

Genetic Fact Sheet

→ **Four-spot megrim**

Lepidorhombus boscii



2022





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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PANDORA Project

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 7.i-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 (Portuguese 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
 - southern 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
Four-spot megrim, <i>Lepidorhombus boscii</i>	2	yes	Yes	no	no	LC

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

FACT SHEET

Four-spot megrim, *Lepidorhombus boscii*

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



Distribution¹

Four-spot megrim, *Lepidorhombus boscii* (Risso, 1810), is a flatfish species distributed in the North-East (NE) Atlantic from the British Isles to the north-western African coasts, and in the Mediterranean Sea. Although adult *megrims* are demersal and fairly sedentary, larvae are pelagic and gene flow could occur at this life stage due to passive transport facilitated by ocean currents. Spawning occurs near the coast from March to June (Campo and Garcia-Vazquez, 2010; and references therein).

Current management status

There are two species of the genus *Lepidorhombus* exploited in the NE Atlantic: megrim, *L. whiffiagonis* (Walbaum 1979), and the four-spot megrim, *L. boscii*, for which fisheries management is carried out with combined TACs set for Megrims, *Lepidorhombus spp.* (Table 2).

In the NE Atlantic, two stocks of four-spot megrim are present: one including west, southwest of Ireland (Divisions 7.b-k) and Bay of Biscay (8.a, b, d) and the second one including the southern Bay of Biscay (8.c) and the Atlantic Iberian Shelf (9.a) (Figure 3.4). In southwest Ireland and Bay of Biscay catches are mainly from France, Spain, UK and Ireland (ICES 2020s). The stock of four-spot megrim in this part of the Atlantic is classified by ICES as a data-limited stock (category 5), only landings data are available and information from survey are limited. Moreover, ICES is not requested to provide information on stock status and fishing opportunities for this stock (ICES 2020s). The management is put in place with a combined TAC set from the European Council for both megrim species, preventing a sustainable fishery management and possibly leading to the overexploitation of one or both species (ICES 2020s). ICES recommend that separate TACs should be set for the two species for a better management of the fisheries. Likewise in the southern Bay of Biscay and in the Atlantic Iberian shelf, four-spot megrim is fished in mixed fisheries directed mainly to hake and anglerfish with Spain becoming the main fishing country in the Atlantic Iberian shelf (ICES 2020s). Although landings are not completely separated by species, advice on stock status and fishing opportunities are

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

given by ICES for each species separately. However, even in this area the two species of megrim are managed under a combined TAC and ICES urges the implementation of separate TACs (ICES 2020s).

Stock units exist for Megrim species (*Lepidorhombus* ssp.) in the Rockall (Division 6.b) and in northern North Sea and west of Scotland (4.a and 6.a). However, catches of *L. boschii* are negligible in these divisions.

Genetic population structure in a nutshell

The available information on genetic population structure confirms the presence of two stocks of four-spot megrim in the NE Atlantic, reflecting the stock units used by ICES. Further studies should focus on the Mediterranean, since only one sample from this region was included to date.

Mismatch

A mismatch is revealed between genetic and management units. Four-spot megrim from Ireland and northern Bay of Biscay are genetically similar based on available data and evidence indicates currently, comprise one unit. However, TACs are set separately for Subarea 7 and Divisions 8.a-b, d, e (Table 2), hence resulting in a mismatch of the management units with genetic and also assessment units.

Summary of genetic evidence

Two studies investigated genetic population structure of four-spot megrim in the NE Atlantic and Mediterranean Sea. Danancher and Garcia-Vazquez (2009) applied a set of newly developed microsatellites to analyse samples from southwest of Ireland (7.j), the Bay of Biscay (8.a-b, d and 8.c), Portuguese waters (9.a) and the Mediterranean Sea. The presence of two distinct populations in the NE Atlantic was revealed (global F_{ST} within the Atlantic 0.145, $P < 0.001$), as well as one in the Mediterranean. The spatial genetic population structure found a match with the stock assessment units currently in use by ICES. Similar patterns of genetic differentiation were reported through a mitochondrial marker (Campo & Garcia-Vazquez 2010). Though, the level of differentiation detected by microsatellites was much higher than the one detected by the mitochondrial marker (global F_{ST} 0.177 and 0.023, respectively). Moreover, the Portuguese and the Mediterranean samples were genetically similar at the

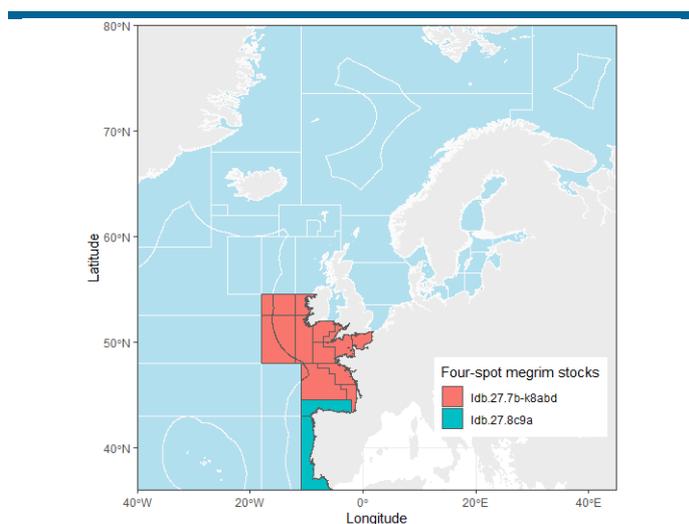


Figure 3.4. Four-spot megrim ICES stock assessment units



mitochondrial marker, probably, due to past colonization events or to extensive larval drift across the Mediterranean from the Atlantic (Division 9.a). The connectivity between the NE Atlantic and the Mediterranean populations should be further explored. The only mismatch present between the genetic population structure and the assessment units is due to a lack of differentiation found between Portuguese and Mediterranean samples by a mitochondrial marker (Campo & Garcia-Vazquez 2010). However, genetic differentiation was revealed between these two basins using microsatellites, solving the mismatch.



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	Differentiated	Mismatch genetic-SA	Mismatch genetic-MZ	LA, LG, MSA	Reference
Four-spot megrim	NE Atlantic, Med	IRE (1), BOB (3), PRT (1), Med (1)	6 (198)	na	na	Ad	Msat (7)	Yes	no	Type II	LG	(Danancher & Garcia-Vazquez 2009)
	NE Atlantic, Med	IRE (1), BOB (2), PRT (1), Med (1)	5 (163)	na	na	Ad	CR (438 bp)	Yes	Type I	Type II	LG	(Campo & Garcia-Vazquez 2010)

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
Four-spot megrim, <i>Lepidorhombus boscii</i>	ldb.27.7b-k8abd			- 7 (Combined TAC with megrim) - 8.a-b, d, e (Combined TAC with megrim)	Genetic unit in Ireland and northern Bay of Biscay
	ldb.27.8c9a			- 8.c, 9, 10; 34.1.1 ^U (Combined TAC with megrim)	



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 Zealand (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.