PANDORA Project - Deliverable No 1.3

Genetic Fact Sheet

Brill

Scophthalmus rhombus

2022

PANDORA

Paradigm for Novel Dynamic
Oceanic Resource Assessments

Gant agreement No: **773713**
Funded by the European Commission within the Horizon 2020 Programme

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.

Project receives funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 773713

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
Brill, *Scophthalmus rhombus*	2	no	no	no	no	LC

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

Brill, *Scophthalmus rhombus*

Number of studies	2
Population structure	✗
Match genetic- Stock assessment units	✗
Match genetic- Management units	✗
Match Stock assessment- Management units	✗

Distribution[1]

Brill, *Scophthalmus rhombus* (Linnaeus, 1758), is a widespread flatfish species in the North-East (NE) Atlantic, that occurs from Norwegian to Moroccan coasts, including the western part of the Baltic Sea, the Mediterranean and the Black Sea. It is a shallow water species. Juveniles are commonly found in inshore waters also in proximity of estuaries while mature individuals prefer offshore waters.

Current management status

ICES currently recognise two stock units in the NE Atlantic for brill (Table 2), one in the Baltic Sea and the other in the North Sea, English Channel, Skagerrak and Kattegat (Figure 3.2).

In the Baltic Sea, brill mainly occurs in the western part of the basin, where the main fishing country is Denmark that accounted for 95% of the catches in the Belt Sea (Subdivision 22) in 1985-2016 (ICES 2020b). Brill in the Baltic Sea and the North Sea is mainly a by-catch species of cod and other flatfish species directed fisheries (ICES 2018a, 2020b). For management purpose a combined TAC for brill and turbot in the North Sea (Subarea 4) and Union waters of division 2.a exists. According to ICES advice, the set of a combined TAC for these two species could lead to overexploitation (ICES 2018a). ICES currently provide separate advices on fishing opportunities and stock status for brill and turbot stocks. These two stocks have also a different geographic extension, with turbot including only the North Sea (Subarea 4), and brill extending into the English Channel, Skagerrak and Kattegat (Table 2). Furthermore, there is a mismatch between the assessment and management units for both species, in fact the TAC is set for subarea 4 and division 2.a whereas neither brill or turbot stock units include division 2.a. Therefore, ICES highlight that in order to guarantee a sustainable fisheries management and avoid overexploitation of one or the other species it is necessary to set separate TACs for brill and turbot (ICES 2018a, 2020c). Ideally, these TACs should match the assessment units, in the case of brill with the addition of the Skagerrak and Kattegat (Divisions 3.a) and the English Channel (Division 7.d and 7.e).

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

Genetic population structure in a nutshell

Genetic studies reported a lack of population structure for brill within the NE Atlantic both with allozyme and microsatellite loci (Blanquer et al. 1992, Vandamme 2014).

Mismatch

Genetic evidence does not support the presence of stock units for brill in the NE Atlantic. Further investigations with more powerful markers are needed to examine if the geographic extension of the current assessment units is supported or not and eventually design optimal management strategies for the species, with units reflecting the real bio-logical population structure of the species, if any.

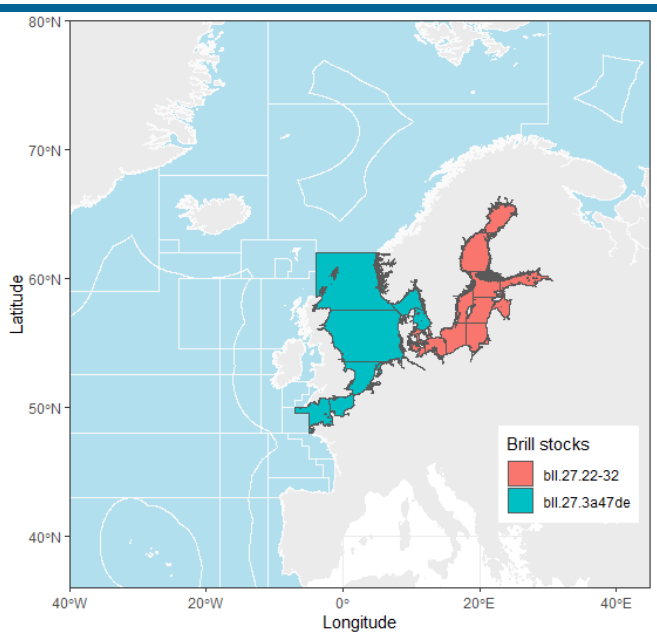

Figure 3.2. Brill ICES stock assessment units

Summary of genetic evidence

The information available on population structure for brill is extremely limited. Only one study analysed genetic variation at allozyme loci and potential geographic differences in the whole distributional range of brill (Blanquer et al. 1992) (Table 1). A lack of genetic population structure within the Atlantic and only a weak differentiation between the Atlantic and the Mediterranean samples was reported (Blanquer et al. 1992). Lack of structure was suggested also at microsatellite loci within the NE Atlantic (Vandamme 2014). Therefore, further studies are needed to test whether brill represents a panmictic population or, rather genetic differentiation exists also within the Atlantic and the Mediterranean. New and more powerful markers should be developed for brill such as SNPs, reinforced by a sampling design that maximise the possibility to detect population structure, focusing on spawning individuals.

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
Brill	NE Atlantic, Med	Kat (1), NS (1), EC (1), PRT (1), Med (2)	6 (117)	na	na	na	All (10)	No	Type I	Type I		(Blanquer et al. 1992)
	NE Atlantic	NS (3), NBTZ (3), EC (2), BI (5), BOB (1), w SPN (1)	23 (879)[8]	na	na	na	Msat (14)	No	Type I	Type I	LG	(Vandamme 2014)

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	Stock assessment unit	Mismatch SA unit - genetics (Type II)	Mismatch SA unit - genetics (Type I)	Management units	Mismatch management unit - genetics
Brill, ***Scophthalmus rhombus***	bll.27.22-32		No differentiation within NE Atlantic (Blanquer et al. 1992, Vandamme 2014)		
	bll.27.3a47de			- 4, 2a [U] (combined TAC with turbot)	No differentiation within NE Atlantic (Blanquer et al. 1992, Vandamme 2014)

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).

For each study the species, 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.