Genetic Fact Sheet

→ Blue Whiting

Micromesistius poutassou

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-management units	IUCN status
Blue whiting Micromesistius poutassou	4	yes	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

1.1 Blue Whiting, Micromesistius poutassou

|	
Number of studies	4
Population structure	✅
Match genetic- Stock assessment units	❌
Match genetic- Management units	❌
Match Stock assessment- Management units	❌

LEAST CONCERN LC

Distribution[1]

Blue whiting, Micromesistius poutassou (Risso 1826), is a pelagic fish of the Gadidae family widely distributed on the shelf edge of the North-East (NE) Atlantic, from the Canary Islands to Spitzbergen (Ryan et al. 2005). It is also present in the North-West Atlantic and in the Mediterranean. Adults migrate in early spring towards spawning grounds where the majority of the catches take place (ICES, 2020a and references therein). Spawning season varies according to latitude, starting in January in the southern areas. Spawning occurs pelagically and eggs and larvae are pelagic. Extensive spawning and feeding migrations are known for blue whiting.

Current management status

Blue whiting is a commercially important species. It is assessed as one stock unit in the Northeast Atlantic and adjacent waters (subareas 1-9, 12, and 14), however TACs are set for several management units (Table 2). The stock identity was questioned by ICES. ICES recognized that the scientific evidence supports the presence of two stocks for blue withing in the NE Atlantic. However, more information is needed for each population to generate separate
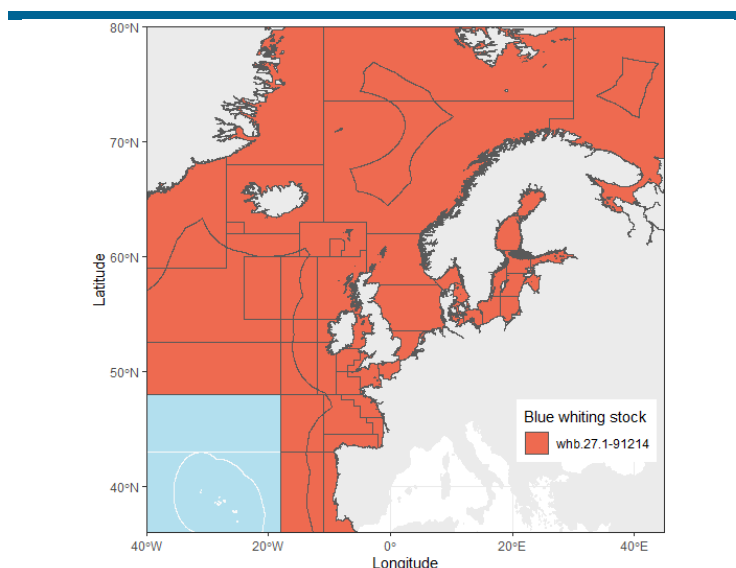
Figure 4.1. Blue whiting ICES stock assessment unit.

advice on stock status and fishing opportunities therefore assessment is still carried out for one stock unit (Figure 4.1). It is a large fishery in the NE Atlantic, with total catches in

2019 of 1 515 527 t, exceeding the recommended catch from ICES (≤ 1 143 629 t), resulting in fishing pressure above sustainable levels.

Blue whiting is mainly fished in the spawning grounds (Subarea 12; divisions 5.b, 6.a-b, 7.a-c), around the Faroes, Rockall and the western European shelf during the first and second quarter of the year (ICES 2020w). It is fished in direct fisheries by pelagic trawlers and in direct and mixed fisheries in the North Sea (Subarea 4 and division 3.a). Catches from the southern areas (subarea 8, 9; division 7.d-k) in 2019 amounted to 130 194 t, representing less than the 10% of the total catches (ICES 2020p). The main fishing countries are Norway, Iceland, the Faroes and Russia.

Genetic population structure in a nutshell

Significant genetic structure was reported for blue whiting, even though one stock unit is considered in stock assessment. Based on genetic evidence, it has been suggested:

- Presence of a local population in the Barents Sea (Giæver & Stien 1998, Ryan et al. 2005).
- Genetic homogeneity in southwest of Ireland (Mork & Giæver 1995).
- Differentiation NE Atlantic- Mediterranean Sea (Ryan et al. 2005).
- Existence of a northern (Hebrides, Rockall, Porcupine, Sulisker and Papa Banks) and southern (Celtic Sea) stock in the NE Atlantic (Was et al. 2008).
- Differentiation of southern Bay of Biscay (8.c), currently managed in a different unit but assessed in the same stock unit of the northern stock (Was et al. 2008).

Mismatch

Significant genetic structure was reported within the NE Atlantic that contrasts with the presence of one stock assessment unit. The existence of separate populations in the Barents Sea, northern and southern of Porcupine Bank (Was et al. 2008), and in south Bay of Biscay (Was et al. 2008) was reported. These findings contrast with the assessment of blue whiting in the NE Atlantic as one stock unit. These mismatches could bias stock assessment and potentially lead to the overexploitation of the weakest populations. Furthermore, a mismatch is evident also between management and genetic units. In fact, the northern and southern Porcupine Bank populations, as well as of the Barents Sea population is carried out as one management unit, despite they most likely represent genetically different units.

Summary of genetic evidence

Several studies have investigated the genetic population structure of blue whiting in the NE Atlantic. No further studies were published after the review conducted by Reiss et al. (2009). Genetic differentiation was detected for blue whiting despite pelagic life-stages and spawning and extensive feeding migrations potentially promoting gene flow. Mork and Giæver (1995) analysed genetic variation at allozyme loci in samples collected west of the British Isles (Southwest of Ireland) during the spawning season for two consecutive

years. No sign of population mixture was reported, in line with the assessment and management unit.

Giæver and Stien (1998) using allozymes studied genetic population structure of blue whiting in its distributional range, including samples from the Mediterranean Sea. The existence of a separate population of blue whiting in the Barents Sea, genetically different from the rest of the NE Atlantic was supported, despite the temporal difference observed between two of the Barents Sea samples. In fact, the population spawning at west of British Isles undertakes feeding migrations into Norwegian waters that can vary annually and explain the genetic similarity with one of the Barents Sea samples. Genetic homogeneity was reported for blue whiting in west of British Isles, the Porcupine Bank and the Norwegian Sea supporting the presence of one stock in these areas. Moreover, the presence of a genetically different populations was suggested also in a Norwegian fjord (Romsdalsfjord), even if not statistically significant. The mismatch between genetics, stock assessment and management units is due to the presence of a local population in the Barents Sea, which has not been taken into account in the current assessment and management units.

Through mini- and microsatellite analysis Ryan et al. (2005) confirmed that blue whiting in the Barents Sea and the Mediterranean are clearly differentiated from the rest of the NE Atlantic. The mismatches between genetics, assessment and management units due to the existence of a local population in the Barents Sea is confirmed. Moreover, genetic heterogeneity was reported for the Hebrides-Porcupine Bank spawning aggregations, that however was not temporally stable.

Was et al., (2008) using 5 microsatellites, reported significant genetic structure within the NE Atlantic for blue whiting, with the Celtic Sea and Bay of Biscay differentiated from the rest of the northern samples (the Hebrides, Rockall, Porcupine, Sulisker and Papa Banks) for which genetic homogeneity was shown. However, temporal variability was detected in the Rockall Bank where one of the temporal replicates differentiated from the others and the northern samples. In contrast to the existing stock unit, a northern and southern stocks was identified in the NE Atlantic, with additional substructure in the southern one. The apparent mismatch is due to the presence of local populations in the Celtic Sea and Bay of Biscay, that are, however, assessed as part of the same stock unit with the rest of the NE Atlantic. The mismatch between genetic and management units is due to the inclusion of the Celtic Sea with the rest of the NE Atlantic subareas rather than considering it as a separate unit. In contrast, the management of southern Bay of Biscay is currently carried out as a separate unit (Table 2).

Temporal variation was reported in the Barents Sea (Giæver & Stien 1998), in the Hebrides (Ryan et al. 2005) and in the Rockall Bank (Was et al. 2008) and should be further investigated. Additional studies are needed to disentangle the spatio-temporal genetic population structure of blue whiting in the NE Atlantic with more powerful markers.

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
Blue whiting	NE Atlantic	BI (1)	2 (130) [1]	y	n	Ad	All (3)	No	no	no		(Mork & Giæver 1995)
	NE Atlantic, Med	Heb (1), SHE (1), FRO (1), BS (5), NOR (35), ICE (1), w IRE (3), CS (1), BOB (1), Med (2)	65 (5025) [10]	y	y	Ad	All (2)	Yes	Type II	Type II		(Giæver & Stien 1998)
	NE Atlantic, Med	ICE (1), Heb (1), Por (1), CS (2), NOR (1), BS (1), PRT (1), Med (1)	11 (850) [2]	y	y	Ad, juv	Minisat (1), Msat (5)	Yes	Type II	Type II		(Ryan et al. 2005)
	NE Atlantic	BI (2), Heb (1), Roc (1), Por (1), CS (1), BOB (1)	16 (755) [9]	Y	Y	Ad	Msat (5)	Yes	Type II	Type II	LG	(Was et al. 2008)

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
Blue whiting ***Micromesistius poutassou***	whb.27.1-91214	Barents Sea local population (Giæver & Stien 1998, Ryan et al. 2005) northern and southern populations (Was et al. 2008); Bay of Biscay (8.c) differentiated (Was et al. 2008)		- 2, 4 [N] - (1, 2, 3, 4, 5, 6, 7, 8a, 8b, 8d, 8e, 12, 14) [U, I] - 8c, 9, 10; CECAF 34.1.1 [U] - 2, 4a, 5, 6 [U] - Faroese waters	Barents Sea local population (Giæver & Stien 1998, Ryan et al. 2005) Northern and southern populations (Was et al. 2008)