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Genetic Fact Sheet

Turbot

Scophthalmus maximus

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PANDORA

Paradigm for Novel Dynamic
Oceanic Resource Assessments

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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.

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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-management units**	**IUCN status**
Turbot, Scophthalmus maximus	17	yes	no	no	no	VU

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

1.1 Turbot, *Scophthalmus maximus*

Number of studies	17
Population structure	✓
Match genetic- Stock assessment units	✗
Match genetic- Management units	✗
Match Stock assessment- Management units	✗

Distribution[1]

Turbot, Scophthalmus maximus L., is an economically important flatfish species. It is distributed from Iceland and Norway, throughout the European coasts and down towards Morocco, including the northern Mediterranean and the Black Sea. Turbot is among the few marine fish species inhabiting the Baltic Sea. It is commonly found between 20-100 m, and spawning occurs in shallow waters between April and August. Turbot in the NE Atlantic is classified as a vulnerable species by the IUCN (IUCN 2019). Eggs and larvae are pelagic except in the Baltic sea where the eggs are demersal due to the lower salinity of the waters (Florin & Höglund 2007).

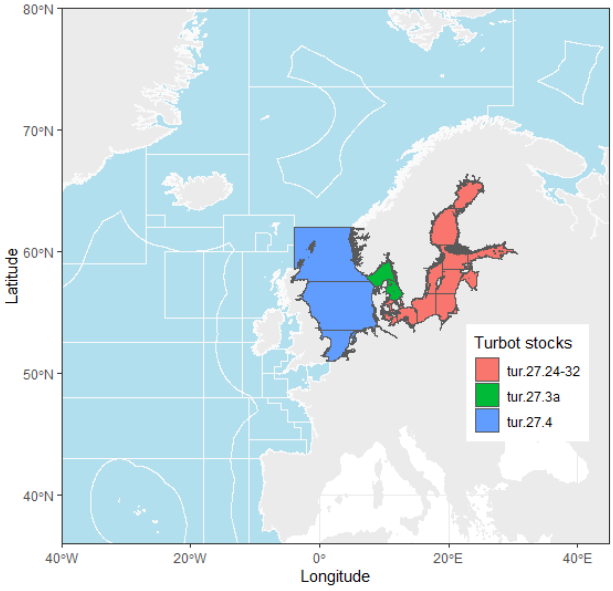

Figure 1 Turbot ICES stock assessment units.

Current management status

Three stock assessment units exist for turbot in the NE Atlantic, namely 1) the Baltic Sea, 2) Skagerrak and Kattegat 3) the North Sea (Figure 3.9). The Baltic Sea stock (SDs 22-32) is mainly fished in the western subdivisions and analysis of survey data indicates that this stock is connected to the nearby turbot in the Kattegat (ICES 2020b). Turbot in Division 3.a (the Skagerrak and Kattegat) is assessed as a separate unit by ICES, it is mainly fished as a by-catch species and landings in 2019 were 204 t (ICES 2020v). ICES recognized this stock

should be reviewed in light of available scientific evidence supporting the connectivity between turbot in 3.a with the North Sea and the Baltic Sea (ICES, 2020b; and reference therein). Hence, the stock of turbot in the North Sea should include also the Skagerrak. Turbot in the North Sea is mainly fished with sole and plaice in mixed flatfish fisheries, and the Netherlands is the main fishing country. While the stocks in the Baltic Sea and Division 3.a are not managed by TACs, turbot in the North Sea is managed with brill under a combined TAC for Subarea 4 and 2.a (European waters) (Table 2). However, ICES provides separate stock assessment advice on fishing opportunities and stock status for brill and turbot. A combined TAC could lead to the overexploitation of the less valuable species (in this case brill). Additionally, this TAC does not match the stock units used for the assessment by ICES, for either of the species. Therefore, ICES highly recommended the management of these species by separate TACs that should match the spatial distribution of the stock unit used in assessment (ICES 2020v).

Genetic population structure in a nutshell

In general, population structure was observed with neutral genetic markers for turbot within the NE Atlantic. However, the presence of locally adapted populations was reported, and genetic evidence suggests the following spatial structure for turbot in its distributional range:

- Baltic Sea and North Sea are genetically different (Nielsen et al. 2004, Vilas et al. 2010, Vandamme et al. 2014), in line with assessment in two different stock units.
- The presence of a hybrid zone was reported in the Skagerrak and Kattegat, where Baltic and North Sea populations mix (Nielsen et al. 2004).
- Turbot in the Skagerrak is part of the same genetic unit inhabiting the North Sea in contrast to the existing stock units, that are separated for turbot in the North Sea (Subarea 4) and in the Skagerrak (Division 3.a) (Prado et al. 2018b).
- Kattegat is genetically part of the same unit of turbot in the Baltic Sea, however they are assessed in two different stock assessment units (Florin & Höglund 2007, Vandamme et al. 2014).
- Potential substructure was detected in the North Sea, where the southern samples were more genetically similar to the British Isles and English Channel while turbot from central and northern North Sea was more similar to the sample from Norway and Iceland (Vandamme et al. 2014).
- Turbot in the Bay of Biscay and Spanish Atlantic coast is weakly, but statistically significant, differentiated from the rest of the NE Atlantic sample (Vilas et al. 2010, Prado et al. 2018b).
- Presence of eastern and western lineages of turbot in the Mediterranean showed (Suzuki et al. 2004).
- In the Black Sea the existence of at least 3 different populations was detected (Turan et al. 2019, Firidin et al. 2020), resulting in a mismatch with the management unit since turbot is managed as one stock.

- Differentiation between turbot inhabiting the Adriatic Sea and the Black Sea was showed (Prado et al. 2018b).

Mismatch

Genetic evidence suggested presence of mismatches between stock assessment units and genetic units. The assessment of turbot in the Skagerrak and Kattegat as one stock unit (Division 3.a) is not supported by genetic studies. In fact, turbot in the Kattegat is genetically part of the same unit present in the Baltic Sea, while turbot in the Skagerrak is part of the North Sea (Subarea 4) population.

Although it is clear that turbot in the Skagerrak and North Sea belong to the same population, the status of turbot in the North Sea and adjacent waters is not. Potential substructure within the North Sea was suggested (Vandamme et al. 2014), as well as a lack of differentiation with the English Channel and British Isles samples, questioning the boundaries of the current stock assessment unit (Turbot in Subarea 4).

In the Black Sea, currently managed as one stock unit, the existence of several populations was reported (Turan et al. 2019, Firidin et al. 2020) resulting in a mismatch. Hence, for a more sustainable fisheries management of Black Sea turbot the presence of these populations should be considered.

Summary of genetic evidence

Turbot is a commercially important flatfish species in the NE Atlantic, Mediterranean and Black Sea and its population structure has been studied with several genetic markers.

Blanquer et al. (1992) using allozymes reported low levels of genetic diversity and absence of structure for turbot in the NE Atlantic (from the Kattegat to Moroccan coast) and Mediterranean Sea. The only sample differentiated was the Aegean Sea. Hence, the mismatch in this study is due to a lack of differentiation between sampling locations (the North Sea and Kattegat) that are assessed as different stocks.

A lack of genetic differentiation was reported also at a finer scale by Bouza et al. (1997) in northwest Spain. In this study samples also of farmed turbot were analysed showing lower levels of genetic diversity than wild samples. The mismatch analysis here is not applicable, since there is no stock assessment or management units proposed for turbot in this region.

In a successive investigation, Coughlan et al. (1998) analysed microsatellite variation in wild and farm samples of turbot form Ireland and Norway. Genetic differentiation was detected between the two farm samples but not between the two wild samples. This lack of differentiation could be due to high levels of gene flow at pelagic life-stages or due to the post-glacial colonization history of the species. In line with previous studies, Bouza et al. (2002) analysing domesticated turbot and wild populations in the Cantabrian Sea and Galician waters, confirmed the absence of structure at this geographic scale and loss of genetic diversity for the samples of domesticated turbot.

In contrast to previous investigations, Nielsen et al. (2004) detected genetic population structure in turbot inhabiting the NE Atlantic and Baltic Sea, despite low level of

differentiation reported within the Atlantic sample (North Sea, Bay of Biscay), as well as within the Baltic Sea. Biologically significant differentiation was observed between the Atlantic/North Sea and the Baltic Sea populations and the presence of a hybrid zone was reported in the North Sea- Baltic Sea transition zone (Skagerrak, Kattegat, Belt Sea) where individuals from both populations mix.

Florin and Höglund (2007), using microsatellites, analysed a total of 11 samples across the Baltic Sea (including temporal replicates) reporting weak genetic structure within the basin (F_{ST} 0.004). Despite the sedentary life-style of turbot, there is no indication for substructure inside the Baltic Sea. Hence, a mismatch with the stock assessment unit exists, due to absence of differentiation between turbot from the Baltic Sea and the Kattegat (Division 3a), currently considered two separate ICES stock units. Vilas et al. (2010) using a combination of neutral and outlier microsatellites confirmed the weak spatial structure of turbot in the Atlantic waters and reported the existence of 3 different populations for turbot in the North Sea, the Baltic Sea and the Atlantic Iberian waters (Cantabrian Sea and Galicia), moreover presence of adaptative divergence between the Baltic Sea- Atlantic group was shown. Therefore, no mismatches are present based on this study.

In Imsland et al. (2014) findings indicated population homogeneity for southern Norway and Icelandic turbot that were; however differentiated from the Irish Sea. The Kattegat sample was the most differentiated from the Atlantic ones, hence no mismatch was revealed with the stock assessment units.

Vandamme et al. (2014) found clear evidence of neutral population structure in the NE Atlantic, indicating the presence of at least three populations, i.e. the Baltic Sea, the NE Atlantic ground and the Irish Shelf, confirming previous studies reporting differentiation between the Baltic and the Atlantic (Nielsen et al. 2004). Including microsatellite loci under selection, substructure was detected with a break in the North Sea between northern and southern Atlantic groups. The mismatch with the stock assessment and management units is evident for the North Sea, because central and northern North Sea samples grouped with the Northern Atlantic (Norway, Iceland) while samples from southern North Sea grouped with the English Channel, British Isles and southern Atlantic. Another mismatch is present due to a lack of differentiation between the Kattegat and the Baltic Sea, assessed as two different stocks. Vilas et al. (2015) analysed, with a combination of microsatellites and SNPs, turbot collected from the Baltic Sea to the Atlantic Iberian waters, including also a sample from a farm. In line with previous studies, the divergence of turbot inhabiting the Baltic Sea and the Atlantic was confirmed. Moreover they reported the presence of candidate genes involved in local adaptation of wild turbot populations experiencing different temperature and salinity conditions. Significant differentiation was found at SNPs only when the Baltic sea or the farm samples were included in the analysis, confirming the lack of structure within the Atlantic. While, for microsatellites all the pairwise comparisons were significant, except between the Cantabrian Sea and the Atlantic Galician coast.

Prado et al. (2018) developed a genetic tool for the identification of fish with farmed origin in the wild, that can be used to evaluate the impact of escapes and restocking activities on wild populations. Significant and high genetic differentiation between farmed and wild populations was observed (mean F_{ST}= 0.059), as well as evidence for adaptation to domestication. Presence of turbot with farmed ancestry was reported especially where restocking has been carried out. Prado et al. (2018b) used SNP analysis to elucidate the genetic population structure of turbot in its distributional range. The study suggested the existence of four main regions i.e., Baltic Sea, NE Atlantic group, Adriatic Sea and Black Sea. Divergence due to local adaptation was detected between the Baltic Sea, the Atlantic and the Black Sea, and temperature and salinity were identified as likely causes. Parallel evolution was observed in the Baltic Sea and the Black Sea, with both basins exhibiting lower salinity. Substructing within the Atlantic sample was shown, with Norway and the southern Atlantic (Bay of Biscay and Atlantic coast of Spain) weakly differentiated from the rest of the Atlantic samples. Hence, a mismatch can be detected for the Skagerrak sample, which is not differentiated from the North Sea and the other Atlantic samples, clearly showing a mismatch with the assessment units (division 3a and the North Sea assessed separately). Moreover, the lack of differentiation between the North Sea and other Atlantic samples should be further investigated. For management purpose the authors suggest these four regions should be considered, as well as the differentiation of the Norway and Spanish samples, and the possible substructure within the Baltic Sea (slightly differentiated north and southern samples).

Le Moan et al. (2019) reported clear differentiation between the North Sea and Baltic Sea populations of turbot, and the presence of only 6 individuals of admixed origin in the Kattegat, the F_{ST} between North Sea and Baltic Sea was 0.044.

In the Mediterranean, Suzuki et al. (2004) analysed mitochondrial DNA variation in turbot, showing the presence of a western and eastern lineage and the existence of endemic haplotypes in the Sea of Azov. A lack of differentiation among samples from the western Black Sea was reported by Atanassov et al. (2011). In the Turan et al. (2019) study, differentiation between the Black Sea and Marmara Sea was supported by both microsatellites and mitochondrial markers. Although turbot in the Black Sea is managed with a TAC, microsatellites revealed additional substructure within the basin where all four samples were significantly differentiated from each other, hence, suggesting presence of a mismatch with the management unit. Previous findings were confirmed by Firidin et al. (2020), that by increasing the number of samples and markers, showed significant differentiation between the southern and northern (Crimea and Sea of Azov) Black Sea. Based on their analysis, the existence of 3 stocks was supported, as well as the presence of admixture between the 2 populations at the southern coasts. These units should be implemented for a more sustainable fisheries management.

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
Turbot	NE Atlantic, Med	NS (2), EC (1), Kat (1), BOB (1), PRT (1), MOR (1), Med (3)	10 (179)	na	na	na	All (6)	Yes	Type I	Type I		(Blanquer et al. 1992)
	NE Atlantic	Gal (3), farm (8)	11 (366)	na	na	na	All (14)	No	na	na		(Bouza et al. 1997)
	NE Atlantic	NOR (1), IRE (1), farm (2)	4 (195)	na	na	na	Msat (3)	Yes	na	na		(Coughlan et al. 1998)
	NE Atlantic	Gal (2), farm (1)	3 (149)	na	na	na	All (17), Msat (12)	No	na	na		(Bouza et al. 2002)
	NE Atlantic	NS (1), NBTZ (4), BAL (2), BOB (1)	16 (706)[8]	y	y	Ad	Msat (8)	Yes	Type I, II	Type I	LG	(Nielsen et al. 2004)
	NE Atlantic, Med	ATL (1), w Med (1), e Med (2), BLS (2)	6 (66)	n	n	n	CR (435 bp)	Yes	na	na		(Suzuki et al. 2004)
	NE Atlantic	Kat (1), BAL (8)	11 (489)[2]	y	y	Ad	Msat (8)	No	Type I	na	LG	(Florin & Höglund 2007)

	NE Atlantic	BAL (1), NS (1), w SPA (2)	4 (190)	n	n	n	Msat (60) [S]	Yes	no	no	LA	(Vilas et al. 2010)
	Black Sea	BLS (4)	4 (76)	y	n	n	CR (432 bp)	No	no	no		(Atanassov et al. 2011)
	NE Atlantic	s NOR (1), IS (1), Kat (1), ICE (1)	4 (201)	na	na	na	Msat (12)	Yes	no	no	LA	(Imsland et al. 2014)
	NE Atlantic	BAL (3), NBTZ (3), ICE (1), w NOR (1), NS (3), EC (2), BI (4), BOB (2), PRT (1)	29 (999)[9]	na	na	na	Msat (17) [S]	Yes	Type I, II[S]	Type I, II[S]	LG, LA	(Vandamme et al. 2014)
	NE Atlantic	NS (1), BAL (1), EC (1), BOB (2), farm (1)	6 (286)	na	na	na	Msat (120) [S], SNPs (136) [S]	Yes	Type I	Type I	LA	(Vilas et al. 2015)
	NE Atlantic, Med	BAL (2), Ska (1), NOR (1), NS (3), ICE (1), BI (4), EC (1), BOB (3), w SPA (1), ADR (1) BLS (2)	20 (672) *	y	na	na	SNPs (755) [S]	Yes	Type I	Type I	LG, LA	(Prado et al. 2018b)
	NE Atlantic	BAL (2), Ska (1), NOR (1), NS (3), ICE (1), BI (4), EC	21 (908)	y	na	na	SNPs (755) [S]	Yes	na	na	LA	(Prado et al. 2018a)

		(1), BOB (3), w SPA (1), farm (4)									
	Black Sea	BLS (4), MS (1)	5 (50)	n	n	n	Msat (5), COIII (bp) [N]	Yes	Type II	Type II	LG	(Turan et al. 2019)
	Black Sea	BLS (12)	12 (414)	y	y	Ad	Msat (6), COIII (bp), cyt-b ()	Yes	Type II	Type II	LA, LG	(Firidin et al. 2020)
	NE Atlantic	NS (4), EC (1), NBTZ (3), BAL (4)	12 (275) **	y	n	n	SNPs (3348) [S]	Yes	Type I	Type I	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
Turbot, ***Scophthalmus maximus***	tur.27.22-32		Lack of differentiation Kattegat- Baltic Sea (Florin & Höglund 2007) (Vandamme et al. 2014)		
	tur.27.3a	Hybrid zone in SKA, Kat between Baltic and NS (Nielsen et al. 2004)			

	tur.27.4	Substructure within North Sea (Vandamme et al. 2014)	Lack of structure NS, BOB (Nielsen et al. 2004) Lack of structure NS and adjacent waters (Prado et al. 2018b) Lack of differentiation Skagerrak and North Sea (Prado et al. 2018b)	- 4, 2a [U] Combined turbot and brill