems, and as such there is the possibility of further mixing with populations from adjacent geographical areas. For example, Health *et al.* (2014) identified the presence of cod with putative ‘Celtic’ genetic signatures from the Irish Sea (ICES Division 7.a) to the southern area of the west of Scotland (ICES Division 6.a). While ICES Division 6.a is part of the assessment of the Northwestern sub-stock, Division 7.a is not.

Genetic studies have revealed the presence of genomic islands of divergence in the cod genome (Hemmer-Hansen *et al.* 2013; Berg *et al.* 2016, 2017, Barth *et al.* 2019, Johansen *et al.* 2020) containing outlier loci, reflecting areas of the genome potentially affected by selection in response to environmental conditions, like salinity and temperature (Berg *et al.* 2016, 2017; Wenne *et al.* 2020). Furthermore, these outlier loci are often located within chromosome rearrangements (Berg *et al.*

2016, 2017) whose frequencies are characteristics of populations (Matschiner *et al.* 2022) and ecotypes (Berg *et al.* 2017; Pampoulie *et al.* 2023). Indeed, cod behavioral ecotypes found in Norway and Iceland were shown to exhibit large inversions on chromosome 1, 2, 7 and 12 (Berg *et al.* 2016, 2017, Pampoulie *et al.* 2023, Johansen *et al.* 2020).

Whole-genome sequencing analysis of the samples collected within GenDC has the potential to further improve the ability to discriminate among genetically differentiated populations within stock and sub-stock units. As such, future research should build on the knowledge generated by the GenDC project and focus on identifying all distinct genetic populations within the current cod stocks units by expanding the spatial sampling coverage. The GenDC project is currently collecting baseline (spawning) cod samples from across the assessment areas (Figure 3.2). However, additional baseline samples from within current sub-stocks could be analyzed to examine the presence of fine scale population structure. In addition, adjacent areas, e.g. Rockall, the Irish and Celtic Seas could be included. These baselines will improve the power to discriminate potentially genetically distinct populations in the assessment areas and improve the estimate of mixing among them.

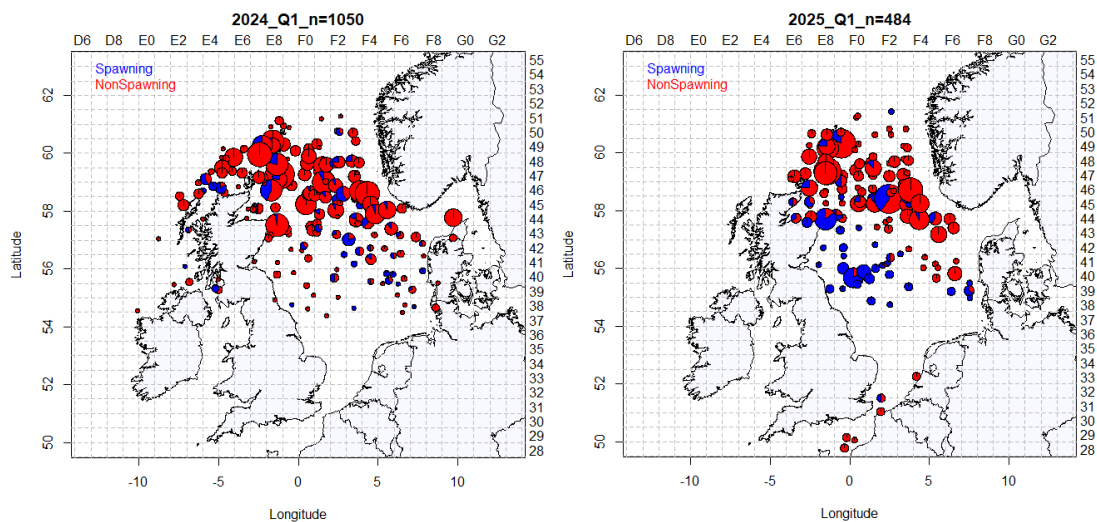


Figure 3.2. The geographic distribution of tissue samples collected during Q1 2024 (a) and Q1 2025 (b).

There is increasing evidence that a single reference genome from a single individual from one population/ecotype is insufficient to capture the full genetic diversity within a species (Thorburn *et al.* 2023). The pangenome represents the complete set of genes of a species; it is composed of core genes, present in all individuals, and variable genes, which are specific to certain populations. The creation of a pangenome for Atlantic cod would allow for a full characterization of genetic diversity in the species, of benefit to the research community as well as fisheries management. This will require significant effort and is not within the scope of the GenDC project. As a species of substantial economic, scientific, academic and conservation interest, Atlantic cod is an ideal candidate for such an effort, which could be undertaken by a future research consortium.

3.2 Tagging

During the workshop, a reanalysis of existing historical tag-recapture programmes from the 1691-2015 period was presented (see 3.5.2). While the results are promising in their support of sub-stocks with limited large-scale movement and mixing, their projection to the present must be done cautiously as the cod population and North Sea ecosystem as a whole have undergone significant changes in the time since.

While easiest to scale up thanks to lower costs, “standard” tag-recapture programs can still be costly (survey and sea time) and are limited in their routine applicability due to a variable passive recapture rate and period. New tagging effort is still strongly encouraged to derive direct, observable knowledge on individual movement across the three sub-stocks and at different life stages. A multi-year tagging program could provide the necessary “baseline” to assess current cod movement and mixing dynamics, in combination to genetics and other methods to confirm sub-stock identity.

Other “tagging” methods may also provide useful data and were mentioned during the workshop. For example, telemetry arrays allow for the precise tagging of individually marked fish equipped with an RFID chip whenever they pass close enough to receivers. International telemetry networks have been gradually implemented along many countries’ coastlines (see the [Fish Intel Network](#) or the [European Tracking Network](#)). More recently they have also been incorporated for monitoring of offshore structures such as wind farms. With the accelerating construction of offshore structures, telemetry could become a practical technology to follow fish movement not only along coastlines but also across open sea.

3.3 Otolith-based methods

3.3.1 Otolith morphology

Otolith morphology in 2D has been used successfully to distinguish between stocks in European seas, including Atlantic cod, although the degree of classification success is variable between stocks (e.g. Campana & Casselman, 1993; Galley *et al.*, 2006; Jónsson *et al.*, 2021). 2D morphology has also been used in combination with microchemistry for a range of stocks (e.g. Longmore *et al.*, 2010; Ferreira *et al.*, 2019, Morales-Nin *et al.*, 2022). The novel approach of 3D otolith morphometry (i.e. 3D sagittal otolith reconstruction from spherical Fourier descriptors; Andrialovanirina *et al.*, 2024a) showed a better classification with more accurate in delineating the stock than those obtained from 2D otolith shape (red mullet, *Mullus barbatus*; Andrialovanirina *et al.*, 2024b). This 3D otolith shape approach combined with environmental data analysis is a very promising tool for stock structure discrimination. Data for 3D otolith shapes are obtained by microtomography, and provide information on the full shape, specific to the individual sampled. Where differences exist between stocks, under genetic, physiological, and environmental control, these differences are therefore more likely to be observed by 3D than by 2D shape analysis. 2D and 3D approaches are easy methods of data collection, and these analyses are relatively low cost. There will be an ICES meeting around these approaches in 2025, with a workshop on emerging methods and technologies for the automated analysis of calcified structures (WKETAC, October 2025).

3.3.1.1 Interest for Northern Shelf Cod

In the context of northern shelf cod, otolith morphology could be a useful tool to develop and analyze in parallel of genetics. A review of available literature during both cod ID workshops showed that otolith morphology supported some levels of population specific signals across the

northern North Sea and west of Scotland areas. Notably, cod from Viking bank exhibited higher classification success against other areas in 4.a and 6.a, supporting some stock structure across those areas (Galley et al, 2006). Within today's sub-stock definition this would suggest otolith morphology as a potential tool to separate Viking cod from the other two sub-stocks. More tests are needed to ascertain whether it can also discriminate Northwestern from Southern.

Otolith morphology could be a simple yet successful method to introduce in parallel to genetic studies. Otoliths are already collected for the purpose of age reading and require only to be imaged for morphology studies. This can easily be done by photographing the otolith using a microscope / magnifying glass camera, even directly on board the vessel for samples collected from surveys. The stratification required would match exactly that of genetic samples meaning that each otolith morphology could be tested against / complement information from genetic analysis (for commercial sources this will depend on what kind of sampling scheme is decided). The development of 3D analysis is much more resource intensive and would likely be more suited as a scientific study rather than a routine tool for monitoring mixing.

A limitation of otolith morphology is that variability in shape stems from both biological (i.e. population-specific growth rates, maturity, etc) and environmental sources (i.e. higher temperatures may affect biomineralization and therefore overall shape). While the two are often correlated, for example a population living in warmer conditions also having faster growth and maturity, this means differences in otolith morphology may be found within an otherwise genetically uniform population due to local environmental differences, for example among cohorts.

Another type of otolith morphology that could be further investigated is the inner morphology of yearly growth rings. The size and contrast of cod translucent growth increments seem to show a significant shift in appearance along a latitudinal gradient in the North Sea, likely to correspond to fish experiencing different peak temperatures and seasonal ranges. It is unclear how prevalent these differences are or whether they can be used to identify individuals down to the sub-stock, but it could likely be a useful diagnostic tool to identify individuals that grew in the southern warmer regions and complement genetic identity. As a result of this first workshop, WKCODSCOPE recommends WGBIOP to organize a dedicated international exchange for sectioned North Sea cod otoliths.

3.3.2 Otolith chemistry

3.3.2.1 Trace elements

Otolith chemistry involves analyzing the elemental composition of fish otoliths, which incorporate environmental chemical signals as the fish and its otoliths grow. Trace elements are found in small but variable quantities in the environment in relation to the movement and mixing of water masses, seafloor composition, freshwater discharge, or external sources. These elements are incorporated in the otolith during biomineralization, and the chemical signatures of fish otoliths at different moments will therefore reflect the water chemistry of different habitats. Transsects of chemical composition from the otolith core (time of spawning) to the edge (time of death) can act as life-long chronological records of an individual fish, thus providing a tool to infer natal origins and migration histories. By comparing signatures across individuals and regions, otolith chemistry can be used to delineate fish stocks, even in the absence of genetic differentiation.

Three case studies in the North Sea were presented during WKCODSCOPE to illustrate.

3.3.2.2 Case study 1 – Atlantic cod in Skagerrak and Kattegat:

This case study builds on two EMFAT funded projects by DTU Aqua (Hemmer-Hansen et al. 2020; Hüssy et al. 2024). In these projects, otolith chemistry (trace elements) was found to be able to distinguish spawning origin between the genetically distinct North Sea and Kattegat stocks

using the elemental composition of otolith cores, especially strontium (Sr), barium (Ba), and manganese (Mn), which reflect environmental conditions such as salinity, coastal/offshore gradients, and hypoxia. Linear Discriminant Analysis (LDA) of otolith chemistry at different life stages indicated larval drift of North Sea cod into the Kattegat during the larval stage. In the Belt Sea and Sound area of the transition zone, two natal origin clusters were identified, but with extensive early life-stage mixing across the transition zone, and only post-settlement ecological separation. Life-stage-based chemical comparisons facilitate inference of migration pathways and spatio-temporal dynamics of stock mixing. Individual-level area assignments reveal ecological separations not evident in genetic data, especially in the transition zone between North Sea and Kattegat stocks.

3.3.2.3 Case study 2 - sand eel:

The investigation originates from ongoing discussions in ICES workshops (notably WKSANDEEL 2022 and 2023), which emphasized uncertainties in population structure and stock mixing boundaries. Otolith microchemistry was explored as a complementary tool to genetic analyses for resolving stock natal origin and movement patterns in DTU Aqua's EMFAF funded TRUST project.

Using samples from multiple cohorts (2016–2020), including both 0- and 1-group individuals, the study applies similar chemical fingerprinting and clustering approaches. Despite a known genetic gradient (northwest to southeast), natal origins remain unidentifiable without baseline data. Nevertheless, three distinct natal origin clusters emerged based on otolith chemistry, with temporal variation across cohorts, suggesting drift-induced changes in origin. Individuals from different natal origins seem to converge in the capture location in late summer as pelagic juveniles, complicating discrete stock assignment.

3.3.2.4 Stable isotopes

Stable isotopes of oxygen from otolith samples have been used to reconstruct temperatures experienced by fishes (e.g. von Leesen *et al.*, 2020, 2021) and fish movements between areas (e.g. Sakamoto *et al.*, 2019), throughout defined periods of their life histories. Data can be obtained across an otolith throughout the entire life of the fish with high temporal resolution. These data are therefore useful for determining the degree of stock mixing within clearly defined temporal periods. Oxygen isotopes in plaice otoliths have also been used with some success in identifying stocks (Darnaude *et al.*, 2014), based on differences in temperatures between areas used throughout the life history. It is worth noting that organic carbon, nitrogen and sulfur stable isotopes from muscle samples have also been used for geolocation of North Sea Atlantic cod and herring feeding areas, with reference to existing isoscape (stable isotope landscape) models, with similar location precision to light-based tagging (Trueman *et al.*, 2017; Wilson *et al.*, 2024). The advantage of stable isotope approaches to stock geolocation are that they can reconstruct locations for individual to population scale, from weeks prior to capture to the entire life history, on a temporally resolved basis, which can be highly valuable in quantifying mixing between stocks, while not relying on tagging studies for geolocation. Spatio-temporal reconstruction of movements, and therefore mixing, can be applied to individuals identified to stocks, and thereby can be useful for quantifying stock mixing outside of sampling periods. Stable isotope studies can provide data for any captured individual, potentially at a lower cost, that can complement and expand tagging and genetic approaches.

3.3.2.5 Interest for Northern Shelf Cod

Otolith chemistry could be a useful tool to be used for quantifying northern shelf cod sub-stock mixing in parallel to genetics, as it can both inform on spatial origin and individual movement over a lifetime. Otolith chemistry proves effective in:

- Identifying natal origin clusters
- Reconstructing life-history migrations
- Revealing spatiotemporal stock mixing patterns

Otolith chemistry has been used to identify natal origin clusters of cod in the Northern Shelf stock (Wright *et al.*, 2018) and to examine nursery to spawning migrations by year-class (Wright *et al.*, 2006; Wright *et al.*, 2018). However, further work to consider year to year variation in natal origin and life-history migrations as well as sub-stock mixing patterns is needed.

These insights are particularly valuable in systems lacking clear genetic differentiation and may also be complementary to genotyping for assessing mixing not only at capture time and location, but across life stages. This could provide important ecological information to resolve individual movement for the sub-stocks, as well as contrast genetic identity for unclear individuals. In case genotyping cannot fully differentiate Northwestern from Southern cod, otolith trace elements may be the most suitable alternative for quantifying mixing.

As detailed in the previous section, the existing routine collection of otoliths for age reading would ensure good availability of samples from survey sources, and a straightforward implementation in an eventual sampling scheme from commercial sources. Additionally, because otoliths are biomineralized structures, they do not degrade over time and can be safely archived over long periods of time. This means otolith chemistry could also be used to elucidate past movement dynamics by utilizing archived samples of northern shelf cod where no other biological data is available (such as genetics). Otolith chemistry is a promising alternative / complement to genetic analysis for routine evaluation of mixing and movement and may also be especially well-suited for hypothesis testing and targeted analyses. A proposal centered on using otolith chemistry for investigating northern shelf cod movement is currently being drafted and will target specific hypothesis testing such as historical mixing.

A significant limitation of otolith chemistry, in particular trace element analysis, is that the associated laboratory workload is both time and resource intensive. Otoliths go through a long preparation process and costly analysis (~ 4-6 times as expensive as genotyping of an individual), and all samples should ideally be centralized and processed at the same facility to prevent laboratory-specific differences. In the context of a sampling scheme from commercial sources to quantify mixing in time and space, this would limit the achievable sample depth.

In addition, otolith chemistry is directly related to the scale and variability of environmental gradients in which the fish grows. While the recent studies presented in this section support its usability even at finer spatial scales within the North Sea, it is important to evaluate whether those gradients exist at scales relevant to the northern shelf cod sub-stocks, and especially how variable they are from year to year as it may affect the discriminating power of otolith chemistry across different year classes.

3.4 Other data types investigated

Some of the data presented in the cod ID workshops weren't found to be relevant to quantifying sub-stock mixing dynamics during WKCODSCOPE.

3.4.1 Cod morphology

There was little evidence of meristic (countable traits, such as number of fin rays or vertebrae) and morphological (general shape and fish morphology) differences among cod in the North Sea that could be representative of population structure.

3.4.2 Life history traits

Persistent patterns of geographic variability in life-history traits were evident across the North Sea, which was a significant argument in support of separating North Sea cod into its existing three sub-stocks to better represent and monitor different productivity regimes. Cod growth and maturity varies along a latitudinal gradient delineated by a depth-driven thermocline, with faster growers to the south and slower growers to the north. Within the northern distribution range (areas 6.a, 4.a and northern 4.b), an additional longitudinal gradient in growth and maturity is evident and separates the Viking and Northwestern sub-stocks.

Life history traits showed however little value to study and quantify mixing during WKCODSCOPE. Population signals were a key finding and argument in support of the current stock structure but cannot be used as a direct stock discriminator due to the inherent inter-individual variability in growth and maturity. It could be a useful diagnostic tool to complement other methods, such as comparing length and maturity at age for genotyped individuals across all sub-stocks.

3.4.3 Drift and dispersal modelling

Like life history traits, during the cod ID workshops the distribution and dispersal of cod eggs and larvae in the North Sea provided evidence of some stock structure and highlighted important nursery areas in Skagerrak. WKCODSCOPE discussed the inclusion of egg and larvae studies in the study of the northern shelf cod sub-stocks but highlighted its limitations as a routine tool. The surveying of spawning success (eggs in Q1, larvae/ 0-group in Q2-4) can be resource-intensive and has little historical data available. The modelling part is also resource-intensive, and since it only partially relies on actual observations it is subject to a number of assumptions (duration of larval stage, swimming ability and potential active movement, etc). It also cannot be used directly to separate a catch of adult fish as it only informs of the potential distribution of juveniles.

3.5 Summary and roadmap on data types

3.5.1 GenDC

The GenDC project, funded by EMFAF-2023-PIA-FisheriesScientificAdvice, aims to enhance stock assessment and sustainable management of marine fisheries through integrated genetic data collection. One of the primary focuses is the Northern Shelf cod stock. As the southern cod component was not separated due to the distinct genetic fingerprint but due to other life history patterns, the initial task for the GenDC project has been to sample spawning cod from the southern area (4C). This is to investigate the possibility of establishing a baseline for this sub stock. Given the low abundance levels of this subpopulation and the minimal targeted cod fishery in the area, all countries fishing in the region have been contacted to participate in the sampling. The GenDC coordinated this in cooperation with the ICES survey working group (IBTS), as well

as through the RCG NANSEA. Currently, most samples have been collected from the IBTS survey, with additional samples obtained from observer trips and other surveys.

Table 3.3. Numbers of genetic samples collected during GenDC and sent to the genetic laboratory to be processed during the project.

Quarter\year	2023	2024	2025
Non-spawning			
1.quarter	0	920	369
3.quarter	369	329	0
Spawning			
1.quarter	0	130	115
3.quarter	0	0	0

The project's goal is to analyze all these sampled spawning cod from the southern area before the next WKCODOSCOPE meeting in the fall, so the results can be incorporated into future sampling designs. Additionally, the project aims to strengthen the baseline between the Viking and Northwestern components with additional samples were some of these have already been collected.

3.5.2 Reanalysis of tagging

To consider the possible extent of mixing of fishable sized cod among the 3 sub-stock areas, tag-recapture data from English and Scottish tag-recapture programmes from the period 1961-2015 were re-analyzed. Release and recapture positions from Data Storage Tagged (DST) cod were also included.

Tag-recapture data were available over all months of the year for the Northwestern and Southern sub-stocks but not for Viking. Tag releases from quarter 1 (spawning period) recaptured after more than 90 days in other months of the year were extracted to obtain an estimate of post-spawning movement for the Northwestern and Southern sub-stocks. The percentage recaptures from release sub-stock areas was 97 and 94% for Northwestern and Southern sub-stocks, respectively (Table 3.4). The total mixing for all tag releases was also considered for the three sub-stocks. Again, the percentage of tagged releases recaptured in the same sub-stock area was 96% for both the Northwestern and Southern sub-stocks (Table 3.5). In contrast, for Viking only 78% remained within the sub-stock area, with 18% moving into the Northwestern sub-stock and 4% into the Southern sub-stock. However, a couple of large Viking releases were made within 1-3 kms of the sub-stock border in ICES rectangles 48E9 and 47E9. Removal of these adjacent release sites reduced the proportion movement from Viking to Northwestern down to 10%, with 86% remaining within Viking. Full details of the tag-recapture re-analysis, together with similar sub-stock re-analysis of DST and otolith chemistry data are given in the working document by Wright (WDX).

The re-analysis of tagging data suggests that while the sub-stock areas do largely reflect groups with little exchange among them, estimates of mixing around the borders of Northwestern and Viking sub-stocks and to a lesser extent between these sub-stocks and the Southern sub-stock would help quantify the current exchange rates. It should also be noted there is also very occasional movement beyond the Northern shelf stock boundaries into adjacent ICES stocks.

Table 3.4. Tag-recapture results for Northwestern (NW) and Southern (S) sub-stock releases in quarter 1 (spawning) that were at liberty for 90+ days and recaptured in other quarters. Viking (V) and other recapture areas were included to show movement beyond NW and S sub-stocks.

Release\Recapture	Numbers recaptured					Proportion recaptured		
	NW	S	V	Other	Total	NW	S	V
NW	949	12	11	4	976	0.97	0.01	0.01
S	69	1583	26	5	1683	0.04	0.94	0.02

Table 3.5. Tag-recapture results for all sub-stocks regardless of time at liberty. Data for Viking includes releases < 3 km from NW sub-stock boundary.

Release\Recapture	Numbers recaptured					Proportion recaptured		
	NW	S	V	Other	Total	NW	S	V
NW	6249	112	157	12	6530	0.96	0.02	0.02
S	191	5559	49	9	5808	0.03	0.96	0.01
V	95	24	417	1	537	0.18	0.04	0.78

3.5.3 Other scientific recommendations and efforts

Moving toward the WKCODSCOPE II at the end of 2025, the genetic analysis central to the GenDC project remains the primary focus for developing methods to monitor and quantify sub-stock mixing in time and space. The discussions on other data types during this first workshop have, however, highlighted the potential for other methods to complement, if not substitute, genetic analysis. In addition, certain ecological aspects of northern shelf cod sub-stocks currently lacking could be investigated to strengthen the assessment.

3.5.3.1 Tools to help quantifying mixing

In the short term, it is recommended that all otoliths from individuals whose genetics have been analyzed for the baseline in GenDC are photographed and a collection curated for shape analysis. This pilot study could inform on whether otolith shape can be used to discriminate between sub-stocks by using known or assumed identity from spawning fish captured in their respective sub-stock areas. In case genotyping does not succeed in separating three sub-stock specific baselines (in particular for Northwestern and Southern cod), the results of this pilot shape analysis may provide additional information to separate them. Longer term, should routine sampling and genotyping of cod be conducted to evaluate mixing, shape analysis of all associated otoliths could be carried out to complement the results and help separate the sub-stocks. Otolith trace elements are promising but costly, and their potential implementation in a routine sampling scheme will be dependent on the effectiveness of genetics. Long term, trace element analysis could be considered as complementary.

3.5.3.2 Tools to strengthen scientific knowledge on the sub-stocks

Several studies have been highlighted for their potential to elucidate ecological differences between sub-stocks. In the short term, differences in otolith annual increment characteristics along a latitudinal gradient should be investigated through an international age reading workshop. The reconstruction of historic natal origin, movement and mixing using archived otolith trace elements should be explored, as it may complement past tagging efforts to evaluate and potentially constrain mixing assumptions in the assessment. It is also of high priority to implement new tag and recapture studies to evaluate contemporary movement of cod.

4 Sampling Strategy

4.1 Research Vessel

Genetic samples (fin clips) have been collected on the North Sea International Bottom Trawl Surveys and other North Sea surveys for the GenDC project (Section 3.5.1). The workshop concluded that this sampling should be continued using the same protocol during surveys taking place throughout the year to contribute to the estimation of the quantity of mixing of the sub-stocks within the stock area.

Surveys identified as possible sources of samples were: NS-IBTS Q1 [G1022], SWC-IBTS [G4748], NSS Q1 [G1758], NS-IBTS Q3 [G2829], BTS [B2453], Q4 SCOWGFS Q4 [G4815], NSS Q4 [G7438], SIAMISS-Q2 [G3745], IE IFGS.

The workshop agreed the aim would be to collect both genetic samples and otoliths to cover both scenarios of genetically determining the sub-stocks or needing to use alternative approaches. The exact requirements for otolith collection should be clarified at the next workshop. It was agreed that collecting samples should be a priority, as they can be stored until funding for the analysis of the samples is available.

4.2 Commercial fisheries

4.2.1 Overall statistical approach

To determine the mixing of substocks within commercial catches requires samples taken directly from the catches themselves. Sampling of catches is more complex than research vessel surveys, where hauls are the usual primary sampling unit and the sampling locations are pre-determined and can cover the whole area of interest. For catch sampling, it is important to cover the temporal and spatial coverage of the catches but in this case, the vessel or fishing trip are usually the primary sampling units and hauls are clustered within trips, and trips clustered within fishing vessels. The estimation procedure should take the multi-stage sampling into account.

When designing a new sampling scheme, it is important to be clear of the aim of the scheme, and to determine the parameter of interest. A short term aim, which could be used in advice is to partition the national and international catch weight by substock. A longer term aim would be to partition the national (and thereafter international) catch numbers-at-age by substock, for use in the substock assessments. The former would require fewer samples than the latter for the same level of precision.

With either aim, we would require to collect both genetic samples and otoliths (as per the current protocol) to cover both scenarios of genetically determining the sub-stocks or needing to use alternative approaches.

It is standard, when designing a new sampling scheme to conduct a pilot survey to both test out the protocols, and also to determine an estimate of the parameter(s) of interest, and hence to determine the ideal sample size. The workshop therefore concluded to attempt pilot surveys as soon as possible, ideally in 2025, but otherwise 2026, and that analysis of these samples should be a priority so that a more formal sampling scheme can be developed.

Following the pilot scheme, the ideal scenario would be to develop a regional sampling scheme, covering all nations fishing the Northern Shelf cod stock. This scheme would have standardised

protocols where necessary but can allow some flexibility. Further work may be required to develop this sampling scheme and to involve national data submitters regarding estimation of catch numbers-at-age by substock.

4.2.2 Practical issues

An efficient method to collect samples is from landings at markets, however locational information collected by this method is likely to be at the statistical rectangle level at best, losing detail on the exact location the cod were caught.

The other alternative is to collect samples onboard fishing vessels, either by scientific observers, or through sampling by industry, e.g. fishing crew. This has the advantage of being able to collect samples from the whole catch rather than just the landings, as well as detailed positional data. The collection of samples through scientific observers would be costly if collected through a new scheme, however could be efficient if carried out as part of typical observer sampling schemes. This would have the added benefit that the data could be used to partition the catch-at-age data used in stock assessments by substock directly using information collected on the same trips, however sample size is usually low. Industry sampling has the advantage of the possibility of a larger sample size, but would require training, and the direct link to estimation of catch-at-age would not be available.

4.2.3 Onboard sampling protocol

Under the GenDC project a protocol for genetic sampling has been developed. The protocol lists the equipment needed, a detailed description of the procedure to follow when taking a tissue sample for genetic analysis and the optimal storage and labelling practices. The protocol has been shared widely with all national correspondents for the DCF program and contact points for non-DCF countries as well as cruise leaders for the IBTS and BITS surveys covering the south-western North Sea to the Eastern Baltic Sea. A request for sample collection from survey and observer programs was made. To ensure the necessary data is collected for sample analysis, a simplified standardized data format was also provided based on the DATRAS format. Using this format means that uploading of the resulting genetic data to DATRAS in the future will be simplified. The protocol was developed based on user feedback and comments are expected from the recent meeting of the ICES International Bottom Trawl Survey Working Group (IBTSWG).

The applicability of the protocol was discussed during the workshop in light of the varying conditions and work flows onboard both research and commercial fishing vessels. The importance of standardized protocols was highlighted. Regulations related to the quantities of alcohol were mentioned which could be overcome by providing pre-filled sampling tubes. The importance of size of the tissue sample was highlighted as was the need to have the samples stored correctly. The use of specially designed tissue collection tools used in some herring genetic sampling programs were discussed, with the main concern being the small size of the tissue sample that is extracted while advantages are ease of use, the lack of additional equipment and space needed and avoiding cross-contamination.

The protocol (Annex 3) can be used as a template and should be reviewed and adapted for any pilot studies or commercial sampling programs and in such cases a suitable data format would be needed.

4.2.4 Brief summary of main cod fisheries and possible sampling approaches by country

4.2.4.1 Scotland

In 2023 Scottish fishing vessels landed 501 thousand tonnes of seafish and shellfish with a gross value of £683 million with vessels most active in ICES Areas Northern North Sea (ICES Area 4.a) and the West of Scotland (ICES Area 6.a). Total landings of demersal species in 2023 amounted to 100,156 tonnes with cod contributing 10,546 tonnes, making it the sixth most valuable species landed in Scotland. In recent years the reduction in advice on Total Allowable Catch has resulted in less directed fishing for cod with catches mainly limited to mixed demersal fisheries by Demersal Trawlers and Seiners with 87% of landings being caught in Northern North Sea (ICES Division 4.a) , 1% in Central North Sea (ICES Division 4.b) and 8% in West of Scotland (ICES Division 6.a).

Sampling of commercial catches at sea are carried out through a Joint Observer Sampling Scheme for sampling biological information on catch on board vessels, carried out under the UK Data Collection Framework (<https://www.gov.uk/guidance/data-collection-framework>). This scheme has the potential to provide opportunities for sampling of cod catches but given that the observers are onboard to carry out a structured sampling scheme, it may be that sample size would be few but could be frequent. Observer trips are carried out throughout the year with sampling stratified on a quarterly basis, targeting main fishing areas (Inshore and Offshore)

Sampling of landings is also carried out at Scottish ports and, again, has potential to provide opportunities for sampling. Sampling is generally carried out on a monthly basis with vessels selected at random. However, fish being landed are usually already cleaned and gutted so it may not be possible to collect sex and maturity data, although whole fish could be brought ashore for sampling, at a cost.

Additionally, the largest Fishermen's Organization (the Scottish White Fish Producer's Association) has indicated that they are very supportive of the efforts being made to improve stock assessment and sustainable management through integrated genetic data collection. They realise that collection of genetic information could be problematic and have offered to help in any way they can, including collection of genetic samples by their own crew. Clearly, this would necessitate a collective effort to provide appropriate training, sampling protocols, pre-prepared vials and sampling tools. Perhaps a short pilot study could be undertaken so as to evaluate the potential of using fishermen to collect samples. An immediate benefit would be that samples could be obtained relatively quickly then analysed at a later stage.

4.2.4.2 England

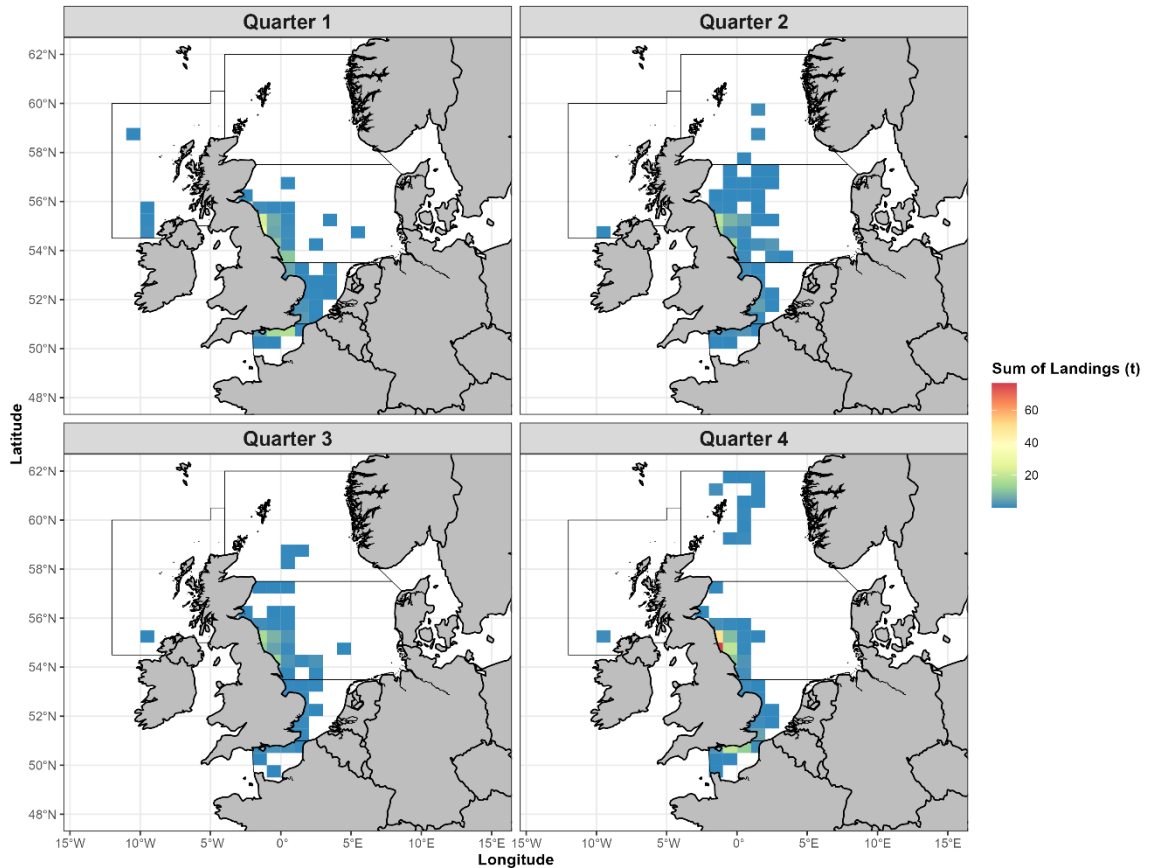


Figure 4.1. Volume of commercial landings of cod per quarter from 2019-2024 for English and Welsh fishing vessels within cod sub-stock assessment areas (iFish 2024).

Vessels taking part in mixed demersal fisheries are responsible for most English and Welsh cod landings during the last 5 years. These vessels use a combination of otter trawls and longlines. Relatively large volumes of cod were also recorded in targeted nephrops trawls. Cefas has an observer program which undertakes biological sampling onshore and at sea. This program is split into two teams which are responsible for distinct fisheries in the north and south of the country. The northern team covers ports from the Scottish borders to the Welsh borders on the west coast and down to Brixham. They work predominately with trawling vessels targeting *Nephrops*, crabs and lobsters, but also on trawlers targeting sole and various species of rays. The southern team works with fisherman operating from ports in Newlyn, Plymouth and Brixham utilising multiple gear types targeting shellfish and demersal species.

4.2.4.3 Norway

4.2.4.3.1 Port sampling programme

The Norwegian port sampling programme covers demersal fish in ICES subareas 1 and 2. It is carried out using a vessel travelling from port to port, operating for around 120 days throughout the year. At each port, samples are taken from any vessels landing within the timeframe that samplers are available, taking length and weight measurements, and extracting otoliths. Samples are taken mainly from fish landed by coastal vessels that land fresh fish, and sampling is done inside the plant. More information about the port sampling programme is available from Hirst et al. (2004) and ICES (2024).

4.2.4.3.2 Norwegian Reference Fleet

The Norwegian Reference Fleet is a group of active fishing vessels that are paid to provide information about their catches and fishing activity. The composition of the fleet aims to cover the commercially important fisheries in Norway and is divided into an offshore and coastal segment. The selection of vessels is an open tender process, which lists a series of required and desired criteria that aim to select a “typical” vessel in the priority fisheries (Clegg & Williams, 2020). If multiple vessels are eligible then the contract is awarded randomly. Contracts last for four years, after which the tender is reoffered. Vessels can re-apply but gain no advantage for previous participation.

Once a contract is awarded, the vessel is fitted with sampling equipment, which include an electronic measuring board and weighing scales connected to a tablet computer that runs the Fish2Data software developed by the Institute of Marine Research. Selected crew are trained in sampling protocols and species identification, and the vessel is allocated an IMR technician as a mentor, who will be the first point of contact for the vessel, and process data deliveries.

Sampling protocols vary between offshore and coastal fisheries and for specific fishing gears. However, as a general rule, offshore vessels record landed catches and fishing activity for each fishing operation. Every third fishing day, offshore vessels also record discards and fishmeal, and take biological samples of selected species. Coastal vessels record landed and discarded catches for each fishing day, taking biological samples on a weekly basis.

In addition to providing data to stock assessments and wider management advice, a core aim of the project is to increase collaboration and strengthen dialogue between researchers and the fishing industry. The mentoring system is a key aspect of this collaboration, as the mentor gains a personal insight into the fishery whilst communicating results and knowledge to fishers. Annual general meetings are held to provide a forum for discussing both the project and fisheries more generally. This is also an opportunity for scientists to present results and chat with fishers.

4.2.4.3.3 Catch Sampling Lottery

The Catch Sampling lottery is a probabilistic survey method used for at-sea biological sampling to gain reliable information on the age- and size-structure of commercial fish stocks. The programme is based on three pillars: probabilistic sampling of hauls, two-way communication of electronic logbooks, and co-sampling (Otterå et al. 2023).

At the heart of the sampling design is the lottery “machine”, which uses the Electronic Reporting System (ERS) to intercept a catch report from a vessel, calculate the sampling probability for that haul, then send a response to the vessel informing them whether a sample is requested or not for that haul. If sampling is required, then crew take a 15 kg sample of fish which is stored on board and delivered alongside the catch upon landing. The delivery site then posts the sample to IMR for processing.

The necessary infrastructure was built during the development in the pelagic fisheries and became integrated in the ERS when the lottery became mandatory in 2018. IMR has also developed a web-based tool to support data processing of lottery samples, tracking requested samples and linking them between ERS reports and IMR’s core database. There is therefore minimal technological development necessary for an expansion to additional fisheries.

A pilot study is currently underway to extend the catch sampling lottery to whitefish factory trawlers. The fleet consists of 38 vessels and accounts for over 30% of the total annual Norwegian catch of cod. Through a collaboration with three vessels, the framework developed in pelagic fisheries has been applied to whitefish factory trawlers to address the practical constraints of applying the sampling design originally tailored for pelagic fisheries.

4.2.4.4 Denmark

4.2.4.4.1 The Danish cod fishery

In the time period 2020-2024 the main Danish cod fishery has been conducted in the North Sea in a trawl fishery with mesh size >120 mm where more than 50% of the catches in average has been cod. This is followed by flyshooters >120 mm with 27% cod and large meshsize gillnetters (120-220 mm) with 17% cod in the landings.

In Skagerrak the largest fraction of cod is landed in the *Nephrops* fishery (mesh size 90-119 mm) where cod is 52% of the total landings. This is followed by the gillnetters with same mesh size as in the North Sea where cod is contributing to 19% of the total landings.

Area	metier_level6	pct_cod
27.3.a.20	OTB_MCD_90-119_0_0	52
27.3.a.20	GNS_DEF_120-219_0_0	19
27.3.a.20	OTB_MCD_>=120_0_0	11
27.4	OTB_MCD_>=120_0_0	50
27.4	SSC_DEF_>=120_0_0	27
27.4	GNS_DEF_120-219_0_0	17

4.2.4.4.2 The Danish sampling program

In Denmark the commercial cod catches are sampled in 2 different programs: the at sea observer program and the market sampling program.

The at-sea observer programme samples for length, age, weight data of landings and discards of demersal species as well as for brown shrimps and deep-water shrimp. All species caught are registered for total weight and length but only selected species for the area (including cod) are collected for age and individual weight. The main aim of the observer trips is to measure the discarded part and only weight by species is recorded for the landed part. Presently, fish that are collected for biological information are brought to the laboratory in land.

Denmark has applied 6 fleet lists (sampling frames) for the at sea observer programme with a similar selection design however, with different target species and effort. The vessel lists are presently covering 3 groups that are targeting cod in the North Sea or Skagerrak:

- Gillnets - Demersal – North Sea and Skagerrak
- Trawler / seiners - Mixed - Skagerrak
- Trawler / seiners - Mixed – North Sea

Effort allocations (observer trips) between the vessel lists are based on the total effort (trips) available allocated according to the numbers of trips in each vessel list group. Each stratum has incorporated a minimum number of 2 trips. Each vessel list is stratified by quarter. Each vessel on a given list has an equal chance of being selected.

The purpose of the marked sampling program is to sample biological samples (age, length, weight) from commercial landings at markets from a list of selected stocks and harbors.

The PSU is defined as harbor*week. The stocks selected for market sampling are listed by the harbors where the fish are sold. The selected harbors are ranked by weight of landings, percentage of total landings, number of landings by harbor and the costs of getting to the harbor, and only harbors where 80% of the landings of the selected stocks are landed have been included in the sampling programme based on the previous year's landing data. The PSUs not included in the sampling scheme are mainly smaller harbors. A total of 23 harbors/ landings sites have been selected based and the list of selected harbors is updated annually based on the previous years' data, and the number of samples per quarter depends on the stock. It is presently not possible to get information on the position a given fish is caught in but SD or ICES square.

4.2.4.5 Sweden

In 2024, Swedish fishing vessels landed 800 tonnes of cod from the Skagerrak, North Sea and the Kattegat. The main cod catches were taken in the demersal trawl fishery, with 53% in the Skagerrak, 47% in the North Sea and less than 1% in the Kattegat. The main part of the landings (87%) was taken by trawls with ≥ 120 mm mesh size, targeting demersal fish in Skagerrak and the North Sea, followed by the mixed demersal trawl fishery in Skagerrak, targeting *Nephrops* and fish (7%).

Sampling of commercial catches at sea is conducted through an on-board observer programme, carried out under the European Data Collection Framework. Observer trips are carried out throughout the year, stratified by quarter and targeting main demersal fisheries. The sampling includes length measurement of all species, and sampling of age and individual weight for discards of cod and plaice. Sex and maturity are not sampled in the commercial sampling. The observer programme mainly covers Skagerrak and Kattegat, with very few occasional trips in the North Sea. It would likely be possible to collect DNA samples from discarded cod, while landed cod might be more difficult to include due to time constraints for the observers.

Sampling of cod landings is carried out at the main market site on the Swedish west coast. The sampling is performed by a subcontractor and hence SLU-Aqua does not fully control the sampling environment. It needs to be investigated if collection of DNA-samples is possible, but considering the more sensitive nature of DNA-sampling (risk of contamination, etc.), the market sampling is probably not well suited for this kind of data collection.

4.2.4.6 Germany

Germany takes North Sea cod mainly in large meshed (≥ 120 mm) otter trawl fisheries (with vessels of 24-40 m LOA). Two types of gadoid fisheries exist in Germany: 1) Most cod is caught in a mixed gadoid fishery targeting cod, haddock and saithe together. 2) The other fishery is targeting saithe only with a minor amount of cod bycatch. Bycatch of cod in other fisheries (e.g., *Nephrops*) is currently very low. In addition, 3) there is a small gillnet fishery (with vessels of 12-18 m LOA) catching cod as well.

Germany only conducts onboard observer trips sampling unsorted catches. This takes place under the DCF. The observers operate year-round. A potential cooperation with the industry to collect small amounts of cod from commercial trips would need to be established first.

4.2.4.7 The Netherlands

In the Netherlands, cod is mainly caught as a wanted bycatch species in mixed demersal fisheries for flyshoot (SSC), otter bottom trawls (OTB) and conventional beam trawlers (TBB). In SSC and OTB, highest landings of cod are with mesh size ≥ 120 mm, whereas for TBB the highest landings are with mesh size 70-99 mm. The highest proportion of Dutch cod landings come from the North

Sea (ICES Subarea 4), though cod is also caught in Skagerrak (ICES Division 27.3.a.20) and the Eastern English Channel (ICES Division 27.7.d).

Within the Netherlands sampling of cod is carried out under the National Data Collection Framework (DCF) in accordance with end-user needs; landings are monitored with market sampling and discards through a self-sampling program with a reference fleet. Biological parameters such as weight and length are collected in both programs, age is only monitored in the market program

4.2.4.8 Belgium

The Belgian cod catches originate from the large meshed (≥ 120 mm) beam trawlers (TBB_DEF_ ≥ 120 ; 85% of Belgian landings in 2024), followed by the otter trawlers targeting crustaceans (OTB_CRU_70-99; 7% of Belgian landings in 2024) and large meshed otter trawlers (OTB_DEF_ ≥ 120 ; 3% of Belgian landings in 2024). The Belgian commercial fishing fleet fishes in all three subareas where the cod substocks reside, from the eastern English Channel (27.7.d) over the southern (27.4.c) and central North Sea (27.4.b) up to south-west of the Norwegian coast (27.4.a). Most catches are realized in the Northern part of Division 27.4.b off the Danish coast in quarter 3 and 4.

Belgium conducts at sea sampling with observers for cod, financed under the Belgian National Data Gathering Programme (DCF) with trips as primary sampling unit. Trips are sampled based on ad hoc selection where the effort distribution of the fleet from the year before is used as guidance. However, this selection is also influenced by the current behaviour of the fleet. Observers register total weights and length for landings and discards. Biological parameters (age, individual weight and length) are determined for 3 and 5 fish per cm class for landings and discards respectively.

5 The way forwards

In the short-term, any results from reanalyses and / or pilot studies relating to mixing rates could compliment the advice for Northern Shelf cod, i.e., advice is provided following ICES guidelines with additional information provided in the 'Issues relevant for the advice' section.

If reanalysis of the tagging data, or other studies, could satisfactorily conclude negligible mixing of the southern sub-stock (e.g., <5%), it may be possible to account for this in the current modelling framework and advice, e.g., by fixing the Q1 landings proportion for the southern sub-stock. However, concerns were raised regarding how multi-stock SAM would then allocate the shared catch-at-age among sub-stocks, given this data cannot currently be split to cod area, even under the assumption of negligible mixing. In this case, satisfactory simulation testing would have to be demonstrated before any change to the model configuration could be considered. If it were to become possible to provide catch-at-age by cod area based on location alone, the catch-at-age for the southern sub-stock could be separated from the northwestern and Viking sub-stocks (which would remain combined) and modelled as a separate fleet within multi-stock SAM (via the fleet-to-stock key; Table 2.1). Both of these options would, however, have to be supported by strong evidence of negligible mixing of the southern sub-stock.

If reanalysis of the tagging data, or other studies, cannot satisfactorily conclude negligible mixing of any of the sub-stocks, it becomes necessary to wait for the results of pilot studies and sampling to inform mixing rates, which could be used (1) to split the data, (2) directly in an assessment model and / or (3) to post-process the results. Intersessional modelling work and simulation studies will be needed to assess the value of the genetic or other stock identification information and inform readiness for a future benchmark, e.g., one year of data may be sufficient or a time-series may be required. If it were to become possible to obtain catch-at-age and other input data by biological sub-stock, then future assessments are not necessarily constrained to multi-stock SAM and could consider modelling individual stocks (similar to those described in Section 2.4) or frameworks that explicitly model movement rates.

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Annex 1: List of participants

Name	Institute	Country (of institute)
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Brian Stock	Institute of Marine Research	Norway
Christophe Pampoulie	Marine and Freshwater Research Institute	Iceland
Côme Denechaud	Institute of Marine Research	Norway
David Murray	Cefas	UK
Edward Farrell	Killybegs Fishermen's Organisation Ltd.	Ireland
Eef Cauwelier	Marine Scotland Science	UK
Elena Balestri	Scottish Fishermen's Federation	UK
Francesca Vitale	SLU	Sweden
Hannah Sterling	DEFRA	UK
Ilaria Coscia	Marine Institute Ireland	Ireland
Imogen Cessford	DEFRA	UK
Jakob Hemmer-Hansen	DTU Aqua	Denmark
Johan Lövgren	SLU	Sweden
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Kate Griffin	Cefas	UK
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Kélig Mahé	IFREMER	France
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Kirsteen MacKenzie	IFREMER	France

Name	Institute	Country (of institute)
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Annex 2: Resolutions

A Workshop on Scoping Data collection for Northern Shelf cod sub-stocks (WKCODSCOPE), chaired by Nicola Walker (UK), Liz Clarke (UK), Côme Denechaud (Norway) and Marie Storr-Paulsen (Denmark), will work on ToRs and generate deliverables as listed in the Table below.

	MEETING DATES	VENUE	REPORTING DETAILS
Year 2025	18-21 March	Copenhagen, Denmark & online	Interim report by 25 April 2025 to FRSG

ToR descriptors¹

ToR	Description	Background	Science Plan Codes	YEAR	Expected Deliverables
	This should capture the objectives of the ToR	Provide very brief justification, e.g. advisory need, links to Science Plan and other WGs	Use codes (<i>max 3 per ToR</i>)		Specify what is to be provided, when and to whom
a	Summarize the sub-stock definition for Northern Shelf cod complex and review the progress of the project GenDC	ToR [a] will summarize discussions captured in previous cod stock ID workshops. GenDC, that aims to improve stock assessment and sustainable management through integrated genetic data collection, have created a sampling protocol and format for the underlying data (based on DATRAS) that has been distributed to the surveys in Q1 for immediate use. Results from current sampling have not been analyzed yet. WKCODSCOPE will collect feedback on the sampling strategy with a view to improve the collection of genetic data for the Northern Shelf cod stock complex and prepare a summary of the data collected in Q1 2025.	Codes 3.3, 3.4, 5.2	2025	Report to be shared with WGAGFA, SIMWG, WGNSSK, EOSG among others

¹ Avoid generic terms such as “Discuss” or “Consider”. Aim at drafting specific and clear ToR, the delivery of which can be assessed

b	Outline (additional) genetic data could be used to further understanding of sub-stock mixing throughout the year to facilitate the provision of advice which can guide area-specific management	which ToR [b] will outline additional genetic data could be used to further understanding of sub-stock mixing throughout the year and the spatio-temporal dynamics.. This will consider the current stock assessment model assumptions and identify future data needs to facilitate provision of advice that can guide area-specific management	Codes 5.2, 5.3, 2025	Report to be shared with WGAGFA, SIMWG, WGNSSK, EOSG among others
c	Draft different sampling strategies according to partial or complete separation of the Northern Shelf and southern components of the Northern Shelf cod complex.	ToR [c] will develop sampling strategies based on 2 scenarios of genetic separation within the Northern Shelf cod and complex. The baseline analysis results from GenDC will provide insights into the feasibility of separating the northwestern and southern components, thereby guiding the sampling strategy. As these results will only be available by Q4 2025, WKCODSCOPE will outline the necessary sampling requirements (e.g., time, area coverage of the 2 possible scenarios (i.e. partial or complete separation of sub-stocks)	Codes 3.3, 2025	Report to be shared with WGAGFA, SIMWG, WGNSSK, EOSG among others
d	Identify what other types of data potentially collected to understand the sub-stock throughout the year.	ToR [d] will discuss alternative discrimination techniques (otolith shape and microchemistry, tagging, drift-based, morphological or phenotypical data) that could be used to quantify the stock-mixing throughout the year and broadly discuss the potential to use those to improve data input to the stock assessment.	Codes 3.3, 2025	Report to be shared with WGAGFA, SIMWG, WGNSSK, EOSG among others

Supporting information

Priority	High, in response to a joint request from EU, Norway and UK.
Resource requirements	Negligible beyond standard Secretariat support
Linkages to ICES committees or groups	There is a very close working relationship with all the groups under FRSG. It is also very relevant to WGNSSK, IBTS, BITS, ISSG, WGBFAS, WGAGFA, SIMWG
Linkages to other organizations	EC, OSPAR, HELCOM, NEAFC, FAO.

Annex 3: Sampling protocol

Protocol for genetic sampling

Equipment:

Paper towels	Laboratory gloves	Pencil
Forceps	Sampling tubes filled with absolute ethanol (close to 100%)	Water-proof marker
Scalpel	Sample tube holder	Tape (paper painters tape)
Scissors	Glass beaker (~ 200ml) filled with absolute ethanol (close to 100%)	

Method:

- A tissue sample = fin clip, piece of gill or muscle tissue
- Sample to be taken from living, recently killed fish or fish frozen to minimum of -20°C The latter must be as soon as possible after thawing
- Minimum 3:1 ratio of ethanol to tissue, i.e. ethanol should make up at least 75% of the total final volume in the tube. Tissue must be completely covered in the sampling tube.

Procedure to follow:

1. Record sample data (i.e., date, location, etc...) and all available biological data (e.g. length, weight, sex, maturity scale and stage, etc...).
2. Collect otoliths for age determination
3. Disinfect scalpel, scissors and forceps
4. Clean the fish skin with a paper towel and discard paper towel
5. Take sample, following one of the procedures below:
 - a. use the scissors to cut a piece of the tail fin (Figure 1.)
 - b. use the scissors to cut a piece of the gill
 - c. use a scalpel to remove skin from muscle tissue and use scissors to cut a piece of the muscle tissue (approx. 2 x 0.5 x 0.5 cm long)
6. Transfer sample to the sampling tube
7. Close the lid firmly, ensure lid clicks into place
8. Clean sampling instruments with a paper towel
9. Place sampling instruments in glass beaker with ethanol for disinfection
10. Ensure no tissue remains on the sampling instruments before taking the next sample

11. Clean the work surface and gloves

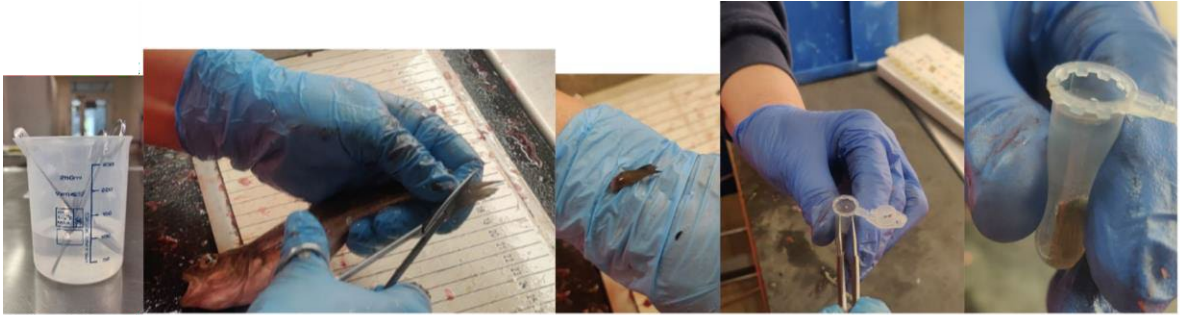


Figure 1. Procedure to following when taking a tail fin clip

Storage:

- Avoid exposing samples to direct sunlight
- Samples preserved in $\geq 95\%$ ethanol can be stored at room temperature, in a fridge or frozen
- Samples are best stored in an insulated sample tube holder
- Sample tubes require individual labels, clearly labelled with a unique identifier

Labelling:

- Each sample tube is labelled with an adhesive heat and ethanol resistant label with information: Survey name, Year, Species, Haul/Station number, Fish number and a unique individual ID. (Figure 2.)

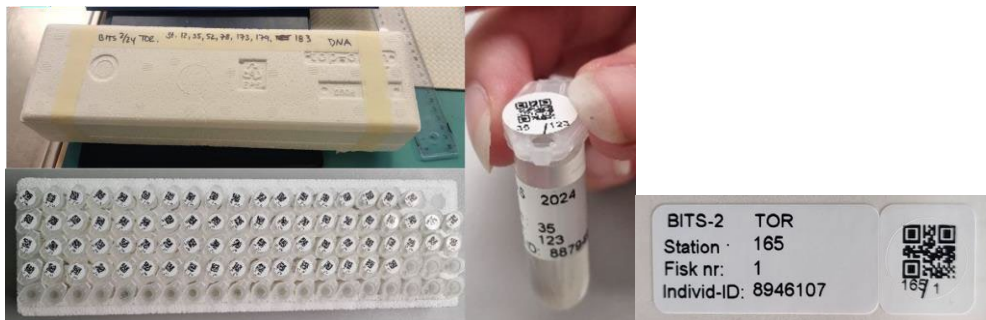


Figure 2. Labelling and storage

- A QR system is recommended where the unique individual ID. is recorded in a QR code
- A QR code can be placed on the lid of the sampling tube (Figure 2.) or on the side of the tube
- When a QR system is not available, pencil is used to label the lid of each individual sampling tube
- All sampling tubes from a haul/station should be clearly identifiable as belonging to the same haul/station.

- Sample tube holder is labelled with information: Survey name, Haul/Station number and number of individual samples in each Haul/Station (Figure 2.).

Version	Version date	Comments			
1	03/12/2024				



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Annex 4: Reviewers' reports

Review of Workshop on Scoping Data collection for Northern Shelf cod sub-stocks (WKCODSCOPE)

Reviewers: Paul Regular (Canada)

Expert group Chair: Côme Denechaud (Norway), Liz Clarke (UK), Marie Storr-Paulsen (Denmark), and Nicola Walker (UK)

Secretariat representative: Lara Salvany (ICES)

Audience to write for: advice drafting group and next year's expert group

General

The WKCODSCOPE report examines stock structure, spatial mixing, and catch monitoring for North Sea cod, with the overarching objective of evaluating whether current management boundaries remain appropriate and to assess the necessary data and analyses to support area-based advice. The report synthesizes a wide range of historical and contemporary evidence (including tagging, genetics, life-history traits, survey data, and catch allocation analyses) to explore both biological structure and management implications.

A major strength of the report is its ambition and breadth. It is rare to see such a comprehensive and explicit re-evaluation of stock boundaries. The report is generally well written, carefully structured, and transparent about uncertainty. Table 3.1 is especially effective, providing a clear overview of the methods considered and helping orient readers before engaging with the detailed analyses. The discussion of spatial allocation of catches and surveys is also strong and clearly demonstrates that allocation assumptions can materially influence assessment inputs.

At the same time, the report raises several important conceptual issues that warrant careful consideration. In particular, there is at times a lack of clarity regarding whether the primary objective is to identify demographically independent biological sub-stocks or to improve management-relevant spatial allocation and mixing estimates. Evidence related to abundance trends, growth, or distribution is occasionally interpreted in the context of stock structure, despite the fact that such patterns can arise from environmental forcing or distributional shifts rather than demographic isolation. These concerns motivate the more detailed technical comments below.

Technical Comments

Biological stock structure versus management units

A recurring issue throughout the report is the conflation of biological stock structure with management units. Several lines of evidence (e.g., differences in abundance trends, growth rates, or spatial distribution) are discussed as potential indicators of stock separation. While informative, these patterns are not sufficient on their own to establish demographically independent stocks, as they may reflect environmental variability, climate-driven shifts, or density-dependent processes. Differences in cohort strength may be more informative, but even these require careful interpretation.

This issue is particularly evident in the treatment of the "Dodger" population. The report notes limited evidence for internal structure within this population, yet sub-components (e.g. North and South) are treated as distinct management units with implied independent reference points. If these components are not demographically independent, then assumptions underlying sub-stock-specific Blim or MSY values become difficult to justify. While local depletion may be a valid management concern, it is conceptually distinct from biological stock separation.

Genetic evidence and delineation

The genetics results suggest subtle differentiation at the scale of the North Sea, but the practical implications for delineating revised stock boundaries are not always clear. For readers without a strong genetics background, it is difficult to determine how the observed differentiation should translate into specific changes to assignment. In particular, when considering Figure 3.1, it is not clear how or whether the current assignment panel should be revised based on these results.

Tagging data and temporal relevance

The report makes effective use of a long and valuable tagging time series, and notes that the cod population and ecosystem have undergone substantial change over the period covered. However, variability through time does not necessarily diminish the relevance of these data for evaluating stock structure and mixing. If demographically meaningful isolation exists, it should manifest as limited mixing, particularly among mature cod during the spawning season, even in the presence of environmental change. In this context, temporal variability in tagging outcomes may provide important information on the strength and persistence of mixing, rather than a reason to discount the data.

Objectives related to mixing and allocation

The analyses related to catch and survey allocation are among the strongest elements of the report. They convincingly demonstrate that fishing in the core areas of management units is more likely to affect cod from those units, while fishing near boundaries is more likely to result in mixed catches. This finding is clearly relevant for spatially explicit management and assessment inputs. However, its implications for biological stock structure are less clear, and at times the report appears to move between these two interpretations without explicitly distinguishing them.

Conclusions

WKCODSCOPE is a high-quality, ambitious, and carefully constructed synthesis that makes an important contribution to ongoing discussions of cod stock structure and management in the North Sea. Its greatest strengths lie in its comprehensive review of evidence, transparent discussion of uncertainty, and clear demonstration that spatial allocation and mixing matter for assessment and management.

However, focusing purely on results presented in this report, evidence of demographic independence of the sub-stocks remains limited. While adult movement patterns, spatial coherence, and some genetic signals are suggestive, they do not yet provide compelling support for assuming independent productivity processes across the proposed sub-units. As such, the report is most convincing when interpreted as a foundation for improving spatial allocation, understanding mixing, and guiding further data collection, rather than as definitive support for the current biological units.

In my view, the WKCODSCOPE report can be used by ICES as a basis to provide advice, provided that appropriate caveats are clearly communicated. Its conclusions are well suited to informing spatially explicit management considerations and motivating further analytical and empirical work. In particular, the report highlights the value of continued investigation into the spatial structure of this stock complex, guided by emerging evidence rather than constrained by existing management boundaries.

Review of Workshop on Scoping Data collection for Northern Shelf cod sub-stocks (WKCODSCOPE), 18-21 March 2025

Reviewers: Ernesto Jardim (IPMA)

Expert group Chair: Côme Denechaud (Norway), Liz Clarke (UK), Marie Storr-Paulsen (Denmark), and Nicola Walker (UK)

Secretariat representative: Lara Salvany (ICES)

Audience to write for: advice drafting group and next year's expert group

General

The report makes a number of recommendations that would imply very substantial financial and logistical investments, particularly in relation to genetic sampling and long-term monitoring. However, these recommendations are presented largely without any assessment of their expected benefits. There is no clear discussion of what social, economic, or sustainability gains would result from such investments, nor how these gains would compare to alternative approaches.

There also appears to be a degree of confirmation bias in the report, in that genetics is treated as the central and, implicitly, preferred solution to the problem of sub-stock identification and mixing. The narrative often reads as circular: a project focused on genetics is used to conclude that further genetic work is required. While genetics is undoubtedly a powerful tool, the report does not sufficiently challenge this assumption or place genetics on an equal footing with other data types and analytical approaches.

For example, modelling approaches such as drift and dispersal modelling are discussed but dismissed relatively quickly, without a thorough examination of their strengths, limitations, and possible roles in hypothesis testing or management support.

Technical comments

A recurring issue throughout the report is the repetition of costly recommendations without a structured evaluation of costs versus benefits. This applies not only to genetics, but also to the implied scale of sampling, laboratory processing, and long-term data handling. Nowhere is there a clear framework for assessing whether the gains in stock discrimination or mixing estimates justify the marginal costs incurred.

The report would also benefit from a more balanced engagement with the modelling literature. There is little reference to studies that rely primarily on models to infer mixing and population structure, as well as to papers that assess the limitations and potential pitfalls of such models. Furthermore, the report should consider the inclusion of parasites as biological tags, which offer a cost-effective and ecologically grounded method for validating contemporary movement and mixing rates between sub-stocks.

Suggest to improve terminology around population, stock and sub-stocks. Although there is a clear and well-written paragraph on page 12 discussing the distinction between populations and sub-stocks, this clarity is not consistently maintained throughout the report.

Genetic differentiation is frequently used as a proxy for defining populations. While this is common practice, it should be more explicitly grounded in the conceptual definition of a population as a self-sustaining group of individuals whose dynamics are biologically connected (Cadrin et al., 2014). Genetic structure alone does not necessarily imply demographic independence, and the report would benefit from a more explicit discussion of how genetic signals translate into management-relevant population units.

There is also an underlying scientific conundrum running through the report. A substantial body of research is reviewed, yet the main conclusion often seems to be that more research is required. While this may be true, it raises the question of whether the proposed next steps are genuinely addressing clearly defined management needs, or whether they risk perpetuating a cycle of data collection without a clear endpoint or decision rule.

Conclusions

Section 5 provides a clear and constructive summary of the process and the way forward, and is one of the stronger parts of the report. Critically it sets simulation testing at the center of decision making.

Review of Workshop on Scoping Data collection for Northern Shelf cod sub-stocks (WKCODOCOPE), 18-21 March 2025

Reviewer - Ian Bradbury (DFO Canada)

General Overview. This report is well written and does a good job of conveying the main intent and outcomes from the workshop. The treatment of the various methods is consistent with the state of the art, and our current understanding of intraspecific diversity within marine species. The authors have done a good job of covering a broad range of subject areas and capturing most of the caveats and limitations associated with each. Moreover, there is an extensive review of stock mixing among many groundfish stocks. In general, I have several broad suggestions, Firstly, I did wonder if the text could be tightened to focus on the question being asked a little more as some of the text and data described does not seem relevant to the terms of reference. For example, why does the text of section two include descriptions of stocks unlikely to present in the region of interest and on Plaice stocks? Perhaps the relevance could be explicitly stated or this text reduced. Secondly, many of the figures and figure captions would benefit from additional details and clarification. Finally, the final section could use a rewrite to more accurately capture the breadth of the report, and the potential implications of the work underway. Overall, the report is well crafted and largely consistent with best practices, and the conclusions generally well supported. Specific comments are listed below.

On the first few pages 2025 is repeatedly provided as the date for the publication, I do wonder if this should be 2026.

Executive summary

“A new project, GenDC aims to resolve these limitations and has collected and will finalizing” should be “will finalize”

“Otolith chemistry provides insights into natal origin, life-history migrations, and mixing patterns”. The missing caveat here is that this is only where stable environmental differences exist.

Section 2 - Current Stock Assessment and Advice

Page 2 – text does not refer to Figure 2.1 explicitly until the end, needs introduction at the start of the section describing conclusions of the North Sea workshop.

Figure 2.1 – the figure caption could be more detailed, refer to the workshop, data types used etc.

General Comment for section 2.4 – why does the text include descriptions of stocks unlikely to present in the region of interest. Why is text on plaice stocks included here? If this is warranted, please make the relevance clear otherwise some of this could be deleted.

Section. 2.4 header – other mixing stocks within ICES, what does this mean? Perhaps this could be clarified.

Section 2.4.2. The ICES SDs are not shown on the map, and the significance of the numbers on the map is not clear.

Section 2.4.3- Arctic cod misspelled Artic.

Section 3 – Investigation of relevance and use of different data types

Table 3.1 - table caption is lacking details, why are genetic and genomic methods not included here, seems an obvious omission.

Section 3.1.1.1 – what is the preservative used in these vials?

Section 3.1.1.2 – For clarity it would be best to not include pool-seq here, which represents quite a different approach. In general pool-seq should be avoided due to an inability to estimate individual multi-locus genotypes and not suited to individual assignment.

Section 3.1.1.2 – I find the presentation of WGS and lcWGS a little confusing. The distinction between these two is sequencing depth. It is unlikely outlier regions would be missed with lcWGS, it just means dealing with genotype likelihoods rather than genotype calls. Larger numbers of samples are always needed for accurate estimation of allele frequency. Given the number of loci assayed with lcWGS can still

exceed millions, it is still highly powered to resolve subtle differences among groups and provide tools for assignment purposes.

see - DeSaix MG, Rodriguez MD, Ruegg KC, Anderson EC. Population assignment from genotype likelihoods for low-coverage whole-genome sequencing data. *Methods in Ecology and Evolution* 2024; 15: 493-510. <https://doi.org/https://doi.org/10.1111/2041-210X.14286>

Section 3.1.1.2 – With respect to SNP Arrays there is no discussion of the limited broad application of SNP arrays and the potential for ascertainment bias to limit future application of inferences based on the dataset. Strand flips may increase the difficulty of merging with other data types, and some thought as the samples being analysed when calling SNPs is required to reduce the likelihood of flipping major and minor alleles.

Section 3.1.13 – Again, I find this section unclear in many locations. For example, the text seems to refer to the impact of ghost or unsampled populations on assignment accuracy. There are methods to deal with this that are not mentioned but in general a comprehensive baseline is optimal.

I would argue that the most robust statistical treatment of genetic assignment currently available is RUBIAS for a variety of reasons. This should be included here - Moran BM, Anderson EC. Bayesian inference from the conditional genetic stock identification model. *Can J Fish Aquat Sci* 2019; 76: 551-560. <https://doi.org/10.1139/cjfas-2018-0016>

Figure 3.1 – This is largely unreadable. Labels on the figure are too small to read.

Page 16 - these inversions and behavioral ecotypes are not limited to Iceland and Norway – see Berg PR, Star B, Pampoulie C, Bradbury IR, Bentzen P, Hutchings JA, Jentoft S, Jakobsen KS. Trans-oceanic genomic divergence of Atlantic cod ecotypes is associated with large inversions. *Heredity* 2017; 119: 418. <https://doi.org/10.1038/hdy.2017.54>

Kess T, Bentzen P, Lehnert SJ, Sylvester EVA, Lien S, Kent MP, Sinclair-Waters M, Morris C, Wringe B, Fairweather R, Bradbury IR. Modular chromosome rearrangements reveal parallel and nonparallel adaptation in a marine fish. *Ecol Evol* 2020; 10: 638-653. <https://doi.org/10.1002/ece3.5828>

Figure 3.2 - Figure Caption needs additional details, please define - IBTS? Q1? Species?

Good point about the pangenome, this is really needed and could be useful in this context.

Section 3.2/3.3 - It will be important to note that integration across methods could be particularly useful, such as exploration of the genomic basis of differing migratory phenotypes, or residents versus migrants etc.

Section 3.3.2.1 – Important to note here that otolith microchemistry is largely environmentally determined and as such requires temporally matched baseline samples and signatures could be subject to change with changing environments.

Section 3.3.2.2 – is there a citation for this example? Some reference is needed.

Table 3.3 - could the details on spatial distribution of samples be provided as well.

Section 4 – Sampling Strategy

Section 4.2.1 - “With either aim, we would require **collection of**”

Section 5. The way forwards

This section does not capture the messages from each proceeding section and the potential future contributions. Strangely it seems limited to tagging data, unclear why. Perhaps a rewrite here would be useful.