# Genetic Fact Sheet

→ **Flounder**

*Platichthys flesus*

2022

# PANDORA

**Paradigm for Novel Dynamic
Oceanic Resource Assessments**

# Genetic Fact Sheets

## Review of available genetic information
## on population structuring in exploited species

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The Blue Growth of European fisheries is at risk due to over-exploitation, unforeseen changes in stock productivity, loss of markets for capture fisheries due to aquaculture, future trade agreements opening European markets to external fleets, and fluctuations in the price of oil and other business costs. All of these risks need to be considered when providing advice needed to sustainably maximize profits for the diverse array of fisheries operating in European waters and to help safeguard the benefits this sector provides to the social coherence of local, coastal communities.

PANDORA aims to:

1. Create more realistic assessments and projections of changes in fisheries resources (30 stocks) by utilising new biological knowledge (spatial patterns, environmental drivers, food-web interactions and density-dependence) including, for the first time, proprietary data sampled by pelagic fishers.

2. Advise on how to secure long-term sustainability of EU fish stocks (maximum sustainable/"pretty good" and economic yields) and elucidate tradeoffs between profitability and number of jobs in their (mixed demersal, mixed pelagic and single species) fisheries fleets. Provide recommendations on how to stabilize the long-term profitability of European fisheries.

3. Develop a public, internet-based resource tool box (PANDORAs Box of Tools), including assessment modelling and stock projections code, economic models, and region- and species-specific decision support tools; increase ownership and contribution opportunities of the industry to the fish stock assessment process through involvement in data sampling and training in data collection, processing and ecosystem-based fisheries management.

The project will create new knowledge (via industry-led collection, laboratory and field work, and theoretical simulations), new collaborative networks (industry, scientists and advisory bodies) and new mechanisms (training courses and management tools) to ensure relevance, utility and impact.

## List of abbreviations

GFCM  General Fisheries Commission for the Mediterranean
ICES   International, Council for the Exploration of the Sea
IUCN   International Union for Conservation of Nature
IUU    Illegal, Unreported and Unregulated
MSY   Maximum sustainable yield
SAC    Scientific Advisory Committee
STECF   Scientific, Technical and Economic Committee for Fisheries
SD    Subdivision
TAC    Total Allowable Catch

## North-East Atlantic ICES subareas, divisions and subdivisions

1) Subarea 1 – Barents Sea
2) Subarea 2 – Norwegian Sea, Spitzbergen and Bear Island
3) Subarea 3
   - Division 3.a, Skagerrak (subdivision 20) and Kattegat (subdivision 21)
   - Division 3.b-c, Sound (subdivision 23) and Belt Sea (subdivision 22)
   - Division 3.d, Baltic Sea (subdivisions 24-32)
4) Subarea 4 – North Sea (divisions 4.a-c)
5) Subarea 5 – Iceland (division 5.a) and Faroes Grounds (division 5.b)
6) Subarea 6 – West of Scotland (division 6.a) and Rockall (division 6.b)
7) Subarea 7
   - Irish Sea (division 7.a), West of Ireland (division 7.b), Porcupine Bank (division 7.c)
   - Eastern English Channel (division 7.d), Western English Channel (division 7.e)
   - Bristol Channel (division 7.f), Celtic Sea (divisions 7.g-h), Southwest of Ireland (divisions 27.7.j-k)
8) Subarea 8
   - North and Central Bay of Biscay (divisions 8.a-b)
   - South Bay of Biscay (division 8.c)
   - Offshore Bay of Biscay (division 8.d), West of Bay of Biscay (division 8.e)
9) Subarea 9 (Portoguese Waters)
10) Subarea 10
   - Azores Grounds (division 10.a) and Northeast Atlantic South (division 10.b)
11) Subarea 11 (incorporated in FAO Fishing Area 34)
12) Subarea 12 North of Azores
   - souther mid-Atlantic Ridge (division 12.a)
13) Subarea 13 (incorporated in FAO Fishing Area 34)
14) Subarea 14 East Greenland, Northeast Greenland (14.a), Southeast Greenland (14.b)

# How to read the factsheets

Genetic structure factsheets are presented for each species. Current knowledge on genetic population structure is summarised and compared with stock units used in assessment and management. The presence of mismatches is emphasised as well as priorities for future work. At the beginning of the factsheets, a summary is presented with green-yellow-red color symbols for 'Population structure', 'Match between genetic and stock assessment units' (units for which scientific advisory bodies, as ICES and the GFCM, provide advice on stock status and fishing opportunities), 'Match between genetic and management units' (units for which TACs are set by the European Council), 'Match between stock assessment and management units'. The information in the factsheet is organized in the following sections:

***Distribution***: general information can be found on the distributional range of the species, with a focus on the NE Atlantic, Mediterranean and Black Sea.

***Current management status***: an overview is provided on the current management and assessment units present for the species in European Seas. The importance of the species for each fishery is included, reporting if the species is mainly a by-catch or if direct fishery exists for the stocks. A mismatch between stock assessment and management units already exists for certain species and it is showed in Table 2.

***Genetic population structure in a nutshell***: provides the key take-home messages, both in terms of current knowledge on genetic population structure and in terms of priorities for future work. In this section, an overall picture of population structure of the species is given, based on considerations on the type of markers, sampling designs and findings of the included studies. It is also discussed if genetic evidence supports the stock assessment and management units currently in use.

***Mismatch***: in this section the mismatch between genetic and stock assessment/ management units is highlighted. Two types of mismatch can be observed. Here, we refer to '*Type I*' mismatch when a genetically homogeneous population is assessed/managed in multiple stock units (oversplitting); while we refer to '*Type II*' mismatch when genetically different populations are wrongly considered part of the same stock assessment/management unit (undersplitting).

***Summary of genetic evidence:*** in this section a more detailed summary of the studies is provided in a chronological way. In general, the type of genetic markers used by different studies depends on the widely available markers at the time. Early studies used allozymes and often reported a lack of differentiation among sample locations. However, later studies using the more highly polymorphic microsatellites and SNPs showed presence of differentiation even in areas where it was not previously detected. Conversely, in other cases presence of differentiation was reported at few allozyme loci, not confirmed

subsequently with strictly neutral markers. This and other contradictions between studies were addressed if possible. Advances in sequencing technology, as well as the use of more sophisticated statistical analysis and sampling design to maximise the detection of population structure have made enormous changes in the awareness we have of genetic structure in marine fish species (Hauser and Carvalho, 2008). Most of the mismatches found in initial studies between genetic population structure and stock assessment and management units were due to a lack of differentiation reported between samples assessed/ managed in different units (referred to as '*Type I*' mismatch in Table 1). However, these mismatches are often solved by more recent investigations, that applied highly polymorphic markers, as well as a sampling design that maximise the chance of detecting population structure, i.e. collecting individuals in spawning aggregations. Particular emphasis should be placed on the sampling season and individuals included in the analysis that are extremely important factors for the detection of population structure in marine fish species (Nielsen et al. 2009b). Moreover, despite in previous studies a neutral background of low differentiation was commonly detected, recently the application of markers under selection allowed the detection of high levels of differentiation and occurrence of locally adapted populations. Therefore, a summary of genetic studies found in literature is provided. For each study, sampling design, temporal and spatial analyses and markers used have been critically evaluated. Strengths and shortcomings of the available studies are reported and based on these considerations an overview is given.

**Table 2.1**. Summary table of available information on genetic population structure and match between genetic, assessment and management units of commercial fish species exploited in the NE Atlantic, Mediterranean and Black Sea.

| Species | No. Studies | Population structure | Match genetic-Stock assessment units | Match genetic-management units | Match stock assessment -manage-ment units | IUCN status |
|---|---|---|---|---|---|---|
| **Flounder,** *Platichthys* spp. | | yes | no | - | - | - |

**IUCN Abbreviations:** NE= Not evaluated, DD= Data Deficient, LC= Least Concern, NT= Near Threatened, VU= Vulnerable, EN= Endangered, CR= Critically Endengered. Eu= Europe, Glo= Global, Med= Mediterranean (IUCN 2021).

# FACT SHEET

## Flounder, *Platichthys flesus*

|  |  |
|---|---|
| Number of studies | 11 |
| Population structure | ✅ |
| Match genetic- Stock assessment units | ❌ |
| Match genetic- Management units | - |
| Match Stock assessment- Management units | - |

RED LIST

**LEAST CONCERN** LC

### Distribution[1]

The European flounder, *Platichthys flesus*, L., is a widespread flatfish species, inhabiting the North-East (NE) Atlantic, from the White Sea to the Mediterranean and the Black Sea (Whitehead et al. 1986b). It is widely distributed in the Baltic Sea, where it is among the few marine fish species that occurs also in the inner part of the basin (Florin & Höglund 2008). In fact, it is a euryhaline species, able to live and tolerate waters with a wide range of salinities, and is correspondingly commonly found in estuaries and lagoons. Adults usually feed in inshore and shallow waters while they migrate to spawn in deeper water during the spawning season. Eggs and larvae are pelagic, thus promoting population connectivity.

The presence of two ecotypes of European flounder in the Baltic Sea with different spawning strategies was known, i.e. the pelagic and demersal spawners. Genetic studies have shown the demersal spawners to represent a different species named Baltic flounder, *Platichthys solemdali* sp. nov. (Momigliano et al. 2018). Although it is not possible to distinguish between the Baltic flounder (*Platichthys solemdali*) and the European flounder by morphological or meristic characters (except for gamete physiology and morphologies), they are genetically different and the absence of hybrids show that there is strong reproductive isolation.  The pelagic and demersal species coexist in the southern as well as in the eastern part of the proper Baltic Sea. These species use the same feeding grounds. However, their spawning grounds differ, with the Baltic flounder spawning demersal eggs (small and heavy) in shallow and coastal areas of the Baltic proper, while European flounder spawning occurs usually in deeper waters, where pelagic eggs are released.

### Current management status

In the NE Atlantic, ICES recognize several assessment units for flounder species (Figure 3.6). A stock unit is present in the North Sea, Skagerrak and Kattegat and another in the Belt Sea and the Sound (SDs 22-23) for the European flounder (*P. flesus*). A stock unit for the Baltic flounder (*P. solemdali)* exists in the northern part of the proper Baltic Sea (SDs

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[1] Further details on symbols and how to read the factsheet are provided on page 16

27, 29–32) (Table 2). The two species (European and Baltic flounders) are assessed jointly, as *Platichthys* spp. in the remaining Baltic subdivisions (SDs 24-25, and SDs 26-28).

In the North Sea stock, the European flounder is caught as by-catch species in flatfish fisheries, mainly for plaice and sole. ICES does not provide advice on fishing opportunities for the North Sea stock (ICES 2018a). European flounder is considered a non-target species and no TAC is set in the area. Previously, this stock was managed together with dab, and a common precautionary TAC for the two species was present, until its removal in 2017 (see ICES, 2018, and references therein).

European flounder in the North Sea, Belt Sea and the Sound (SDs 22 and 23) is mainly a by-catch species of direct cod fisheries or flatfish mixed-fisheries, and catches are mainly from the Belt Sea.

Both species of flounders are present in West of Bornholm, Southern Central Baltic–West subdivisions (SDs 24 and 25). Advice is given by ICES at the level of *Platichthys* spp. Correspondingly, the proportion of the two species for stock assessment are not separated (ICES 2020b). A total of 11 815 t was landed in 2019, mainly from subdivision 25 (ICES 2020b). The assessment of two different species as one stock unit is considered dangerous and could lead to the overexploitation of either species (ICES 2020b).

Likewise, both species are present in eastern Gotland and Gulf of Gdansk (SDs 26-28) and their relative proportions are not separated for assessment and management (ICES 2020b). Moreover, a decreasing trend in landings was reported from ICES for this stock, that in 2019 were 2740 t (ICES 2020b).
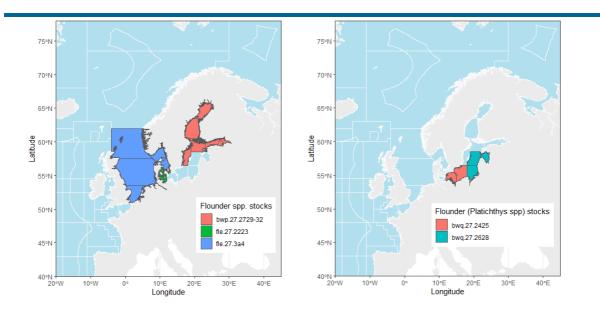


**Figure 3.6.** Flounder stock assessment units. Left, European flounder (fle.27.2223; fle.27.3a4) and the Baltic Flounder stocks (bwp.27.2729-32). Right, the mixed flounder species stocks.

While in the rest of the Baltic, European flounder is the most common flounder species, in the Baltic Proper (SD 27, 29-32) *P. solemdali* is the prevalent one (ICES 2020b). Hence, a stock unit for the Baltic flounder (*P. solemdali*) is present in subdivisions 27, 29-32. Since both species are present in the central Baltic (SD 28) and *P. flesus* seems to be the

predominant one, subdivision 28 is not included (ICES 2020b). Although it is assumed that the Baltic flounder species is the prevalent in the proper Baltic Sea, previous analysis showed that the two species co-occur and their proportion has changed since the 1980s. According to ICES the majority of the catch are from SD 29, however the proportion of the two species are not separated. In fact, there are not morphological or meristic characteristics that readily allow assignment of individual to either species, and currently only genetic methods and gamete physiology and morphology (eggs shape and sperm mobility) allow clear separation.

## Genetic population structure in a nutshell

Genetic evidence shows European flounder is structured within the NE Atlantic, and that a cryptic species exists in the Baltic Sea (Momigliano et al. 2018). For the European flounder, the presence of separate populations in the Faroe Islands and Bay of Biscay was supported (Hemmer-Hansen et al. 2007b). Genetic differentiation was reported between *P. flesus* inhabiting the North Sea and the Baltic Sea (e.g., Momigliano et al. 2017, Le Moan et al. 2019a).

Moreover, genetic evidence supports the two flounder species in the Baltic Sea:

- Genetic homogeneity for the Baltic species (*P. solemdali*) that can be considered a genetic unit (Hemmer-Hansen et al. 2007b, Florin & Höglund 2008).
- European flounder in the Sound and western Baltic subdivisions (SDs 24,25,26) are genetically one unit (Florin & Höglund 2008, Momigliano et al. 2017).
- Presence of hybrids between North Sea and Baltic Sea pelagic flounder in the Sound (Momigliano et al. 2017) as well as in the transition zone (Le Moan et al. 2019a).
- Co-occurrence of pelagic and demersal flounder species in the central and northern Baltic Sea (SDs 27, 29,32) (Momigliano et al. 2018, 2019).
- The presence of demersal individuals in West of Bornholm and southern Central Baltic subdivisions (SDs 24, 25) (Le Moan et al. 2019a).

## Mismatch

The pelagic Baltic Sea population can be considered a genetic unit, no suggestions of substructure were found despite several stock assessment units exist (Table 2), resulting in a mismatch. Likewise, the Baltic Sea flounder represent a genetically homogeneous unit. Mixing of the two species is not limited only to subdivisions 24, 25 and 26, 28, as considered by ICES. Presence of mixing between pelagic and demersal species was showed in the Baltic proper and Gulf of Finland, and it is not taken into account in fishery assessment.

Also in the inner part of the Baltic Sea the two species co-occur (Momigliano et al. 2019) and their proportion could fluctuates based on environmental variables, as currents that allow larvae and eggs dispersal of the pelagic spawners. The exploitation of two different species morphologically indistinguishable could lead to the overexploitation of the weakest stock components, hence more sustainable fisheries management practices should be implemented.

## Summary of genetic evidence

Population structure of European flounder in its distributional range was studied initially by allozymes (Galleguillos & Ward 1982). Although they did not detect any differentiation within the NE Atlantic samples, differentiation between the Atlantic, the Adriatic and the Black Sea flounders was detected, confirming the presence of subspecies in the Adriatic Sea, *P. flesus italicus*, and the Black Sea, *P. flesus luscus* (Galleguillos & Ward 1982). Likewise, by including more localities within the Atlantic, a weak pattern of isolation by distance was reported by Borsa et al. (1997). The analysis supported the differentiation between flounders inhabiting the NE Atlantic and the Mediterranean Sea, and also intrabasin genetic differences were detected between the western part, the Adriatic Sea and the Aegean and Black Sea. Therefore, based on the genetic structure pattern found, the Gibraltar strait, the Siculo-Tunisian Strait and the Peloponnese Peninsula were suggested as potential barriers to gene flow (Borsa et al. 1997).

Based on microsatellite data, significant and temporally stable differentiation was found within the NE Atlantic by Hemmer-Hansen et al. (2007b), who reported the existence of several populations, namely the Faroe Islands, Bay of Biscay and the benthic spawners population in the Baltic Sea. Notably, this was the first study reporting genetic differentiation between pelagic and demersal spawners in the Baltic Sea: a genetic barrier was identified between North Sea – Bornholm (pelagic spawners) and Gotland (benthic spawners) in the eastern Baltic (Hemmer-Hansen et al. 2007b).

Hemmer-Hansen et al. (2007a) used a candidate gene (*Hsc70)* approach to study local adaptation in flounder across the NE Atlantic. The differentiation levels between flounders inhabiting the North Sea and the Baltic Sea at neutral loci was 0.02 while 0.45 at *Hsc70*, suggesting the existence of adaptive divergence despite putatively high levels of gene flow between these populations, highlighting the importance of using genetic markers under selection to determine whether locally adapted populations exist despite low levels of differentiation at neutral markers.

Florin and Höglund (2008) focussing on the North Sea, the Baltic Sea and the transition zone supported the existence of three genetically different populations, *i.e.* a demersal population in the northern Baltic Sea; a pelagic population in the western Baltic including the Sound (SD 23) and another one in the North Sea, Skagerrak and Kattegat. The genetic differences between the demersal and pelagic spawners population was confirmed and their mixing in some of the Baltic Sea subdivisions was showed.

Through SNP marker analysis Momigliano et al. (2017) provided evidence that the demersal spawners population in the Baltic Sea represent a distinct species, arising from a rapid event of ecological speciation, where the spawning behaviour is the trait under selection promoting reproductive isolation. The new species was successively described as the Baltic flounder, *Platichthys solemdali* (Momigliano et al. 2018). Moreover, the differentiation between the European flounders (*P. flesus*) inhabiting the Baltic Sea, the North Sea and the transition zone was confirmed also by SNPs (Momigliano et al. 2017), and presence of hybrids was demonstrated especially in the transition zone.

In the Baltic proper, considered to be inhabited only by the demersal species, pelagic flounders were found, showing that the two species co-occur. The reproductive isolation was confirmed by an absence of hybrids between the two species. Hence, a multispecies fishery management should be implemented for sustainable management of flounders' fisheries in the Baltic Sea.

Since the two species cannot be distinguished morphologically, a genetic tool was designed by Momigliano et al. (2019, 2018) in order to assign individuals to the flounder species of origin in areas where the Baltic flounder and the European flounder co-occur in the Baltic Sea. This genetic tool uses 6 loci under selection that are highly discriminatory between the two species.

This tool was applied to analyse DNA from archived otolith samples in order to monitor spatio-temporal changes (1976–2011) in stock composition of flounder fisheries from the Aland Sea and Gulf of Finland (Momigliano et al. 2019). The study confirmed that both species of flounder are present in this part of the Baltic Sea and that the relative proportion of each species have showed spatio-temporal fluctuations, depending on environmental variables in the Baltic. The importance of monitoring the contribution of different component (in this case species) to mixed-stock fisheries in a spatiotemporal manner was emphasized in order to avoid the overexploitation of the less productive component and implement assessment and management measures for each species individually.

Reis-Santos et al. (2018) studied population structure of flounder across the NE Atlantic, using otoliths composition and microsatellite analyses. No information about demersal and pelagic spawners were given for the Baltic Sea samples. Microsatellites indicated genetic differentiation between the Polish and Swedish coast of the Baltic Sea and absence of differentiation between North Sea, the Polish Baltic Sea (SD 26) that are currently in two different stock assessment units. The integrated analysis indicated the presence of four groups in the NE Atlantic, i.e. (1) the Norwegian coast; (2) the Baltic Sea; (3) the southern North Sea and the Bay of Biscay; (4) the Galician shelf and Atlantic Iberian coasts (division 9.a).

Le Moan et al. (2019a) using a SNP panel reported the presence of both the demersal and pelagic species in the Baltic Sea. The strong differentiation between the two flounder species was confirmed by an absence of hybridization between them. Likewise, their mixing was confirmed, two demersal individuals were found in the South-west Baltic (SD 24) and Bornholm Sea (SD 25) that are considered habitat of the pelagic flounders. While for the European flounder, *P. flesus*, differentiation was supported between the North Sea and Baltic Sea population ($F_{ST}$ 0.013 and highly significant), and with a continuum of hybridization through the transition zone between these basins.

**Table 1.** Summary table of genetic population structure studies of commercial marine fish species exploited in the North-East Atlantic Ocean, Mediterranean and Black Sea.

| Species | Region | Sampling locations | No. Samples (Number of individuals) | Spawning | Maturity | Life stage | Genetic Marker | Differentiation | Mismatch genetic-SA | Mismatch genetic- MZ | LA, LG, MSA | Reference |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Flounder** | NE Atlantic, Med | UK (3), Belt (1), ADR (2), BLS (2) | 7 (270) | na | na | Ad, juv | All (38) | Yes | Type I | na | | (Galleguillos & Ward 1982) |
| | NE Atlantic, Med | NS (4), BAL (2), Kat (1), BOB (2), PRT (5), Med (4) | 18 (796) | y | na | Ad | All (8), mtDNA (RFLP) | Yes | Type I | na | LG | (Borsa et al. 1997) |
| | NE Atlantic | FRO (1), NOR (2), NS (4), IS (1), BAL (5), BOB (1) | 22 (1062) [9] | y | y | Ad, juv | Msat (9) | Yes | Type I | na | LG | (Hemmer-Hansen et al. 2007b) |
| | NE Atlantic | FRO (1), NOR (2), NS (3), IS (1), BAL(4), BOB (1) | 20 (809) [8] | y | y | Ad, juv | Msat (9)[N]; *Hsc70* [S] | Yes | Type I [N] | na | LA, LG | (Hemmer-Hansen et al. 2007a) |
| | NE Atlantic | NS (1), Ska (1), Kat (1), NBTZ (1), BAL (16) | 20 (960) | y | y | Ad | Msat (7) | Yes | Type I | na | LG | (Florin & Höglund 2008) |
| | NE Atlantic | ENG (1), FRA (3), PRT (1) | 5 (250) | no | na | Ad, juv | Msat (8); COI (689 bp); candidate gene [S] | Yes | na | na | LG | (Calvès et al. 2013) |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| NE Atlantic | NS (2), NBTZ (1), BAL (10) | 13 (282) | Y | y | Ad | SNPs (2051) [S] | Yes | Type I | na | LA, LG | (Momigliano et al. 2017) |
| NE Atlantic | BAL (4) | 4 (69) | y | y | Ad | SNPs (5861) [S] | Yes | Type I | na | LA, MSA | (Momigliano et al. 2018) |
| NE Atlantic | NOR (1), BAL (2), NS (1), BOB (1), Gal (1), PRT (1) | 7 (318) | na | na | Ad | Msat (12) | Yes | Type I | na | LG | (Reis-Santos et al. 2018) |
| NE Atlantic | BAL (2) | 21 (444) [19 H] | na | na | Ad | SNPs (5) [S] | Yes | Type II | na | LA, MSA | (Momigliano et al. 2019) |
| NE Atlantic | NS (1), NBTZ (3), BAL (4) | 8 (214) | y | na | na | SNPs (5472) [S] | Yes | na | na | LA, LG | (Le Moan et al. 2019a) |

The following abbreviations are used for the geographic locations: North-East Atlantic (NE Atlantic), Mediterranean Sea (Med), Northwest Atlantic (NWA), Adriatic Sea (Adr), Aegean Sea (Aeg), Africa (AFR), Alboran Sea (Alb), Atlantic (Atl), Atlantic Iberian (Atl IB), Australia (AU), Azores (Azo), Baltic Sea (BAL), Barents Sea (BS), Bay of Biscay (BOB), Black Sea (BLS), British Isles (BI), Canada (CAN), Canary (Cn), Cantabrian Sea (Cant), Celtic Sea (CS), English Channel (EC), Faraday Seamount (Far), Faroe Islands (FRO), fjord (fj), Galicia (Gal), Greece (GRC), Greenland (GRL), Gulf of Cadiz (GC), Gulf of Lion (GoL), Hebrides (Heb), Iceland (ICE), Ionian Sea (Ion), Ireland (IRE), Irish Sea (IS), Irminger Sea (Irm), Kattegat (Kat), Lake Mogilnoe (Mog)Lofoten (Lof), Madeira (Mad), Marmara Sea (MS), Mid-Atlantic Ridge (MAR), Morocco(MOR), Namibia (Nam), New Zeland (NZL), Newfoundland and Labrador (NL), North Sea (NS), North Sea-Baltic Sea Transition zone (NBTZ), Norway (NOR), Nova Scotia (Nov), Porcupine Bank (Por), Portugal (PRT), Reykjanes Ridge (Reyk) , Rockall Bank (Roc), Russia (RUS), Scotian Shelf (SS), Scotland (SCO), Shetland (SHE), Sicily (SIC), Skagerrak (Ska), Spain (SPA), Svalbard and Jan Mayen (SJM), Tasman Sea (TS), Tunisia (TUN), Tyrrhenian Sea (Tyr), White Sea (WS); north (n), south (s), east (e), west (w), central (c); Norwegian Coastal Cod (NCC), North-East Arctic Cod (NEAC).

Sampling locations (for abbreviations see below) and in brackets the number of samples are shown; the total number of samples and individuals analysed is reported, as well as the number of temporal replicates in superscript or (*) if multiple temporal replicates are included. The spawning, maturity and life-stage of samples included are summarised as follow, *Spawning*: y= if samples collected in spawning season/grounds are included, na= not available, no= samples outside spawning season/grounds. *Maturity*: y= mature individuals included; na= maturity not available; no= immature individuals. *Life-stage*: Ad= adult; juv= juveniles; lar= larvae; eg= eggs; na= not available. Genetic markers (All= allozymes; Msat= microsatellites; Minisat= minisatellites; SNPs= Single Nucleotide Polymorphisms; mtDNA= mitochondrial DNA; Cyt-b= cytochrome b; COI= Cytochrome c Oxidase subunit I; COIII= Cytochrome c Oxidase subunit III; CR= Control Region; RAPD= Random Amplified Polymorphic DNA); number of loci or base pairs analysed in brackets, in superscript S= if at least one locus is under selection, N= neutral markers (only if neutrality was tested). Differentiation, if genetic differentiation was detected (Yes, No). Mismatch genetic- SA= mismatch of the genetic units found and the stock assessment units. Mismatch genetic- MU = mismatch of genetic units with the management units. We refer to '*Type I*' mismatch when a genetically homogeneous population is assessed/managed in multiple stock units (oversplitting); while we refer to '*Type II*' mismatch when genetically different populations are wrongly considered part of the same stock assessment/management unit (undersplitting). LA= Local Adaptation, LG= Landscape Genetics, MSA= Mixed Stock Analysis.

**Table 2.** Mismatch between stock assessment (SA) units and genetic population structure (Type I and II explained) and mismatch between management and genetic units.

| Species | Assessment unit | Mismatch SA unit - genetics (Type II) | Mismatch SA unit - genetics (Type I) | Management units | Mismatch management unit - genetics |
|---|---|---|---|---|---|
| Flounder, ***Platichthys flesus*** | fle.27.3a4 | Hybrids of NS and BS pelagic flounders in the transition zone (Le Moan et al. 2019a) | | - | |
| | fle.27.2223 | The Sound (23), southern Baltic (24,25,26) genetically one unit (Florin & Höglund 2008) presence of NS and Baltic Sea pelagic flounders in SD 23 (Momigliano et al. 2017) | | - | |

| Flounder, *Platichthys* spp. | [bwq.27.2425](#) | **no differentiation between pelagic flounder in SD 25,26,28 (Momigliano et al. 2017)** | | - |
| | [bwq.27.2628](#) | | | - |
| Baltic flounder, *Platichthys solemdali* | [bwp.27.2729-32](#) | SD 26,27,28,29,32 demersal and one unit (Florin & Höglund 2008)<br><br>presence of pelagic flounders in SD27, 29, 32 (Momigliano et al. 2018) | No differentiation between SD 28 (benthic) and SD 29 (benthic) (Hemmer-Hansen et al. 2007b) | - |
| Flounder, *Platichthys flesus* | [fle.27.3a4](#) | Hybrids of NS and BS pelagic flounders in the transition zone (Le Moan et al. 2019a) | | - |