Small Pelagic Fish: 2022

Range-wide genetic stock delineation of the European sardine (*Sardina pilchardus*) using whole genome sequencing (Pool-Seq)

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Stephen J. Sabatino, Susana Garrido, João Neves,
Bruno Louro, Adelino V.M. Canário, Cymon J. Cox,
Gianluca De Moro and António Múrias Santos

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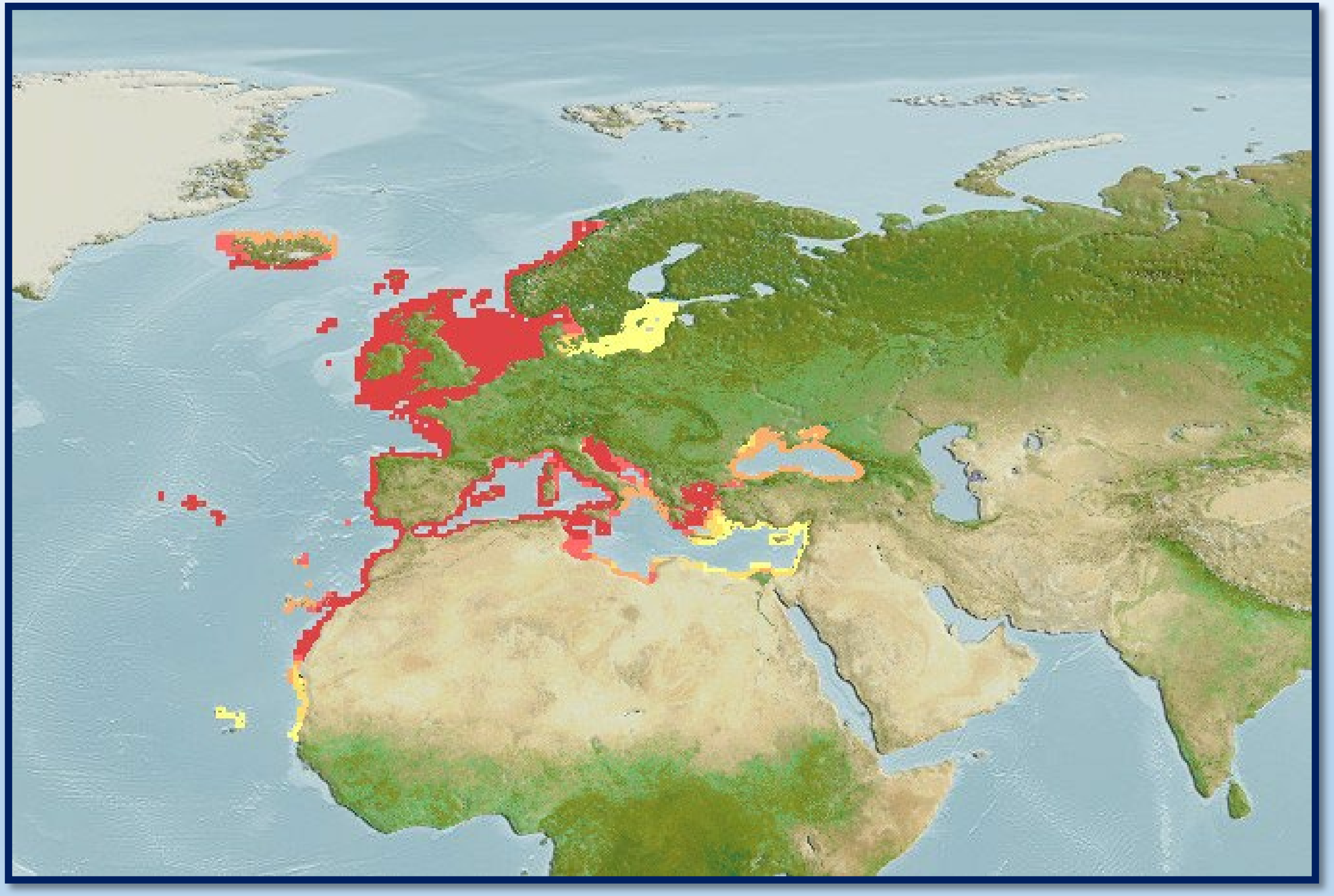
U.PORTO FACULDADE DE CIÊNCIAS UNIVERSIDADE DO PORTO
CIBIO Centro de Investigação em Biodiversidade e Recursos Genéticos
ipma instituto português do mar e da atmosfera
CCMAR Centro de Ciências do Mar

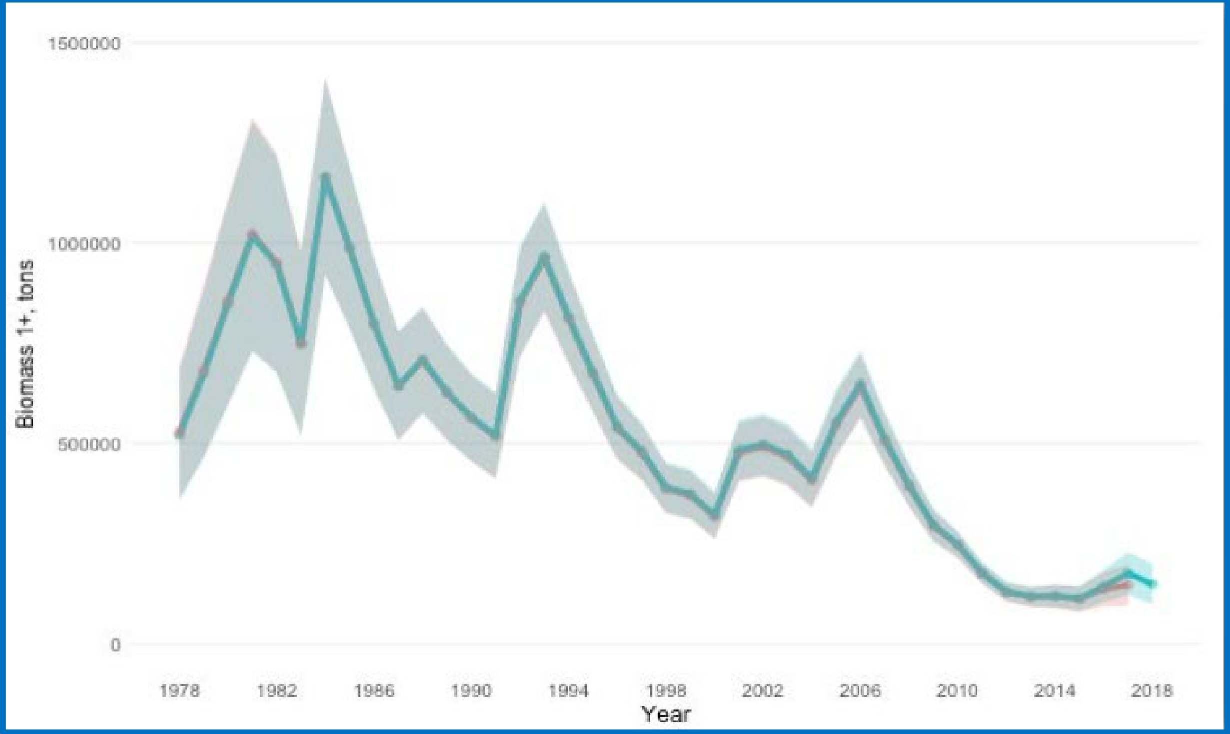
INTRODUCTION

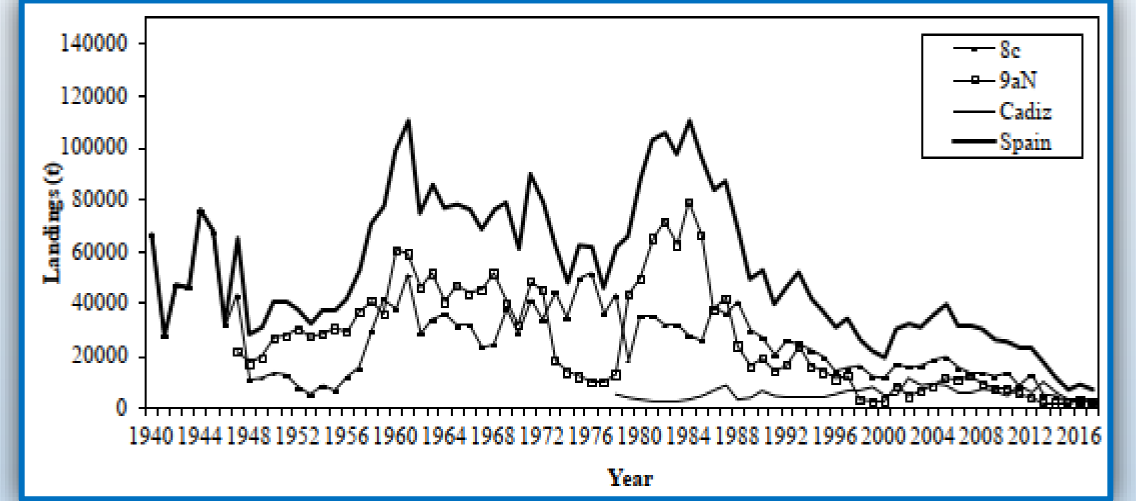


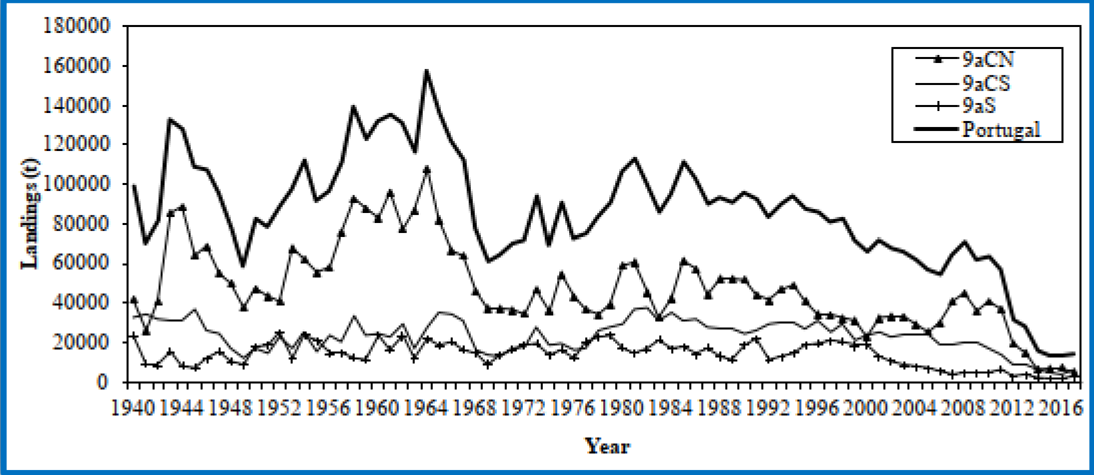
Relevant fisheries resources

Source of income for local economies

INTRODUCTION





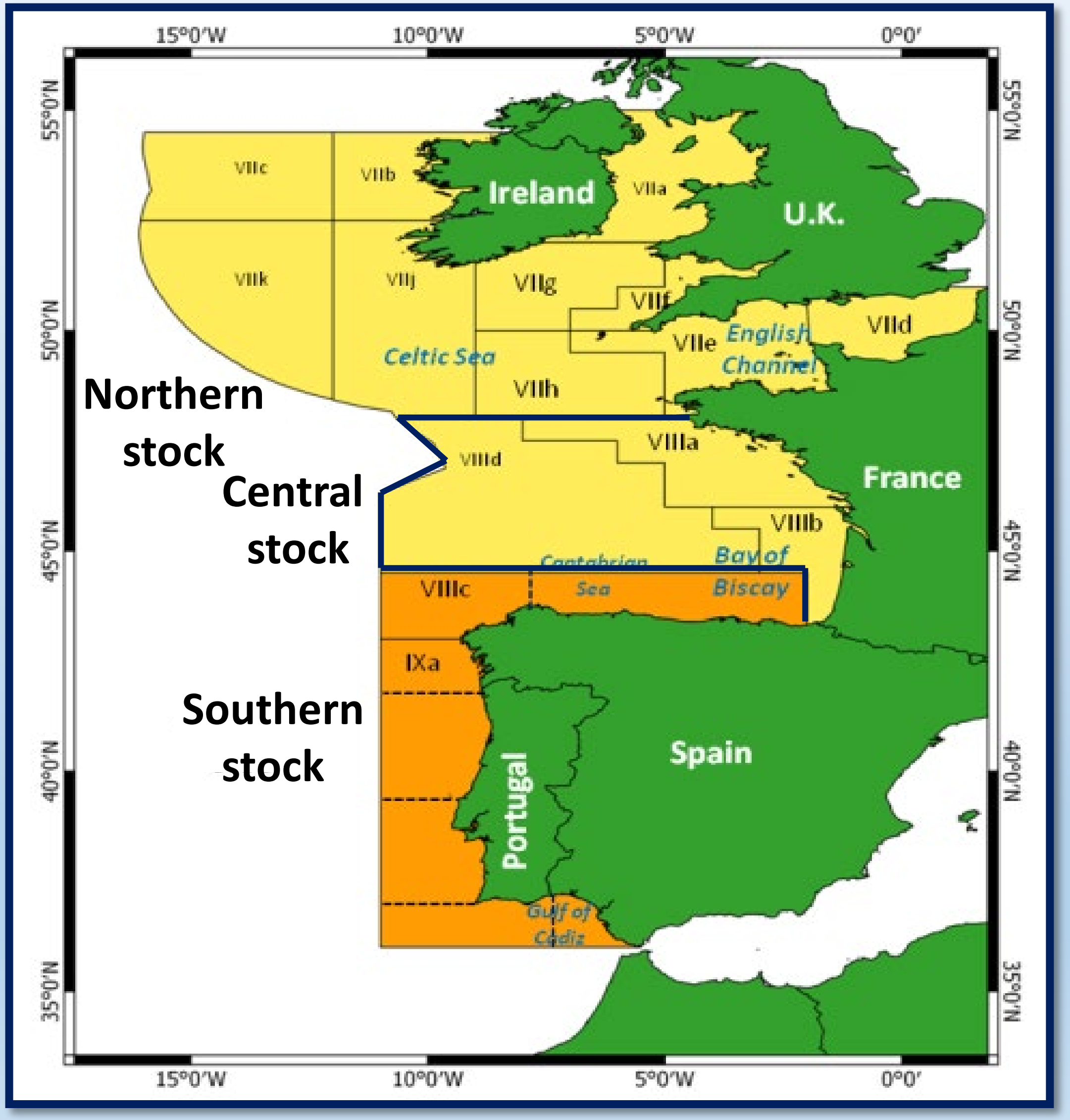


- Fishing restrictions and quota limitations
- Premature closures of fishing seasons

ICES 2018

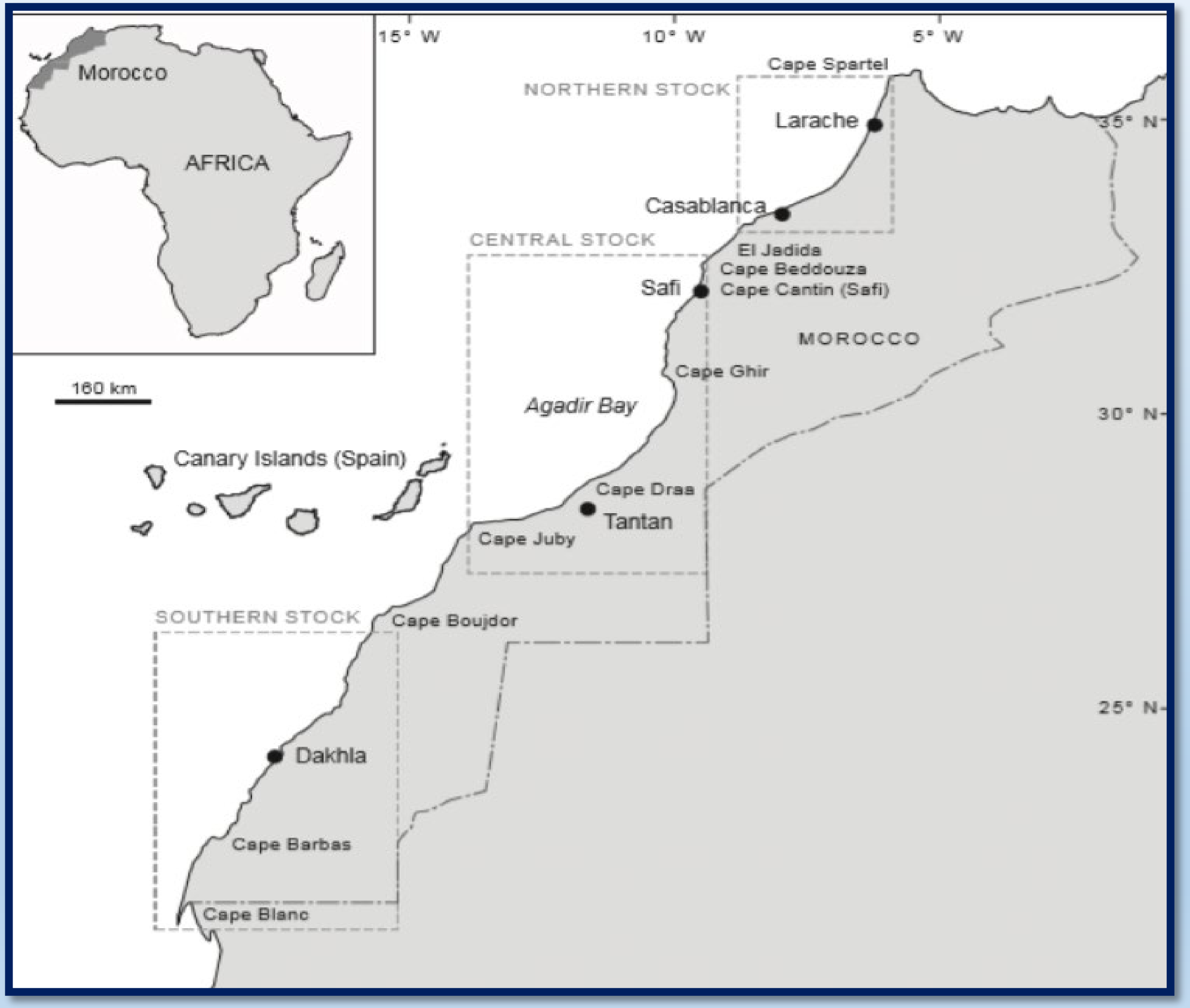
INTRODUCTION

European Atlantic waters



ICES 2019

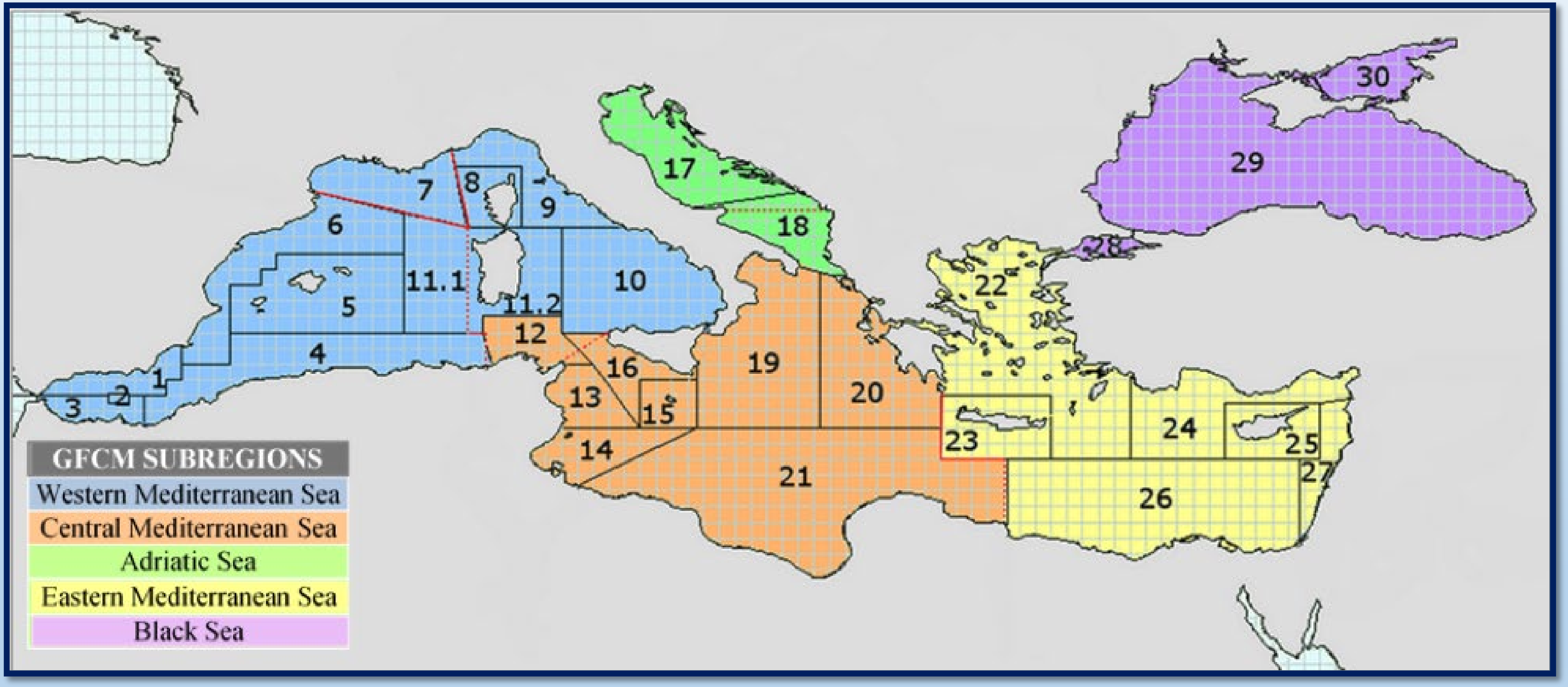
Atlantic African coast



FAO 2019

INTRODUCTION

Mediterranean



GFCM Geographical subareas (GSAs)

INTRODUCTION

Population structure of the European sardine *Sardina pilchardus* from Atlantic and Mediterranean waters based on otolith shape analysis

João Neves [a,b,*], Alexandra Almeida Silva [b,c], Ana Moreno [b], Ana Veríssimo [d], António Múrias Santos [a,d], Susana Garrido [b,c]

Major population's separation area for sardine (*Sardina pilchardus*) and hake (*Merluccius merluccius*) revealed using otolith geochemistry on the Atlantic coast of Morocco

Maylis Labonne [a], Hicham Masski [b,*], Sophia Talba [b], Imane Tai [b], Khalid Manchih [b], Rachid Chfiri [b], Raymond Lae [c]

Evidence for meta-population structure of *Sardina pilchardus* in the Atlantic Iberian waters from otolith elemental signatures of a strong cohort

A.T. Correia [a,b,*,1], P. Hamer [c], B. Carocinho [d], A. Silva [e,1]

INTRODUCTION

Low coverage whole genome sequencing reveals the underlying structure of European sardine populations

EUROPEAN SARDINE | FISH | GENOMICS/PROTEOMICS | LOW COVERAGE SEQUENCING | POPULATION GENETICS - EMPIRICAL | POPULATION STRUCTURE

Rute da Fonseca, Paula Campos, Alba Rey de la Iglesia, Gustavo Barroso, Lucie Bergeron, Manuel Nande, Fernando Tuya, Sami Abidli, Montse Pérez, Isabel Riveiro, Pablo Carrera, Alba Jurado-Ruzafa, Andre Machado, Miguel Fonseca, Elsa Froufe, L Filip

Signature of an early genetic bottleneck in a population of Moroccan sardines (*Sardina pilchardus*)

Touriya Atarhouch [a,b], Lukas Rüber [c,1], Elena G. Gonzalez [c], Eva M. Albert [c], Mohamed Rami [b], Allal Dakkak [b], Rafael Zardoya [c,*]

Evidence of a genetic cline for *Sardina pilchardus* along the Northwest African coast

M. Chlaida, V. Laurent, S. Kifani, T. Benazzou, H. Jaziri, and S. Planes

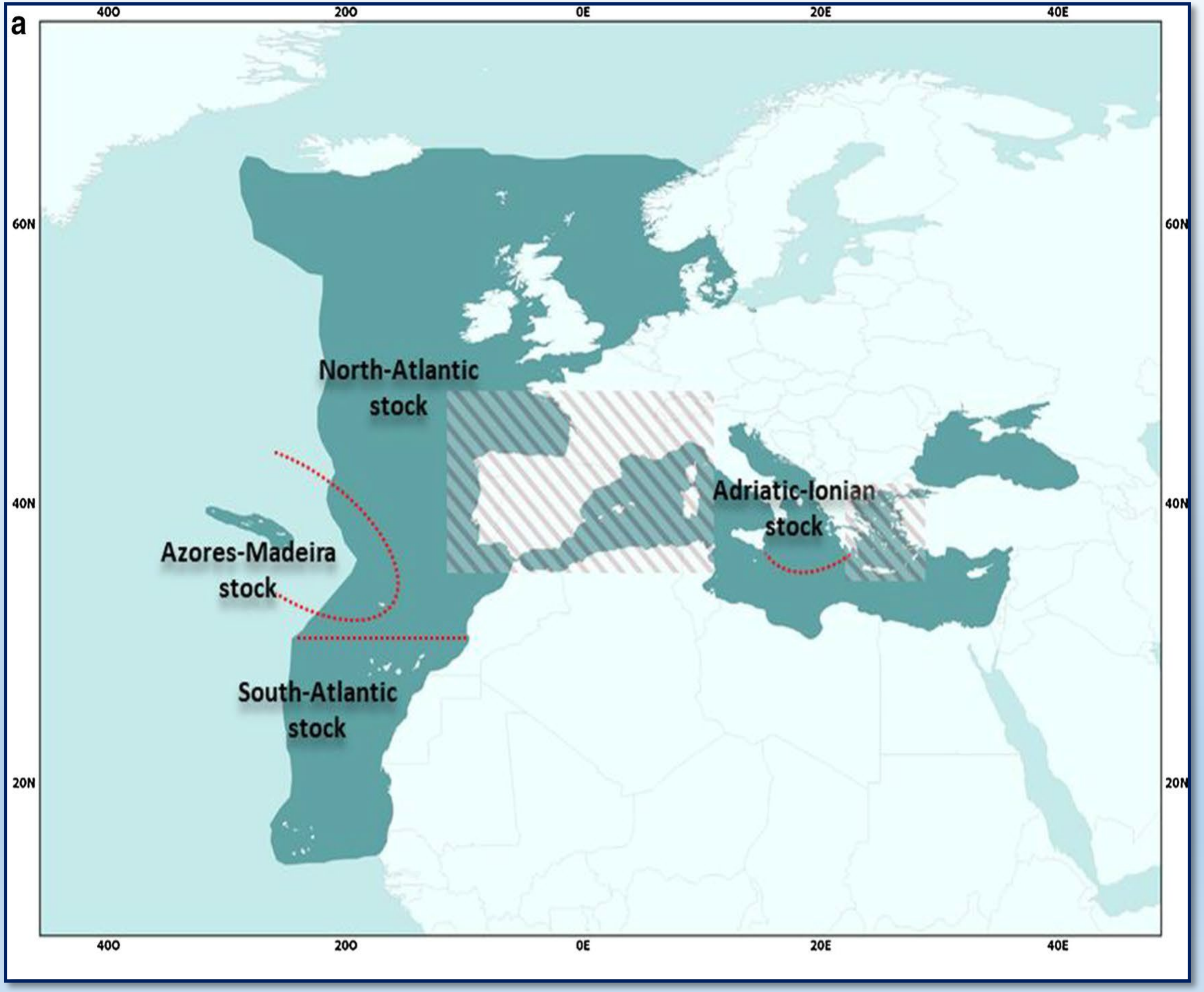
Evidence for microsatellite hitchhiking selection in European sardine (*Sardina pilchardus*) and implications in inferring stock structure

PANAGIOTIS KASAPIDIS [1], ALEXANDRA SILVA [2], GIANPAOI
and ANTONIOS MAGOULAS [1]

Searching for a stock structure in *Sardina pilchardus* from the Adriatic and Ionian seas using a microsatellite DNA-based approach

PAOLO RUGGERI [1], ANDREA SPLENDIANI [1], SARA BONANOMI [1,4], ENRICO ARNERI [2], NANDO CINGOLANI [3], ALBERTO SANTOJANNI [3], SABRINA COLELLA [3], FORTUNATA DONATO [3], MASSIMO GIOVANNOTTI [1] and VINCENZO CAPUTO BARUCCHI [1,3]

INTRODUCTION



Caballero-Huertas *et al*. 2022

NO CLEAR CONSENSUS !

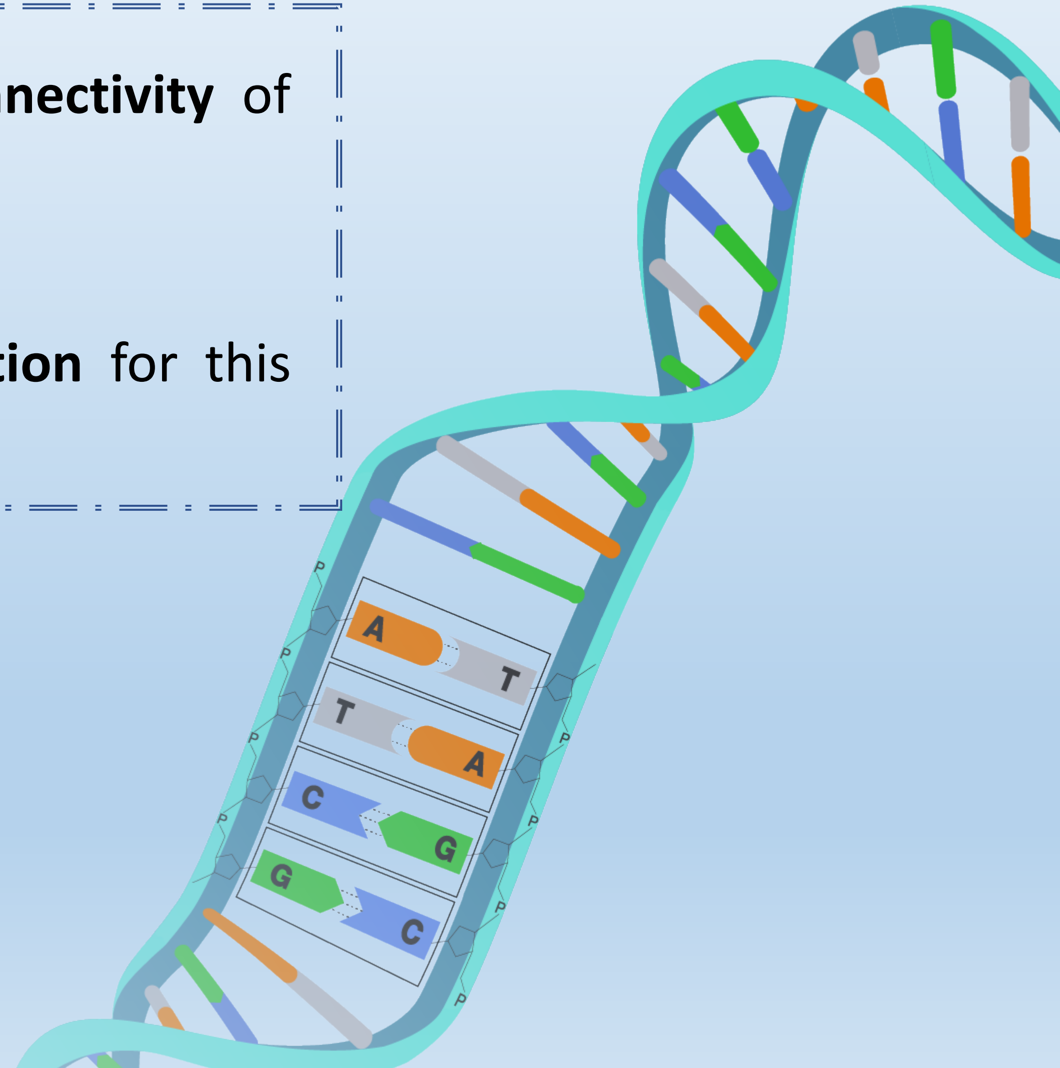
OBJECTIVES

We used **whole-genome sequencing of pools** of individuals (**Pool-Seq**) sampled across **most of its distribution range**, to:

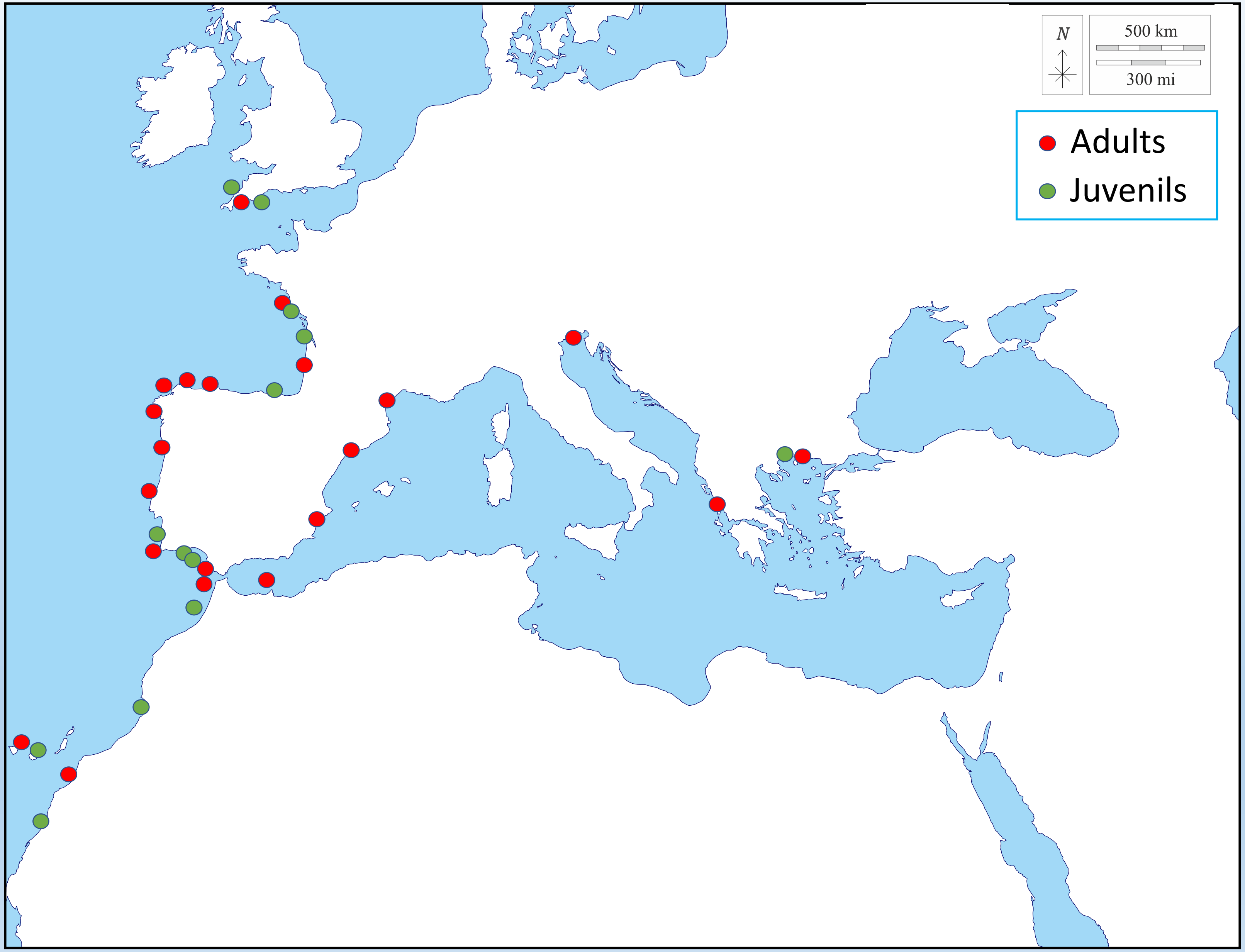
- investigate the **genetic structure and spatial connectivity** of European sardine populations

- try to reach a **consensual reliable stock delineation** for this species

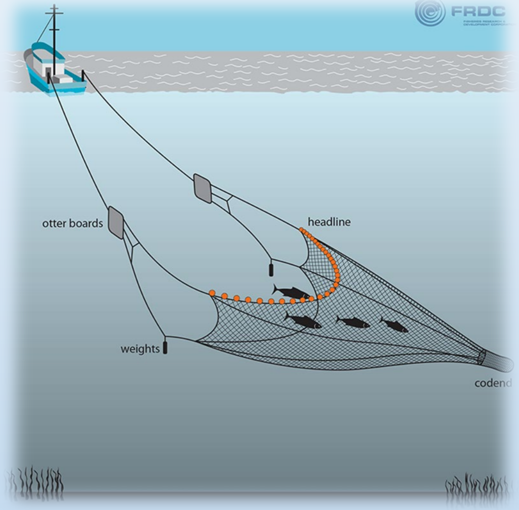
Proper management and conservation of this important fishery resource



MATERIALS & METHODS



Annual research surveys:
Pelagic trawls



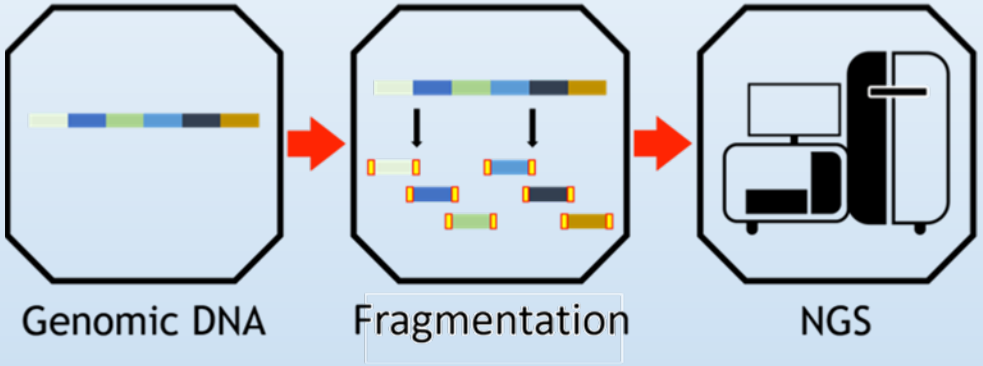
Commercial landings:
artisanal fleets

MATERIALS & METHODS

DNA Extraction

34 Pools: 25 inds.

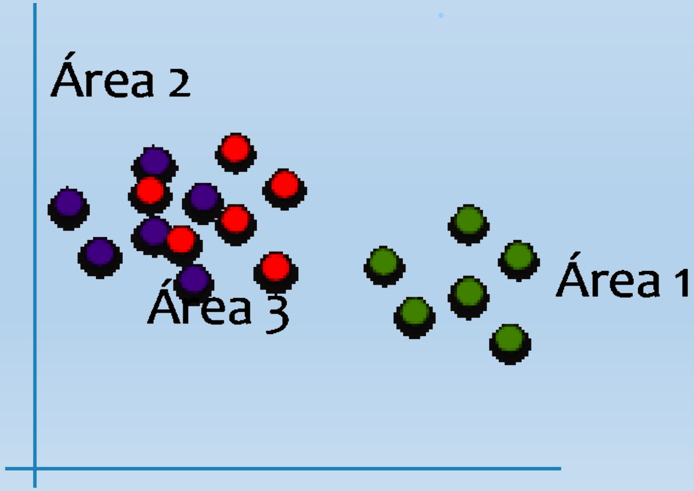
Whole Genome Sequencing (WGS)



- Paired-end reads
- 151 bp reads length
- TrueSeq Nano DNA Library
- Illumina platform (NovaSeq 6000)

Bioinformatic analyses

Population structure



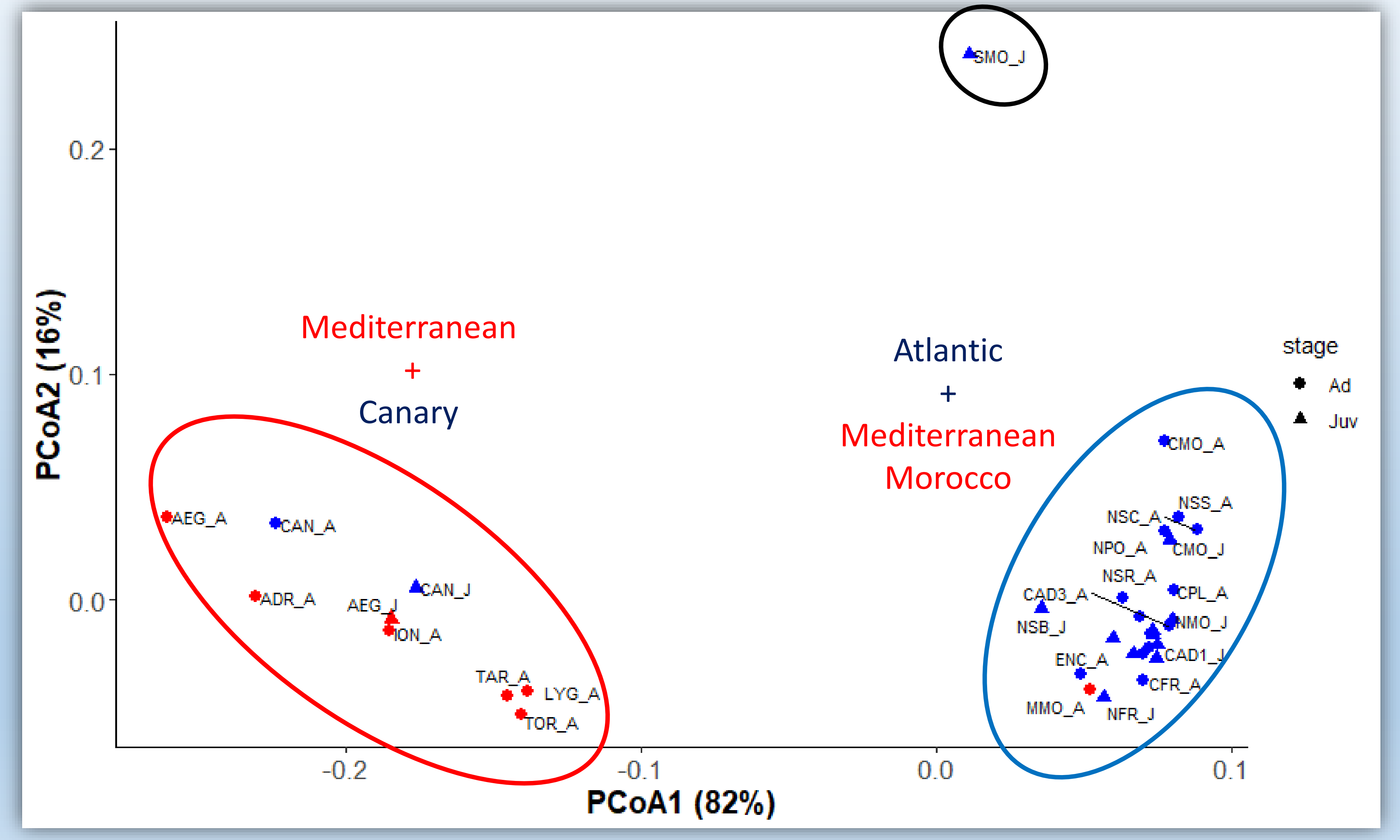
RESULTS & DISCUSSION

Fst Values

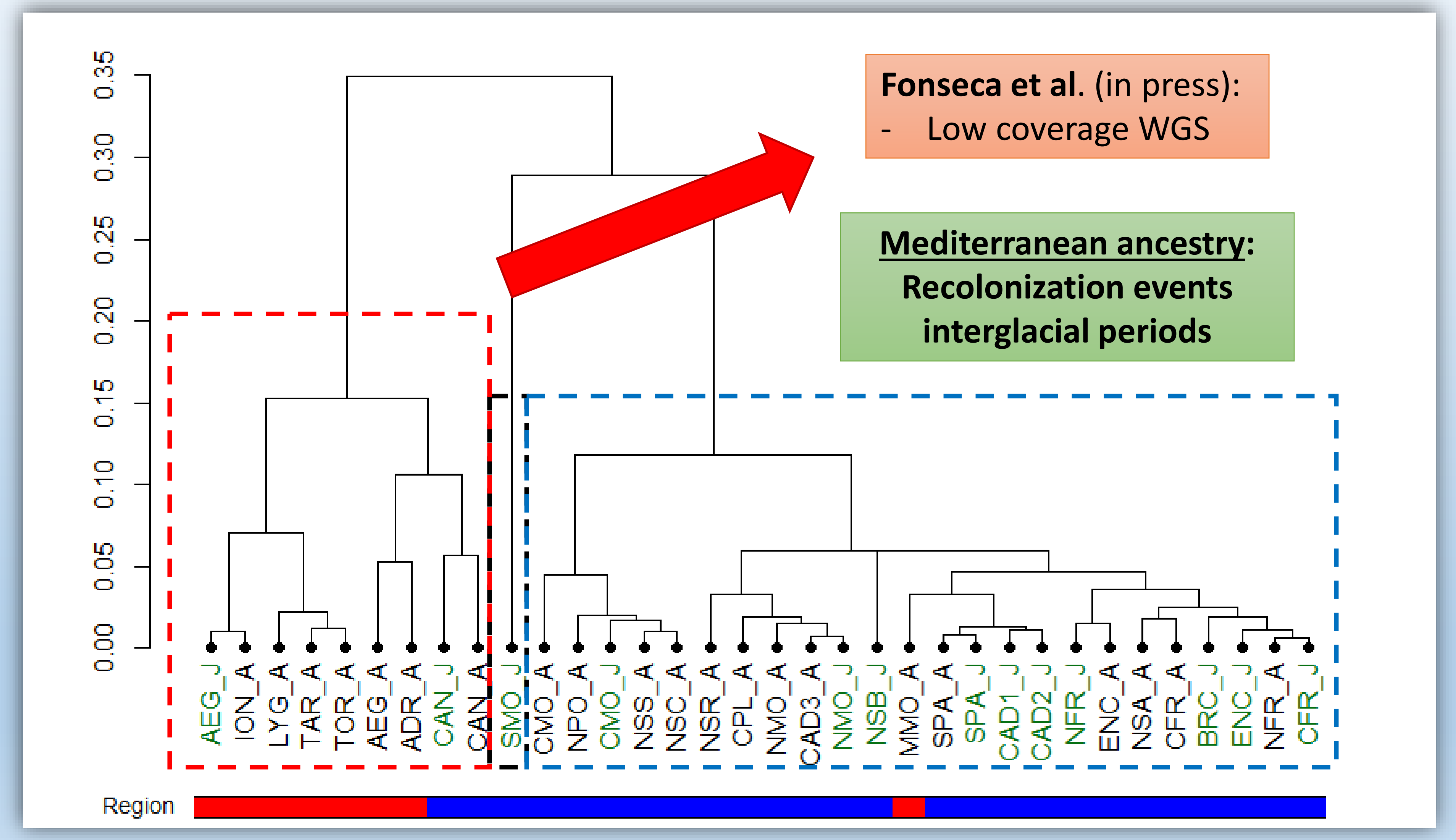
	AEG_A	AEG_J	SPA_A	CAD1_J	CAD2_J	CAD3_A	NPO_A	CPL_A	SPA_J	CAN_J	CAN_A	NSA_A	LYG_A	TAR_A	TOR_A	ION_A	ADR_A	NFR_J	NFR_A	CFR_J	CFR_A	ENC_A	BRC_J	ENC_J	MMO_A	SMO_J	NMO_A	NMO_J	CMO_A	CMO_J	NSS_A	NSC_A	NSR_A	NSB_J
AEG_A		0.021	0.067	0.063	0.064	0.068	0.086	0.072	0.067	0.051	0.048	0.069	0.027	0.029	0.028	0.024	0.018	0.056	0.070	0.069	0.061	0.058	0.068	0.067	0.061	0.142	0.074	0.071	0.089	0.076	0.079	0.080	0.067	0.070
AEG_J	0.021		0.054	0.054	0.053	0.054	0.066	0.058	0.054	0.044	0.045	0.052	0.027	0.026	0.023	0.012	0.021	0.049	0.054	0.054	0.050	0.050	0.053	0.055	0.051	0.124	0.058	0.056	0.072	0.064	0.065	0.063	0.058	0.058
SPA_A	0.067	0.054		0.009	0.011	0.010	0.015	0.010	0.011	0.052	0.065	0.015	0.041	0.044	0.039	0.054	0.058	0.016	0.015	0.014	0.014	0.019	0.018	0.016	0.012	0.038	0.012	0.011	0.016	0.013	0.013	0.012	0.015	0.024
CAD1_J	0.063	0.054	0.009		0.010	0.009	0.016	0.009	0.010	0.053	0.065	0.015	0.038	0.043	0.039	0.054	0.056	0.014	0.015	0.014	0.012	0.017	0.018	0.015	0.011	0.039	0.012	0.010	0.016	0.011	0.011	0.012	0.012	0.024
CAD2_J	0.064	0.053	0.011	0.010		0.009	0.014	0.010	0.010	0.052	0.063	0.016	0.038	0.042	0.037	0.052	0.055	0.015	0.015	0.015	0.015	0.019	0.018	0.015	0.012	0.040	0.014	0.012	0.018	0.012	0.015	0.014	0.017	0.027
CAD3_A	0.068	0.054	0.010	0.009	0.009		0.012	0.009	0.009	0.053	0.066	0.013	0.041	0.045	0.040	0.054	0.058	0.016	0.014	0.013	0.014	0.019	0.017	0.015	0.011	0.036	0.011	0.010	0.015	0.012	0.012	0.012	0.015	0.024
NPO_A	0.086	0.066	0.015	0.016	0.014	0.012		0.012	0.012	0.065	0.080	0.014	0.054	0.057	0.052	0.065	0.073	0.021	0.014	0.013	0.017	0.023	0.017	0.014	0.019	0.037	0.013	0.013	0.018	0.016	0.015	0.012	0.020	0.029
CPL_A	0.072	0.058	0.010	0.009	0.010	0.009	0.012		0.009	0.060	0.073	0.013	0.047	0.050	0.045	0.059	0.064	0.015	0.013	0.012	0.013	0.019	0.016	0.014	0.013	0.034	0.011	0.010	0.014	0.013	0.011	0.011	0.015	0.025
SPA_J	0.067	0.054	0.011	0.010	0.010	0.009	0.012	0.009		0.053	0.066	0.013	0.042	0.044	0.040	0.053	0.058	0.015	0.014	0.013	0.014	0.018	0.016	0.014	0.013	0.038	0.012	0.011	0.016	0.013	0.013	0.012	0.016	0.024
CAN_J	0.051	0.044	0.052	0.053	0.052	0.053	0.065	0.060	0.053		0.015	0.051	0.032	0.032	0.029	0.043	0.038	0.052	0.056	0.057	0.052	0.054	0.056	0.058	0.047	0.120	0.055	0.054	0.070	0.062	0.064	0.064	0.060	0.057
CAN_A	0.048	0.045	0.065	0.065	0.063	0.066	0.080	0.073	0.066	0.015		0.064	0.034	0.032	0.030	0.046	0.036	0.061	0.068	0.069	0.063	0.063	0.067	0.069	0.060	0.140	0.070	0.069	0.087	0.076	0.079	0.079	0.072	0.070
NSA_A	0.069	0.052	0.015	0.015	0.016	0.013	0.014	0.013	0.013	0.051	0.064		0.042	0.042	0.036	0.053	0.055	0.011	0.010	0.009	0.009	0.012	0.009	0.010	0.017	0.049	0.013	0.014	0.020	0.018	0.015	0.013	0.015	0.016
LYG_A	0.027	0.027	0.041	0.038	0.038	0.041	0.054	0.047	0.042	0.032	0.034	0.042		0.014	0.014	0.026	0.017	0.037	0.046	0.046	0.039	0.039	0.045	0.045	0.033	0.112	0.045	0.044	0.061	0.049	0.053	0.053	0.044	0.048
TAR_A	0.029	0.026	0.044	0.043	0.042	0.045	0.057	0.050	0.044	0.032	0.032	0.042	0.014		0.012	0.026	0.016	0.037	0.045	0.046	0.039	0.039	0.044	0.045	0.038	0.117	0.048	0.048	0.065	0.053	0.056	0.056	0.047	0.047
TOR_A	0.028	0.023	0.039	0.039	0.037	0.040	0.052	0.045	0.040	0.029	0.030	0.036	0.014	0.012		0.023	0.015	0.033	0.039	0.041	0.035	0.034	0.038	0.040	0.034	0.110	0.044	0.043	0.060	0.049	0.052	0.051	0.044	0.041
ION_A	0.024	0.012	0.054	0.054	0.052	0.054	0.065	0.059	0.053	0.043	0.046	0.053	0.026	0.026	0.023		0.021	0.051	0.055	0.055	0.052	0.051	0.054	0.055	0.050	0.125	0.056	0.055	0.072	0.065	0.065	0.063	0.060	0.058
ADR_A	0.018	0.021	0.058	0.056	0.055	0.058	0.073	0.064	0.058	0.038	0.036	0.055	0.017	0.016	0.015	0.021		0.048	0.059	0.059	0.052	0.049	0.055	0.057	0.050	0.136	0.063	0.062	0.081	0.069	0.072	0.071	0.061	0.058
NFR_J	0.056	0.049	0.016	0.014	0.015	0.016	0.021	0.015	0.015	0.052	0.061	0.011	0.037	0.037	0.033	0.051	0.048		0.012	0.010	0.008	0.008	0.010	0.010	0.019	0.052	0.019	0.017	0.023	0.018	0.016	0.016	0.012	0.016
NFR_A	0.070	0.054	0.015	0.015	0.015	0.014	0.014	0.013	0.014	0.056	0.068	0.010	0.046	0.045	0.039	0.055	0.059	0.012		0.009	0.010	0.013	0.010	0.010	0.019	0.045	0.015	0.015	0.020	0.019	0.015	0.013	0.016	0.018
CFR_J	0.069	0.054	0.014	0.014	0.015	0.013	0.013	0.012	0.013	0.057	0.069	0.009	0.046	0.046	0.041	0.055	0.059	0.010	0.009		0.009	0.012	0.009	0.009	0.019	0.044	0.015	0.014	0.019	0.017	0.013	0.012	0.013	0.017
CFR_A	0.061	0.050	0.014	0.012	0.015	0.014	0.017	0.013	0.014	0.052	0.063	0.009	0.039	0.039	0.035	0.052	0.052	0.008	0.010	0.009		0.008	0.010	0.010	0.017	0.047	0.015	0.014	0.020	0.016	0.014	0.014	0.011	0.015
ENC_A	0.058	0.050	0.019	0.017	0.019	0.019	0.023	0.019	0.018	0.054	0.063	0.012	0.039	0.039	0.034	0.051	0.049	0.008	0.013	0.012	0.008		0.010	0.010	0.022	0.054	0.020	0.019	0.025	0.020	0.018	0.017	0.012	0.013
BRC_J	0.068	0.053	0.018	0.018	0.018	0.017	0.017	0.016	0.016	0.056	0.067	0.009	0.045	0.044	0.038	0.054	0.055	0.010	0.010	0.009	0.010	0.010		0.008	0.022	0.051	0.019	0.018	0.023	0.020	0.017	0.016	0.015	0.016
ENC_J	0.067	0.055	0.016	0.015	0.015	0.015	0.014	0.014	0.014	0.058	0.069	0.010	0.045	0.045	0.040	0.055	0.057	0.010	0.010	0.009	0.010	0.010	0.008		0.020	0.046	0.016	0.016	0.021	0.017	0.015	0.013	0.013	0.017
MMO_A	0.061	0.051	0.012	0.011	0.012	0.011	0.019	0.013	0.013	0.047	0.060	0.017	0.033	0.038	0.034	0.050	0.050	0.019	0.019	0.019	0.017	0.022	0.022	0.020		0.047	0.013	0.012	0.020	0.016	0.017	0.017	0.018	0.025
SMO_J	0.142	0.124	0.038	0.039	0.040	0.036	0.037	0.034	0.038	0.120	0.140	0.049	0.112	0.117	0.110	0.125	0.136	0.052	0.045	0.044	0.047	0.054	0.051	0.046	0.047		0.037	0.035	0.029	0.031	0.033	0.033	0.044	0.059
NMO_A	0.074	0.058	0.012	0.012	0.014	0.011	0.013	0.011	0.012	0.055	0.070	0.013	0.045	0.048	0.044	0.056	0.063	0.019	0.015	0.015	0.015	0.020	0.019	0.016	0.013	0.037		0.009	0.015	0.014	0.012	0.011	0.018	0.023
NMO_J	0.071	0.056	0.011	0.010	0.012	0.010	0.013	0.010	0.011	0.054	0.069	0.014	0.044	0.048	0.043	0.055	0.062	0.017	0.015	0.014	0.014	0.019	0.018	0.016	0.012	0.035	0.009		0.013	0.012	0.011	0.010	0.015	0.023
CMO_A	0.089	0.072	0.016	0.016	0.018	0.015	0.018	0.014	0.016	0.070	0.087	0.020	0.061	0.065	0.060	0.072	0.081	0.023	0.020	0.019	0.020	0.025	0.023	0.021	0.020	0.029	0.015	0.013		0.015	0.013	0.013	0.019	0.029
CMO_J	0.076	0.064	0.013	0.011	0.012	0.012	0.016	0.013	0.013	0.062	0.076	0.018	0.049	0.053	0.049	0.065	0.069	0.018	0.019	0.017	0.016	0.020	0.020	0.017	0.016	0.031	0.014	0.012	0.015		0.013	0.012	0.015	0.027
NSS_A	0.079	0.065	0.013	0.011	0.015	0.012	0.015	0.011	0.013	0.064	0.079	0.015	0.053	0.056	0.052	0.065	0.072	0.016	0.015	0.013	0.014	0.018	0.017	0.015	0.017	0.033	0.012	0.011	0.013	0.013		0.009	0.013	0.022
NSC_A	0.080	0.063	0.012	0.012	0.014	0.012	0.012	0.011	0.012	0.064	0.079	0.013	0.053	0.056	0.051	0.063	0.071	0.016	0.013	0.012	0.014	0.017	0.016	0.013	0.017	0.033	0.011	0.010	0.013	0.012	0.009		0.013	0.022
NSR_A	0.067	0.058	0.015	0.012	0.017	0.015	0.020	0.015	0.016	0.060	0.072	0.015	0.044	0.047	0.044	0.060	0.061	0.012	0.016	0.013	0.011	0.012	0.015	0.013	0.018	0.044	0.018	0.015	0.019	0.015	0.013	0.013		0.019
NSB_J	0.070	0.058	0.024	0.024	0.027	0.024	0.029	0.025	0.024	0.057	0.070	0.016	0.048	0.047	0.041	0.058	0.058	0.016	0.018	0.017	0.015	0.013	0.016	0.017	0.025	0.059	0.023	0.023	0.029	0.027	0.022	0.022	0.019	

RESULTS & DISCUSSION

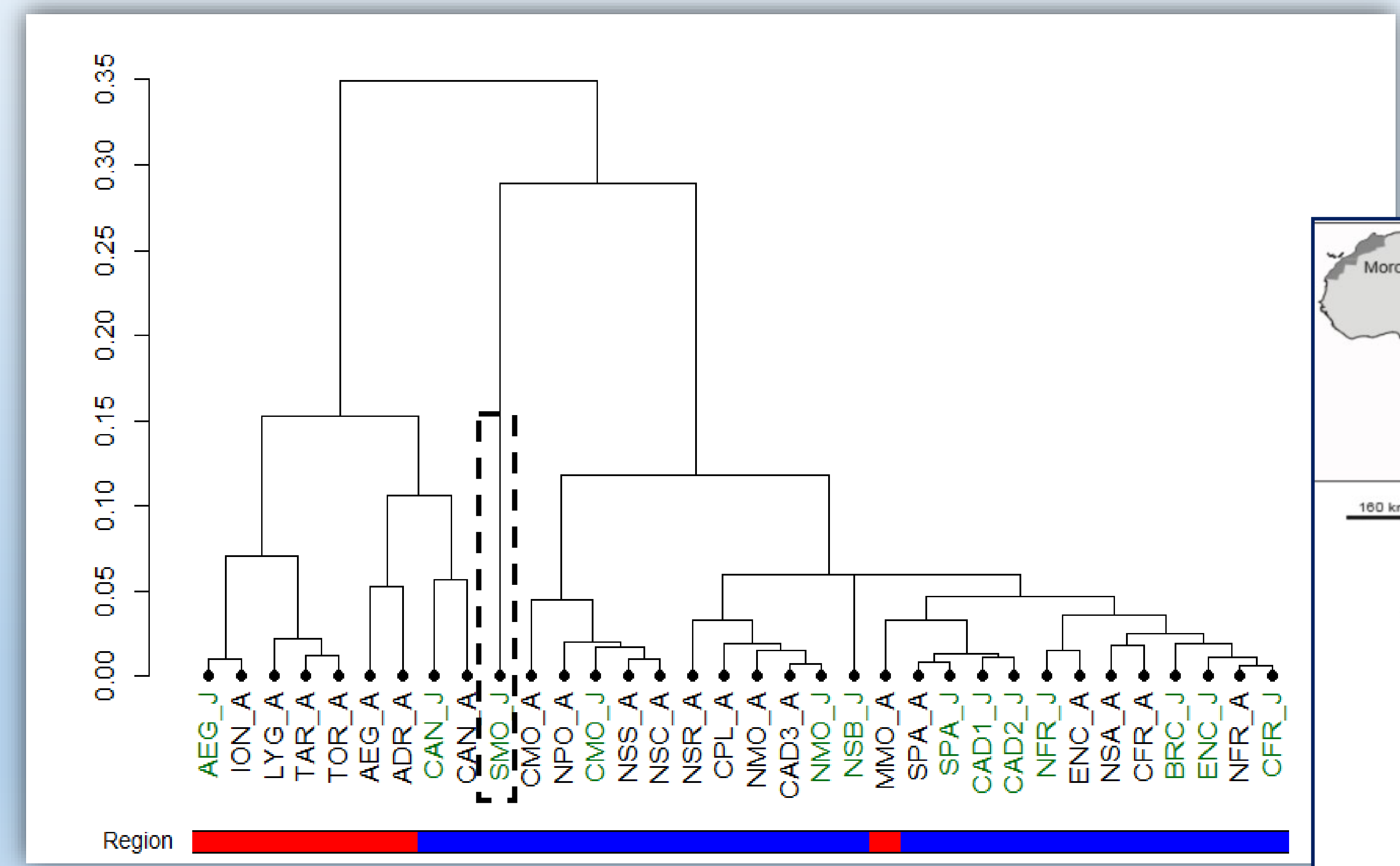
PCoA All populations



RESULTS & DISCUSSION



RESULTS & DISCUSSION

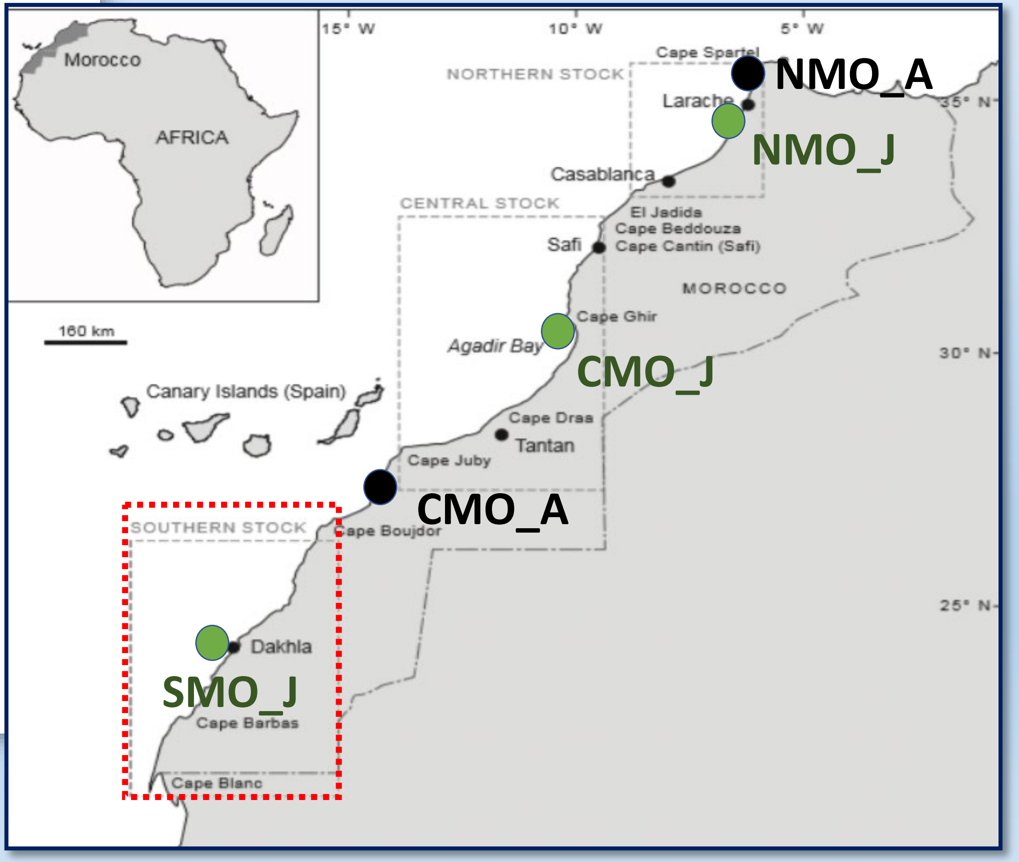


Bay of Agadir:

- Labonne et al. (2022) – Otolith geochemistry
- Chlaida et al. (2009) – Allozyme

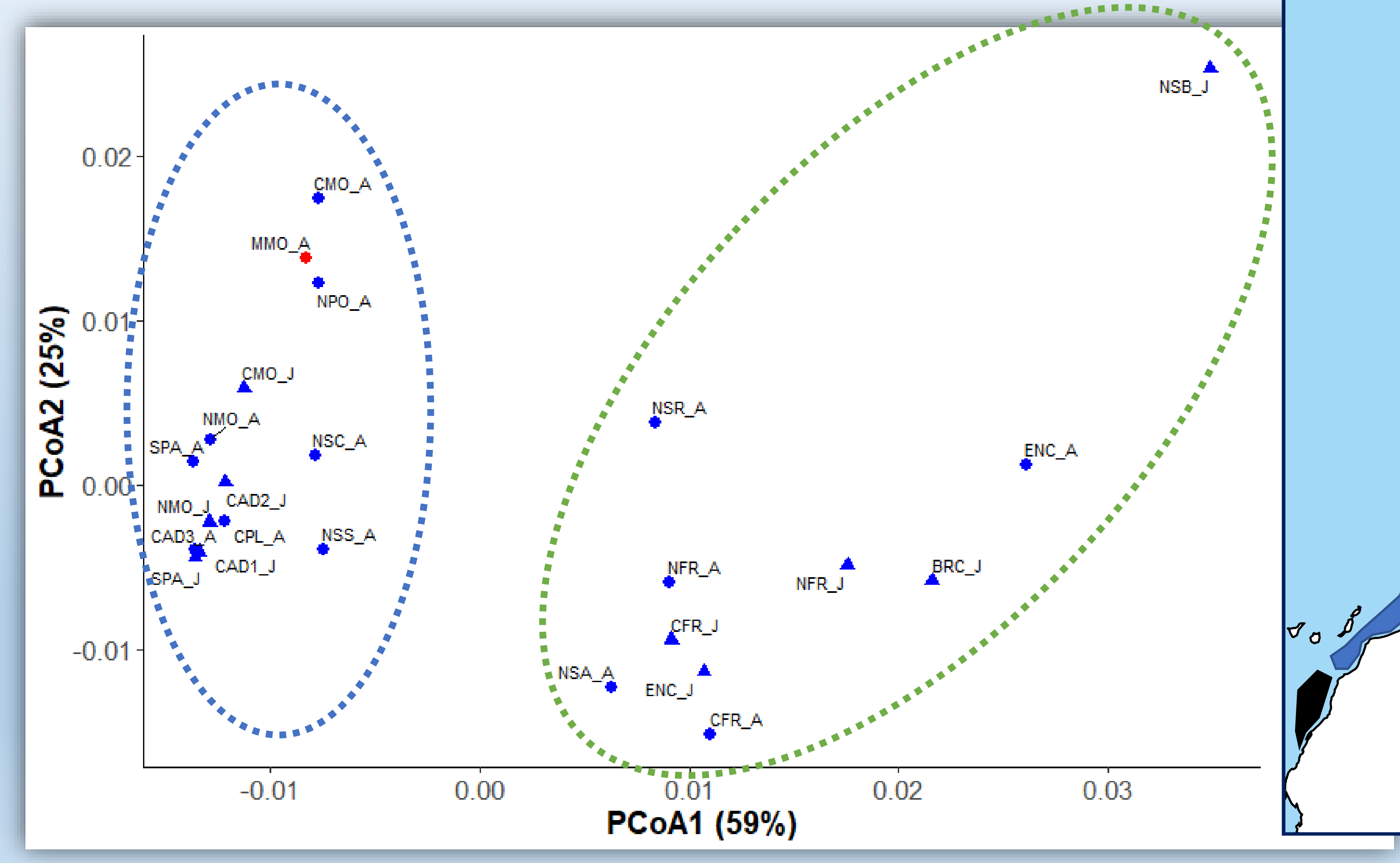
Genetic homogeneity:

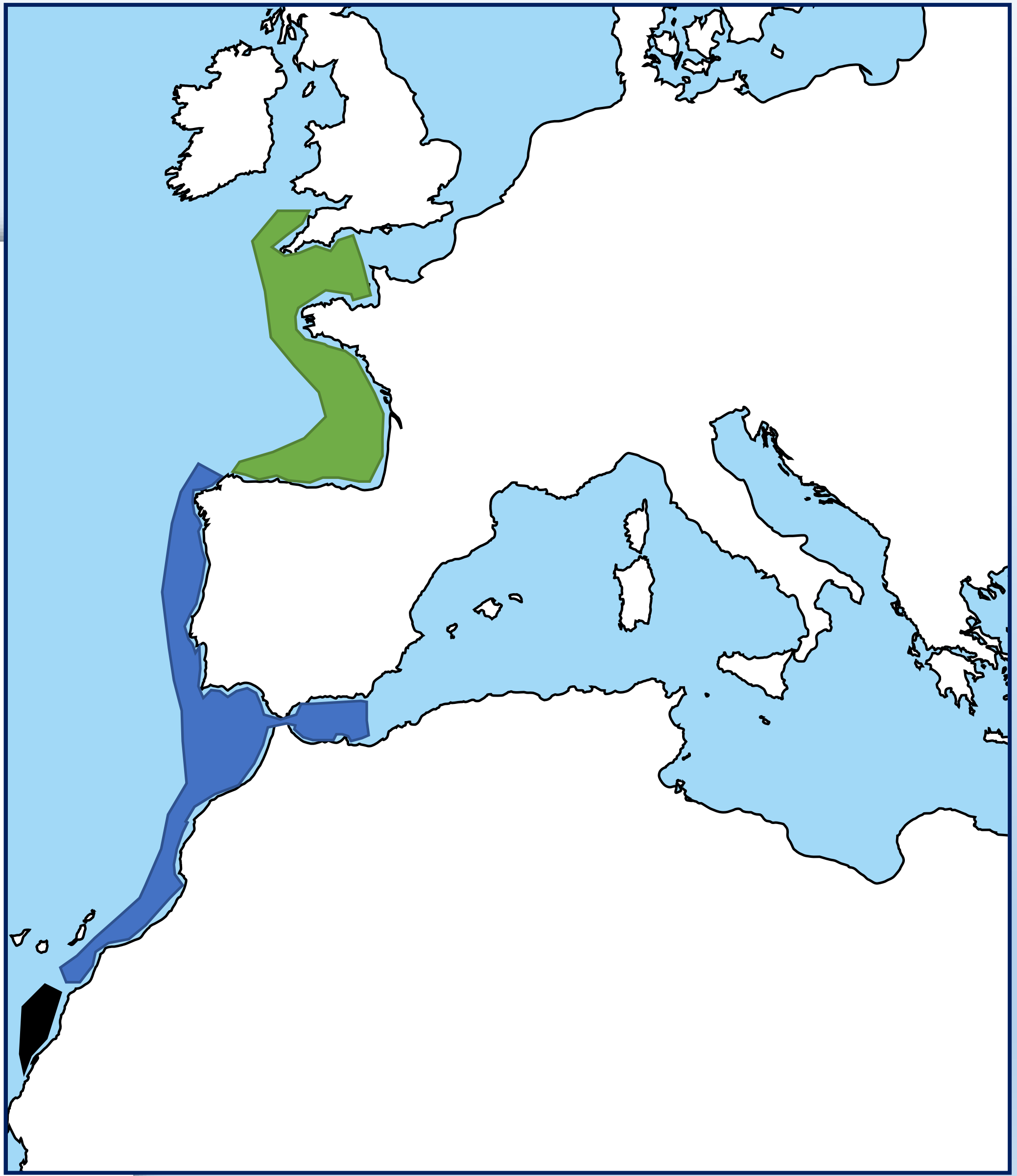
- Baibai et al. (2012) - Microsatellites



RESULTS & DISCUSSION

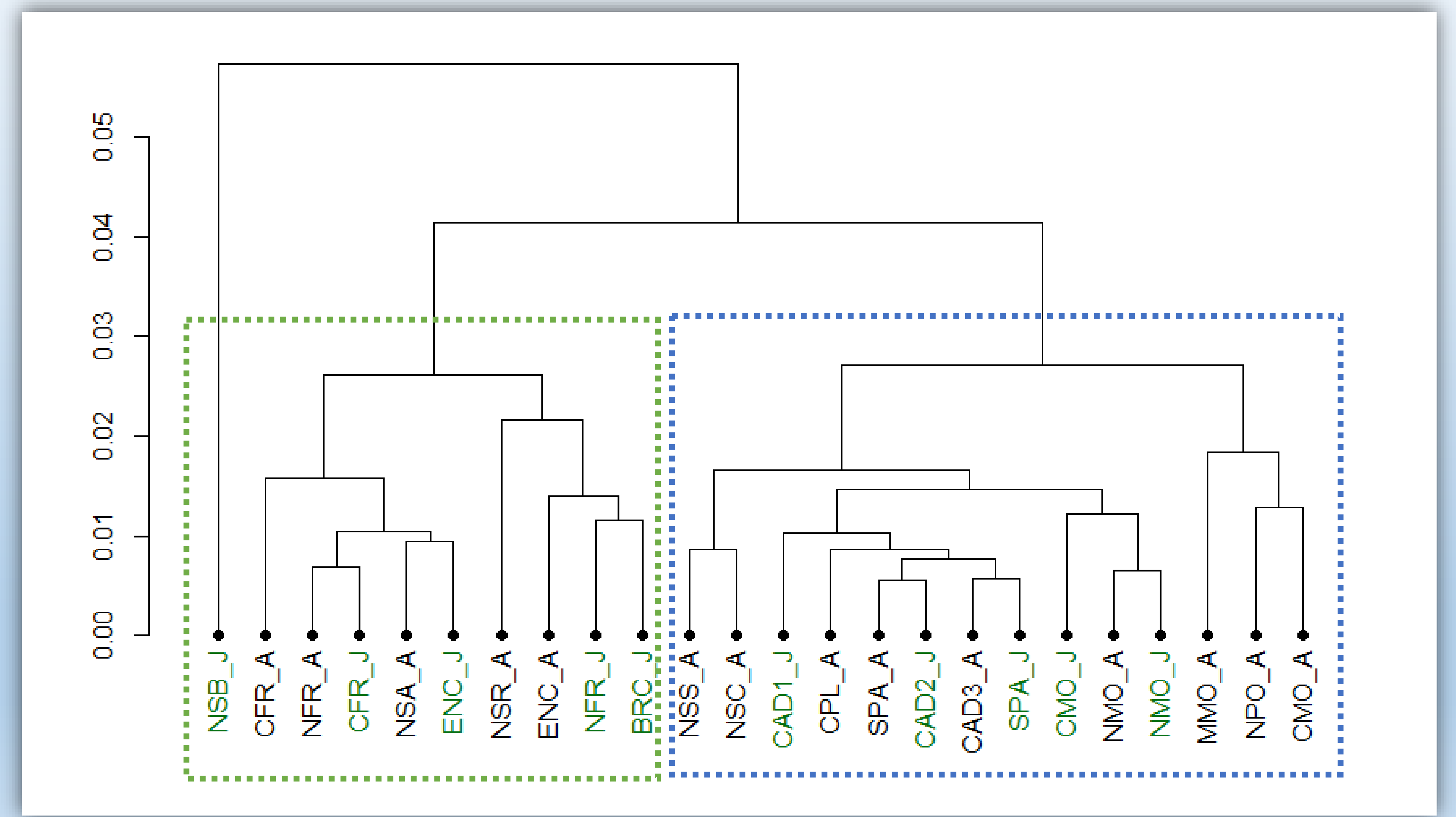
PCoA Atlantic + Mediterranean Morocco populations





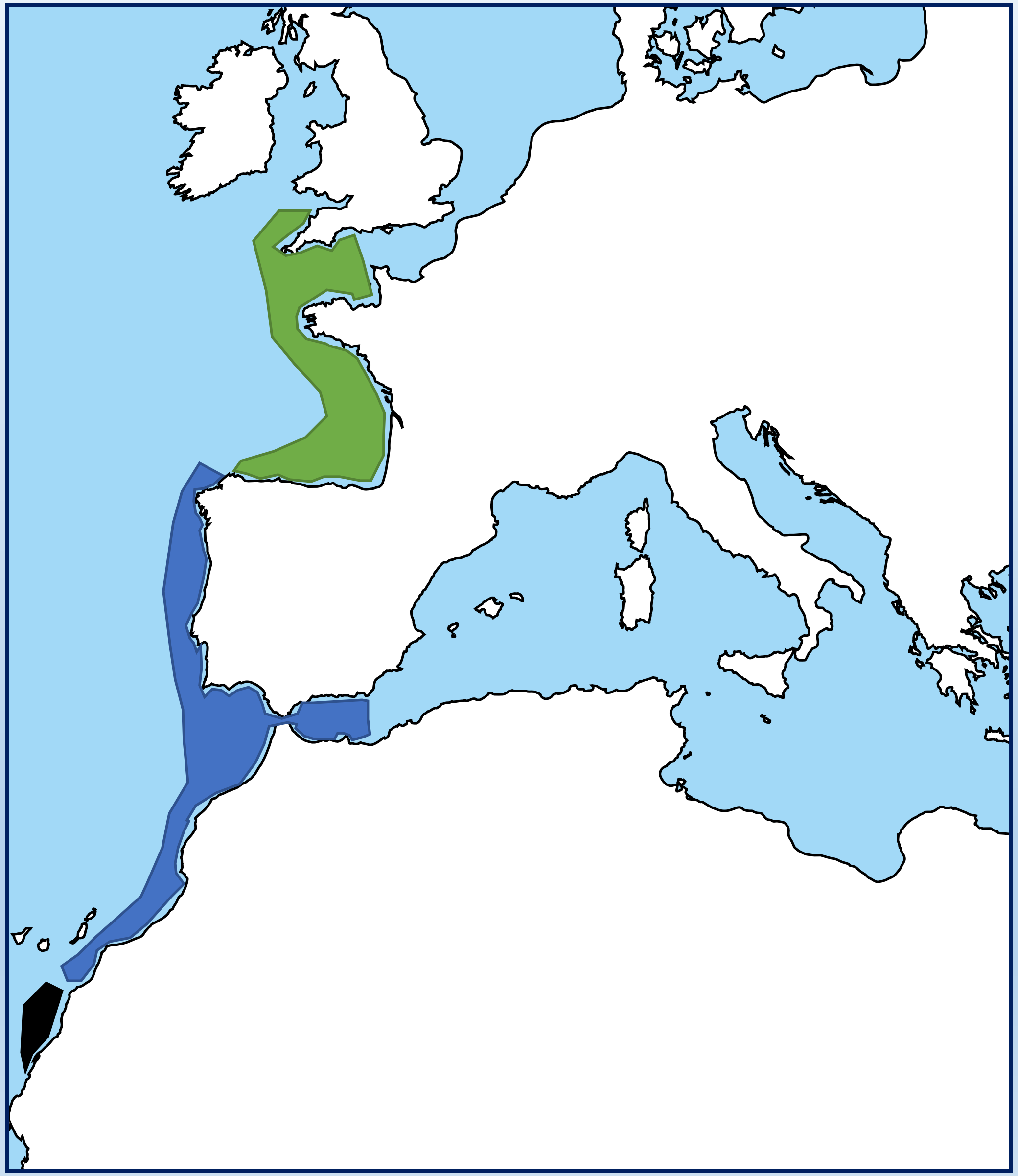
RESULTS & DISCUSSION

Atlantic + Mediterranean Morocco populations



RESULTS & DISCUSSION

Atlantic + Mediterranean Morocco populations



✓ **Bay of Biscay** ≠ Iberian populations

- Atarhouch et al. (2006) – mtDNA control region

✗ Bay of Biscay ≠ Iberian populations

- Kasapidis et al. (2012) – microsatellites
- Fonseca et al. (in press) – low coverage WGS

✓ **Morocco** = Western Iberian populations,

✗ but ≠ Moroccan stocks

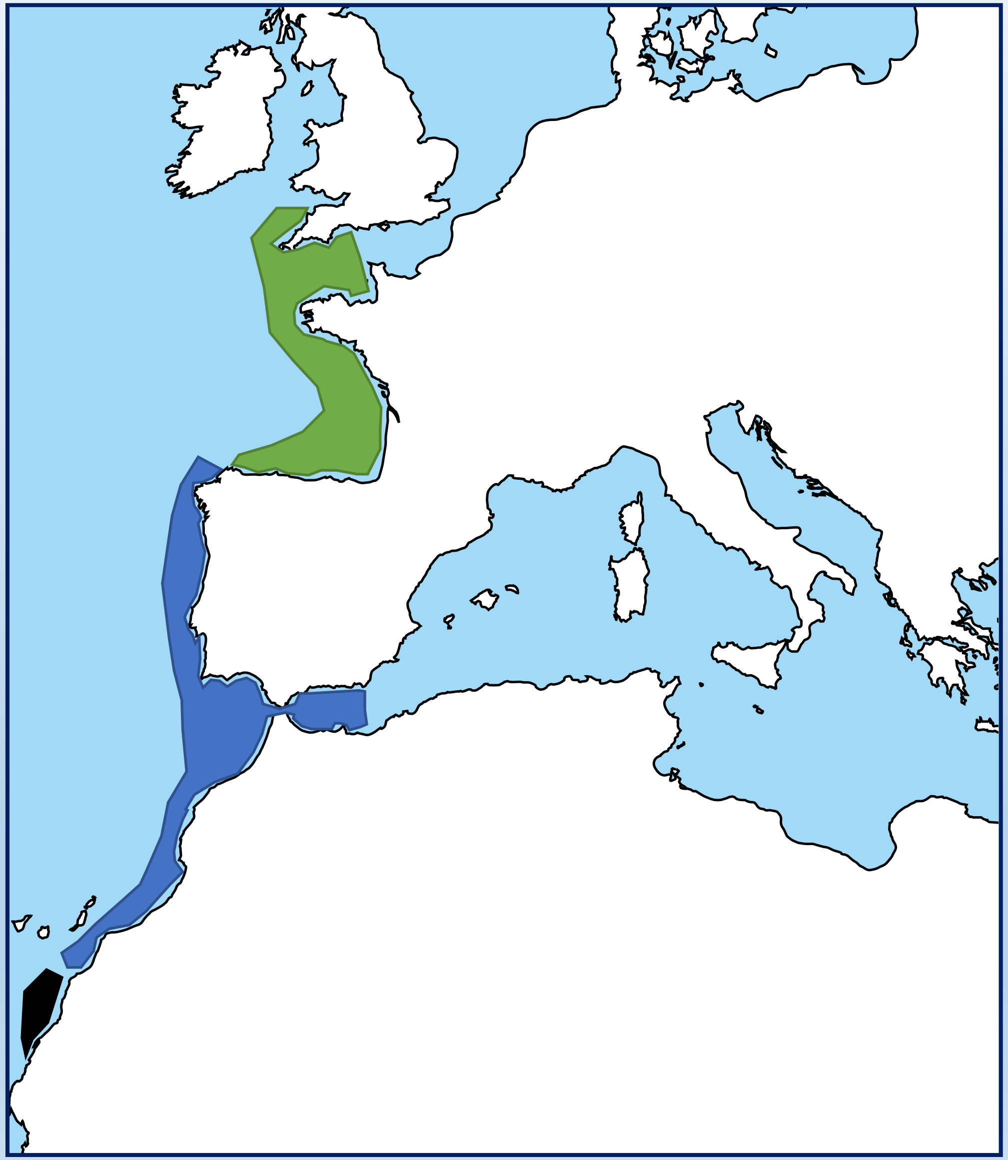
- Laurent et al. (2009)
- Chlaida et al. (2009) – allozymes

✓ Genetic homogeneity Moroccan coast

- Baibai et al. (2012) – mtDNA control region and microsatellites

RESULTS & DISCUSSION

European Atlantic waters



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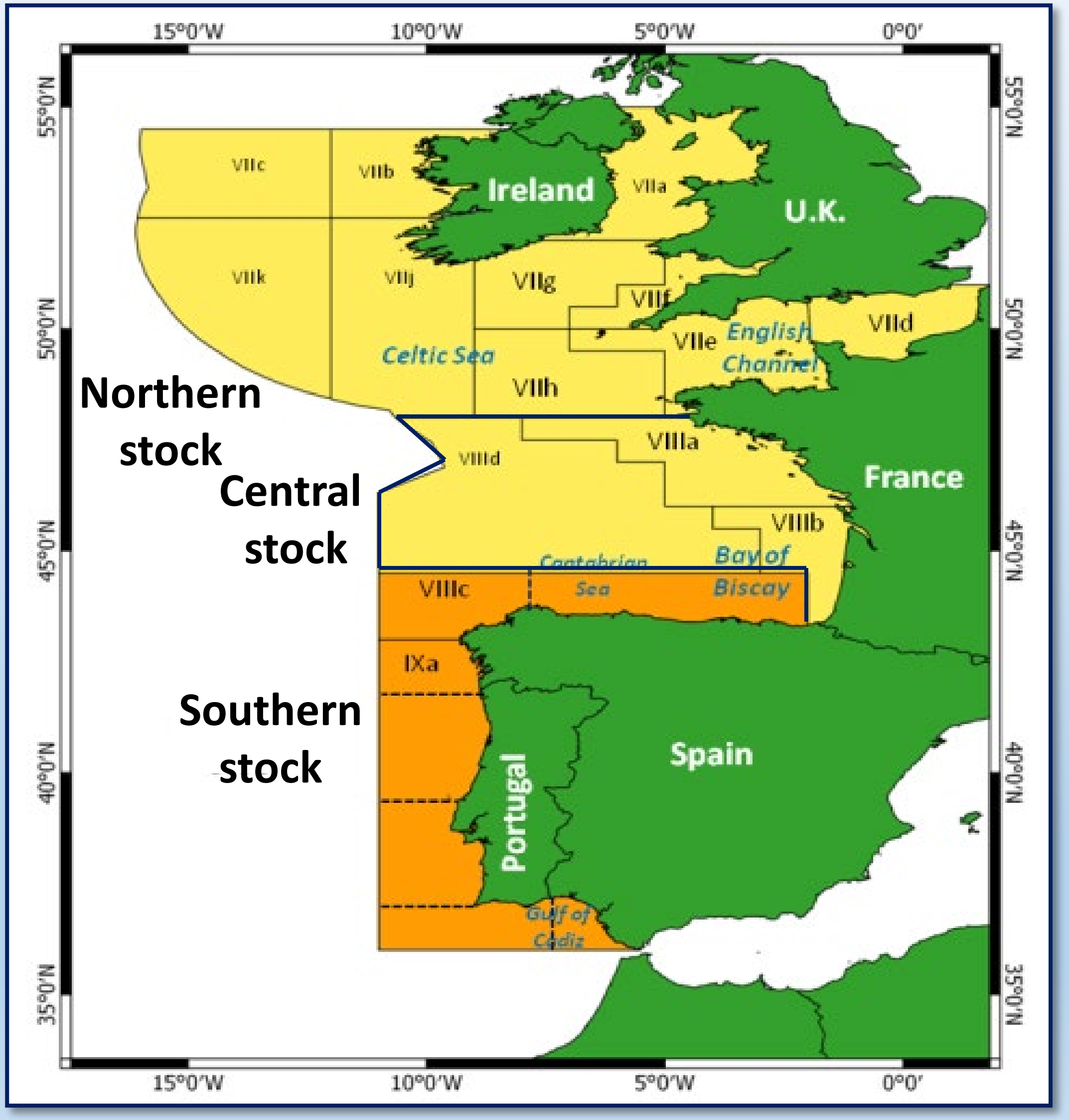
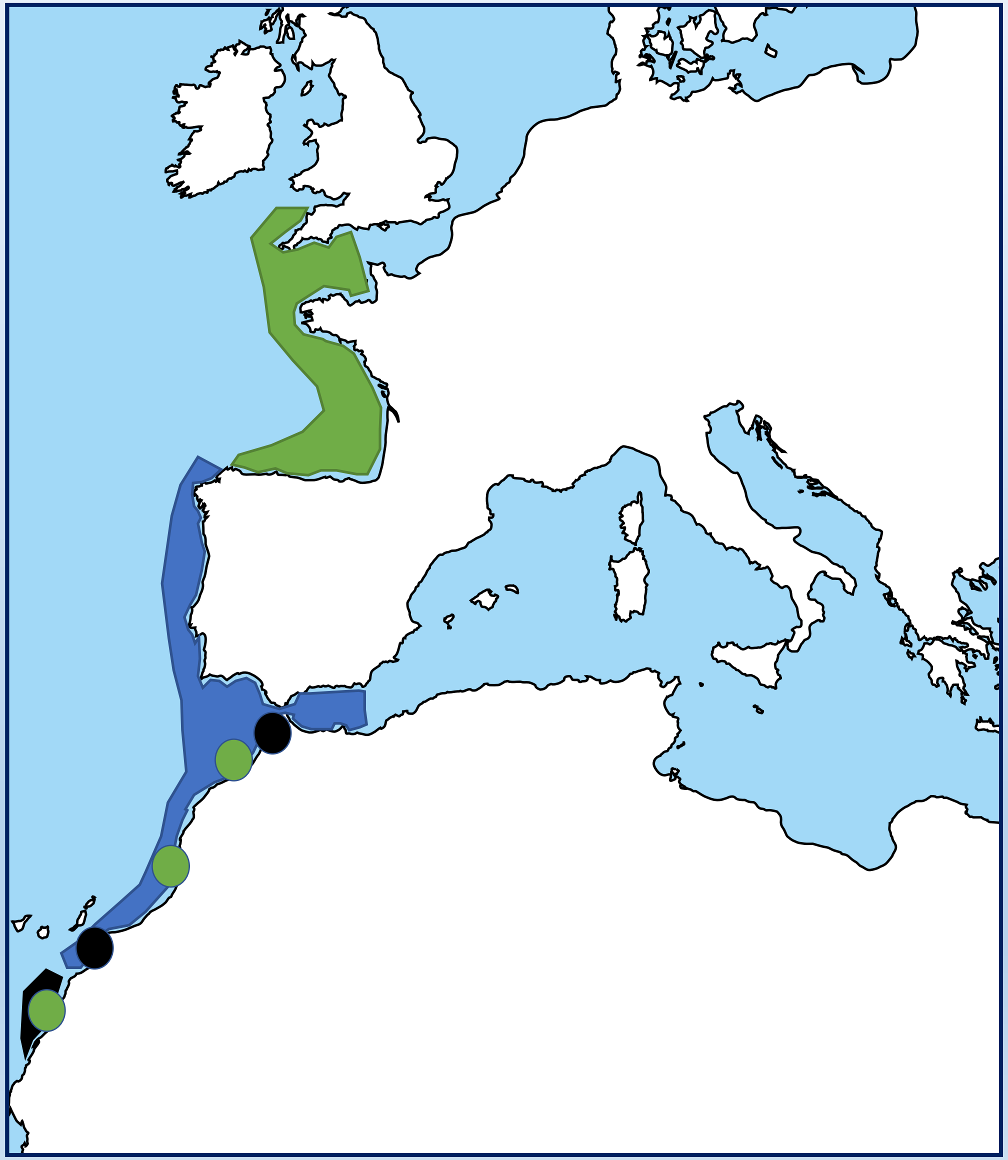


RESULTS & DISCUSSION

Atlantic African coast



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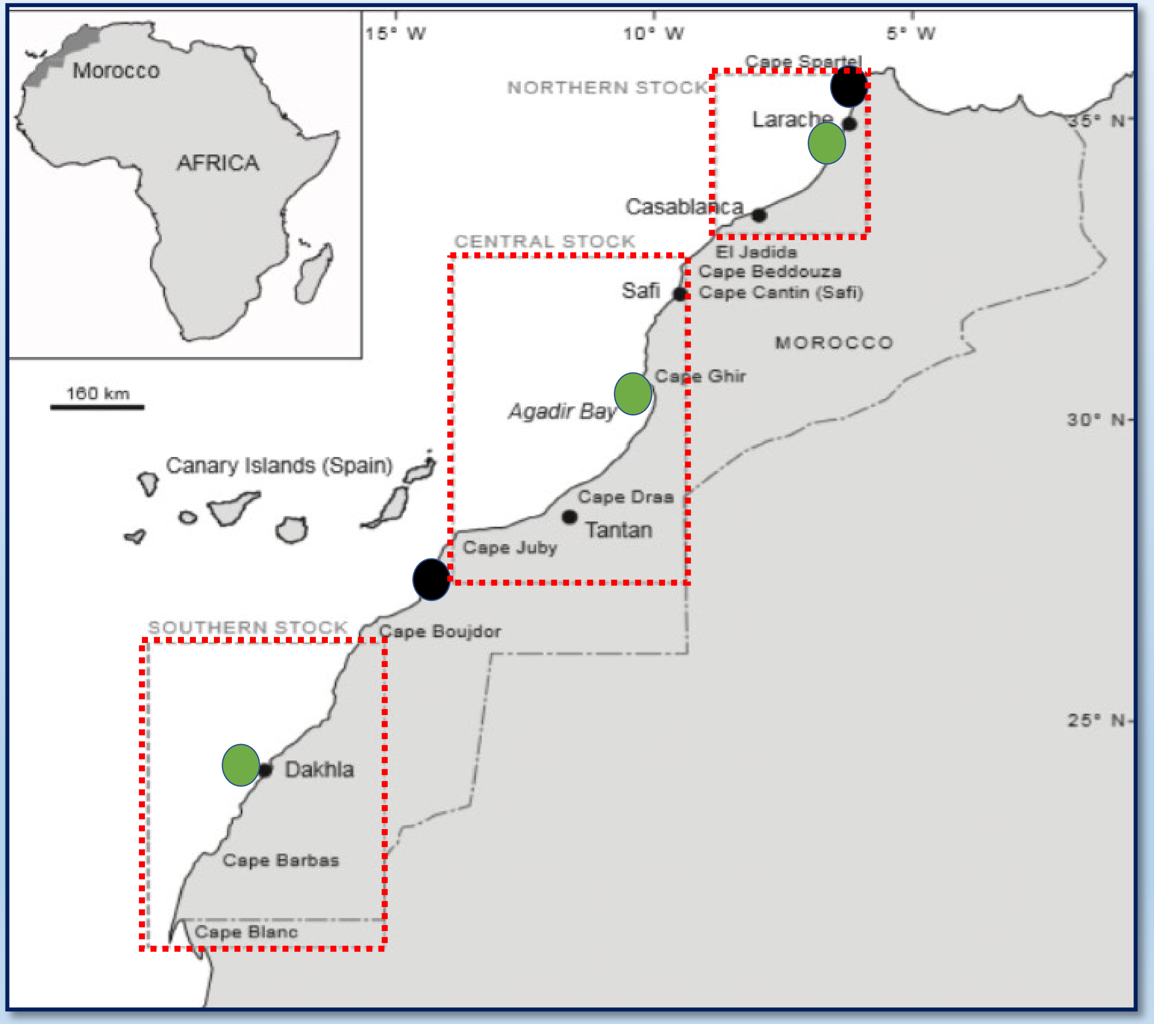
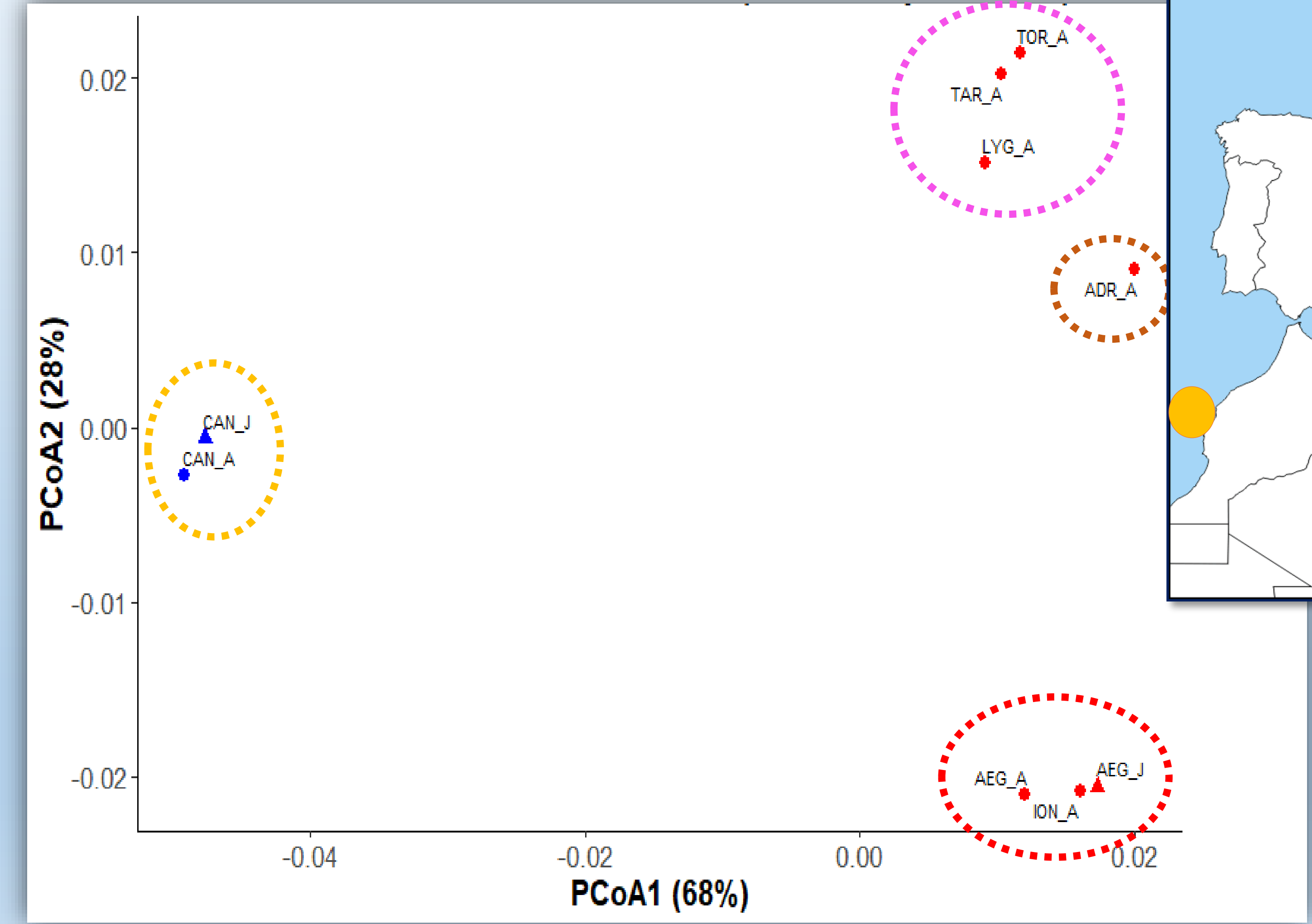
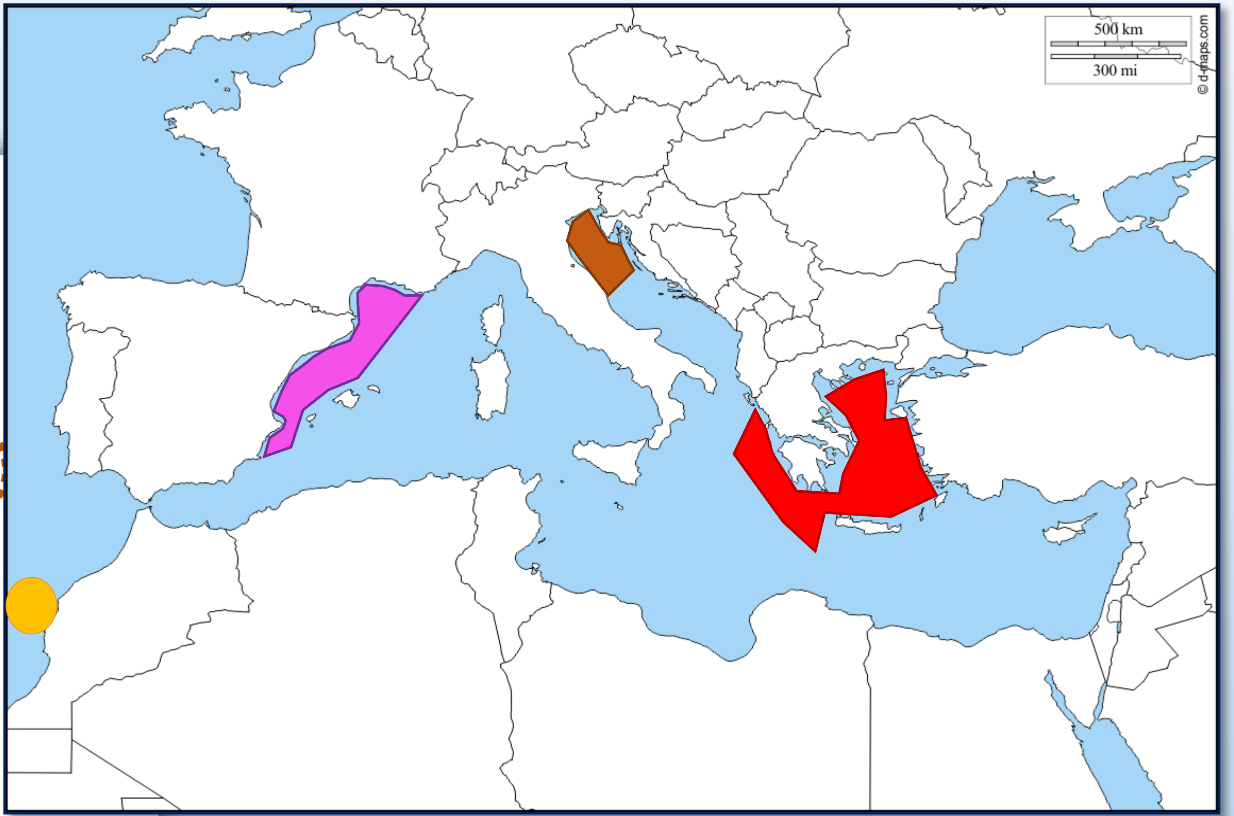


RESULTS & DISCUSSION

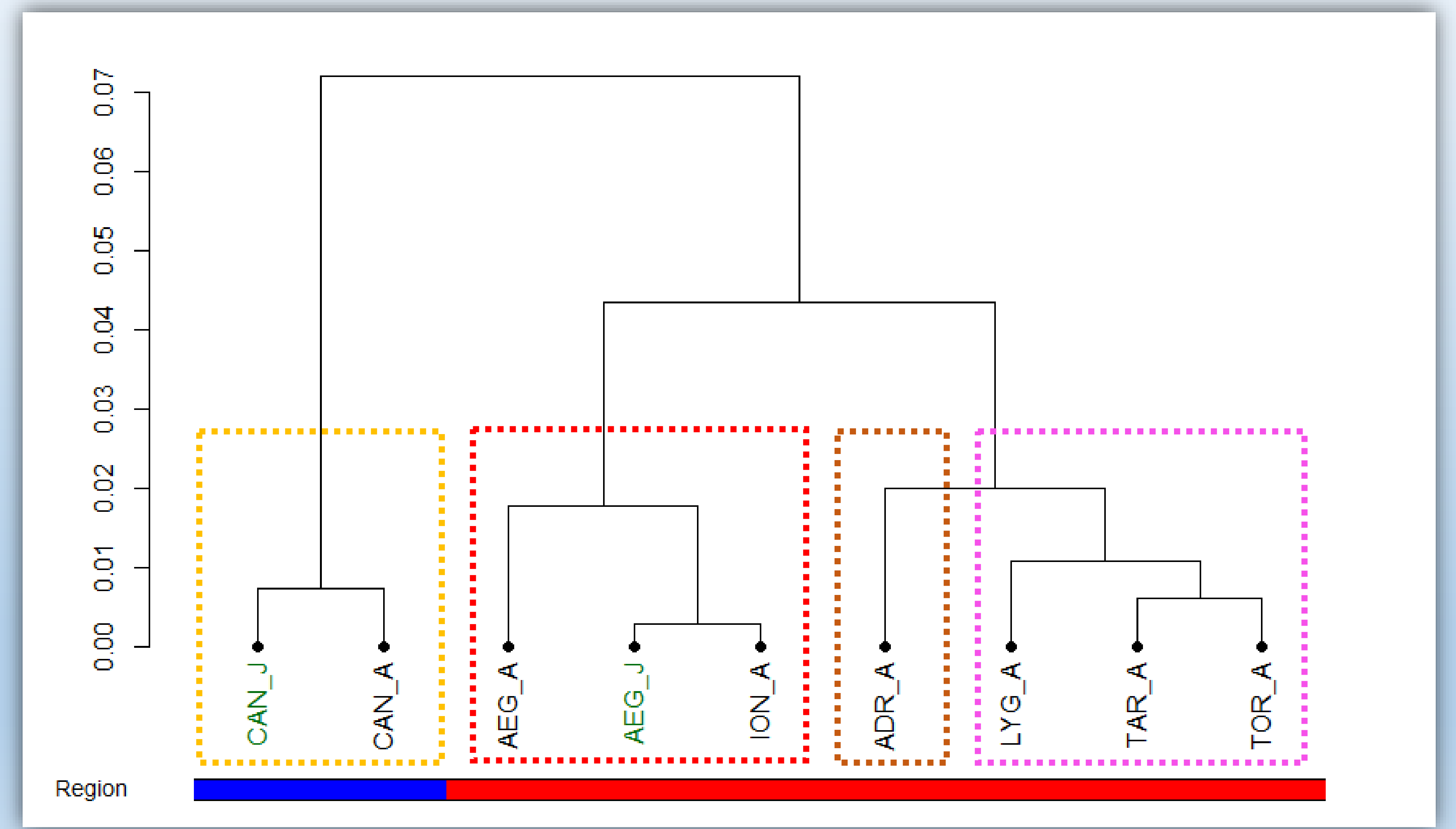
PCoA Mediterranean + Canary populations





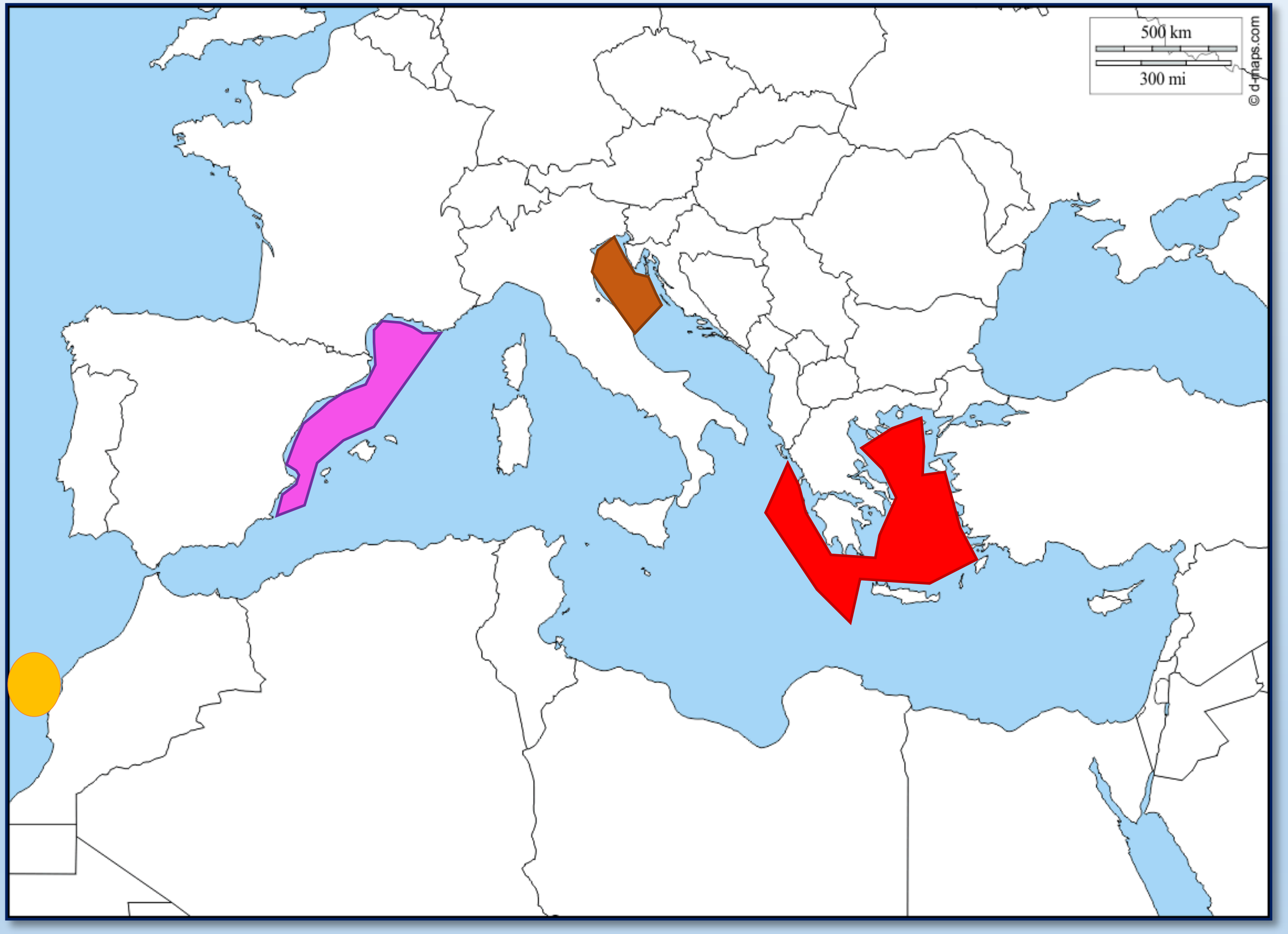
RESULTS & DISCUSSION

Mediterranean + Canary populations



RESULTS & DISCUSSION

Mediterranean + Canary populations



✓ Eastern Mediterranean *vs* Western Mediterranean

✗ Adriatic Sea ≠ Ionian Sea

- Rugerri et al. (2013) – microsatellites
- Tinti et al. (2022) – mitochondrial DNA

✗ Aegean = Ionian

- Spanakis et al. (1989) – allozymes

Western Mediterranean populations:

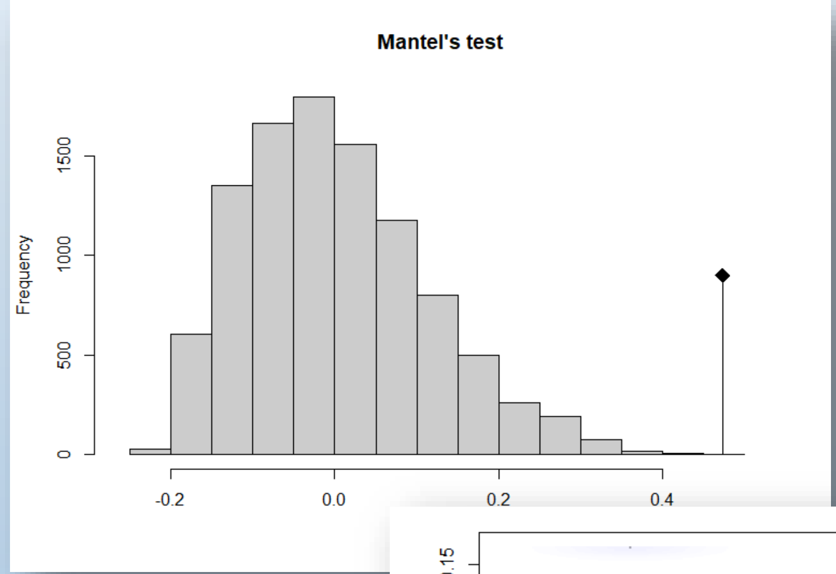
✓ Kasapidis et al. (2012) – microsatellites

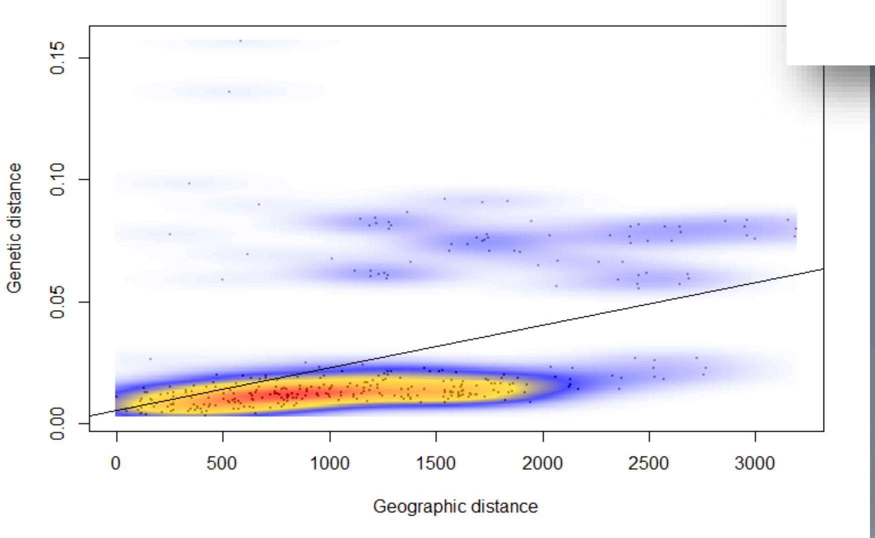
✗ Fonseca et al. (in press) – low coverage WGS

RESULTS & DISCUSSION

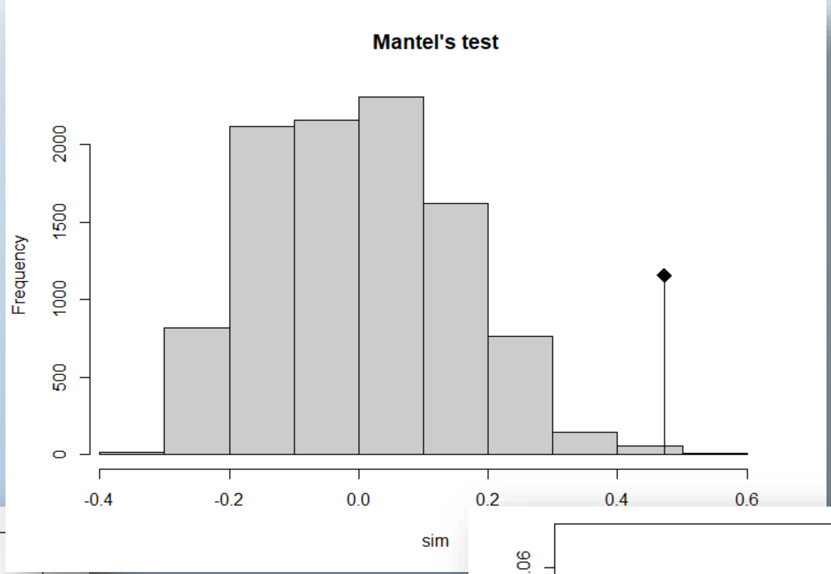
Isolation By Distance (IBD)

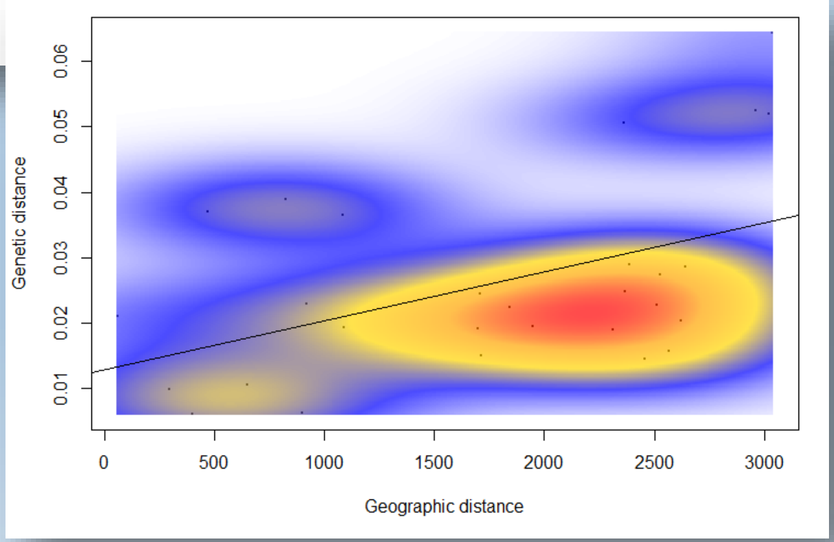
ATLANTIC





MEDITERRANEAN

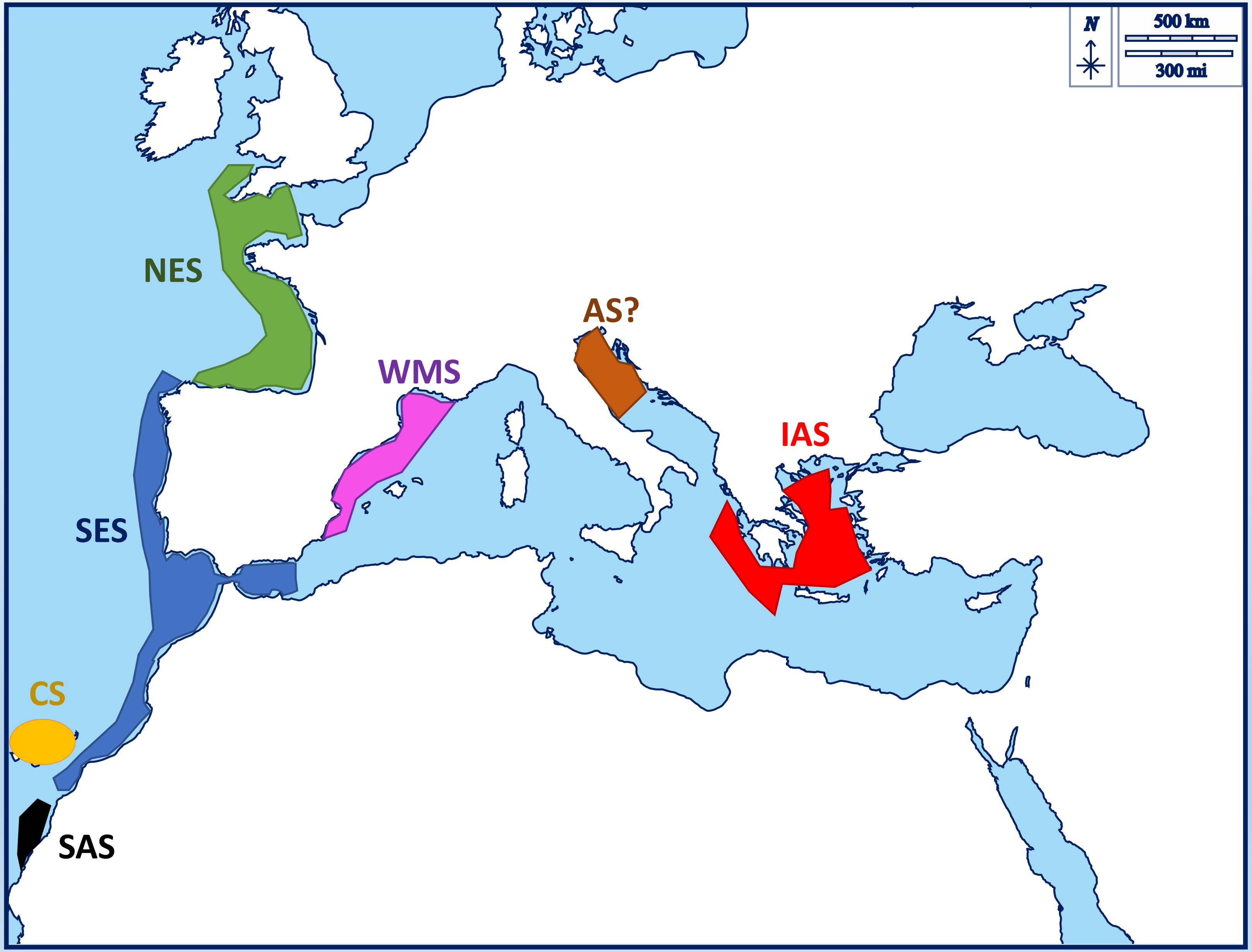




CONCLUSIONS

Genetic stocks

- Northern European stock **(NES)**
- Southern European stock **(SES)**
- Southern African stock **(SAS)**
- Canarian stock **(CS)**
- Western Mediterranean stock **(WMS)**
- Ionian-Aegean stock **(IAS)**
- Adriatic stock **(AS)** ?



CONCLUSIONS

- There are still **discrepancies** when it comes to delimiting sardine populations, varying depending on the approach used, but also with the temporal and spatial scale considered.
- There is a **mismatch** between the genetic stocks and the managed stocks currently defined based on administrative/political interests.

↓

A **re-assessment of sardine stocks** currently considered for management purposes is necessary.
To this end, the integration of **different approaches** and the **temporal monitoring** of sardine populations covering as much as possible the **whole geographical distribution** of this pelagic species should be a priority.


THANK YOU FOR YOUR ATTENTION!