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**EUSKO JAURLARITZA  
GOBIERNO VASCO**



# Multiple chromosomal inversions shape the evolutionary history of lineage divergence and admixture in the European sardine

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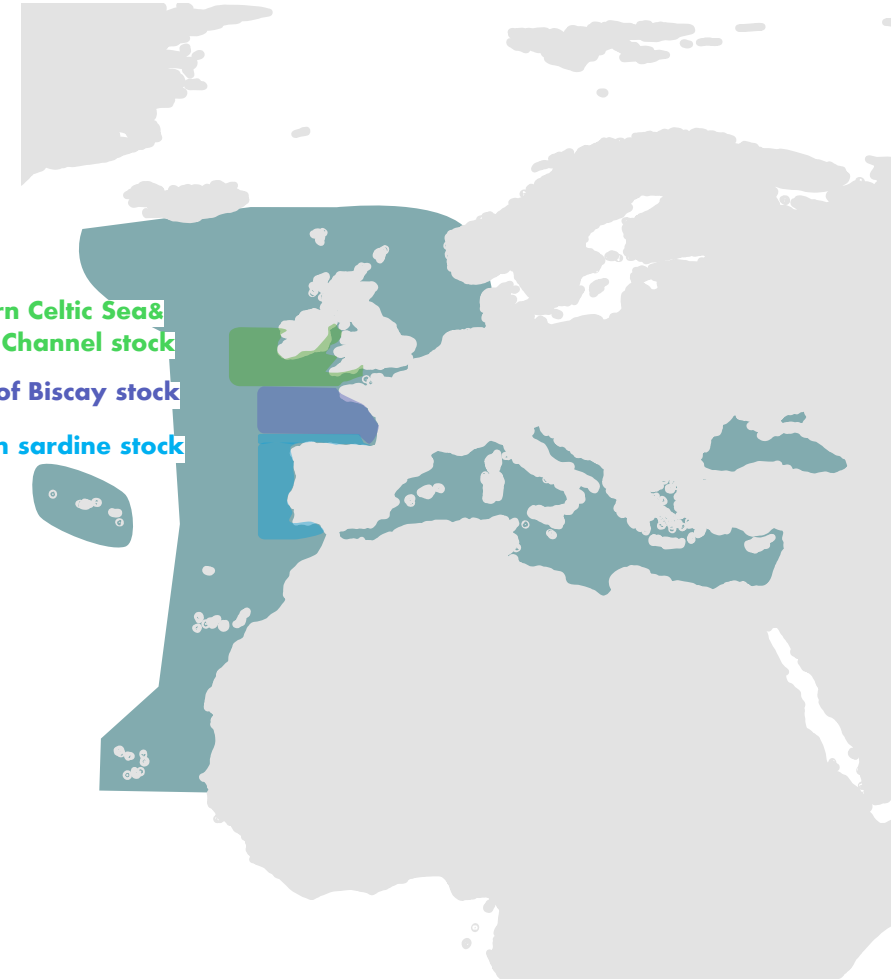
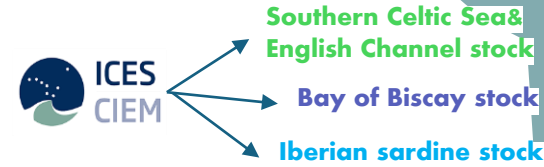
<sup>3</sup> Institut National de Recherche Halieutique (INRH), Centre Régional d'Agadir, Laboratoire de Génétique des Populations Halieutiques, Agadir, Morocco

# Introduction

## The European pilchard (*Sardina pilchardus*)



- SPF of high **ecological** and **economic** importance in the **NE Atlantic**.
- Currently **assessed** as **three units** in Atlantic European Waters (**ICES**)



# Introduction

## The European pilchard (*Sardina pilchardus*)

- **SPF** of high **ecological** and **economic** importance in the **NE Atlantic**.
- Currently **assessed** as **three units** in Atlantic European Waters (**ICES**)

- **Population structure – Consensus and Contradictions**

**Consensus:** North N.Atlantic, South N.Atlantic, and Mediterranean populations

**Uncertain Boundaries:** the Alboran Sea and the Moroccan coast

**The NE Atlantic:** no structure vs. Isolation by Distance (IBD)

**Structuring:** at outlier loci



## Objectives:

1. Resolve current uncertainties in **population structure and connectivity** of European sardine within the Northeast Atlantic
2. Understand why previous studies produced **contradictory results**
3. Zoom into the **drivers of population divergence**

# Methods

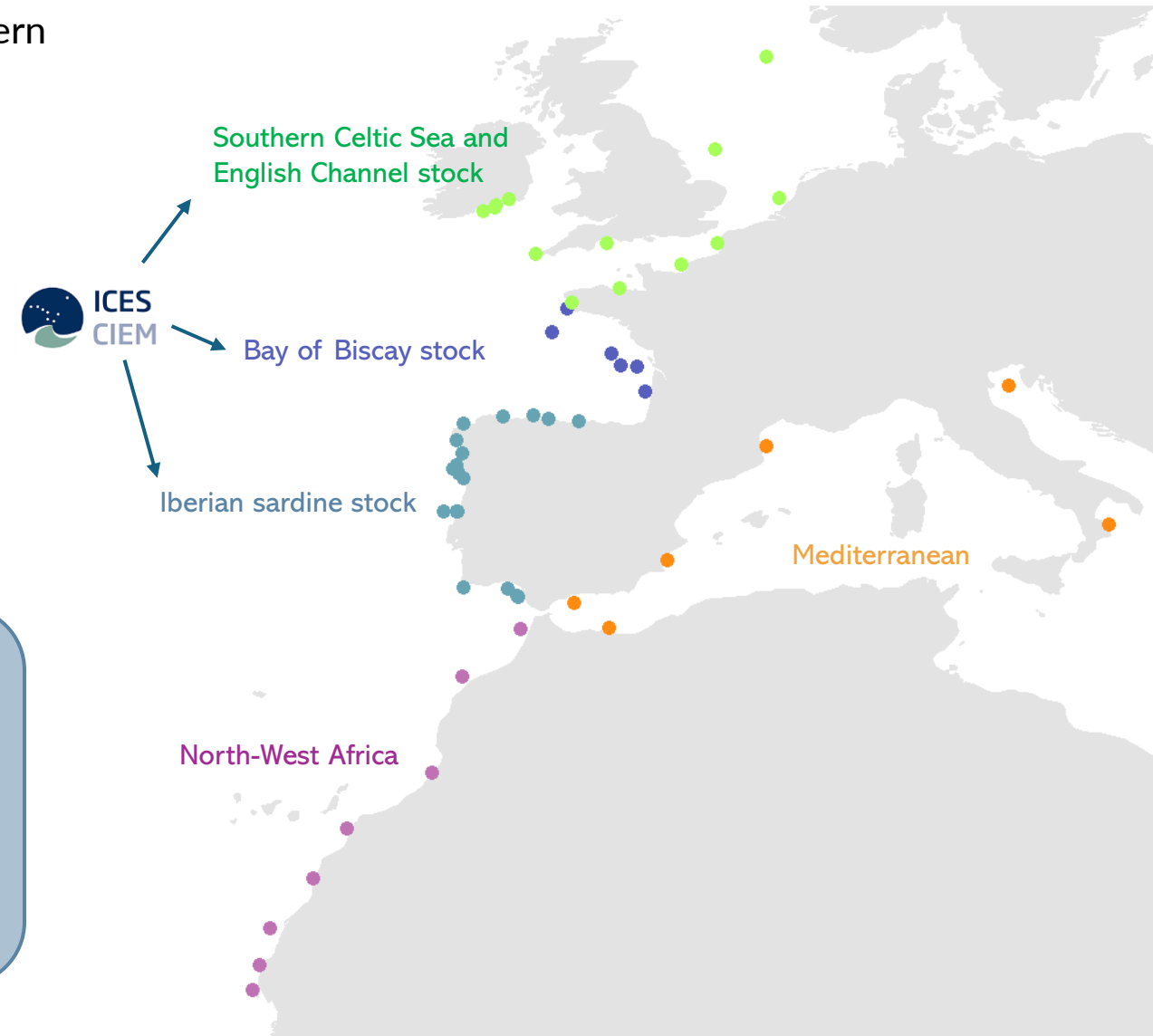
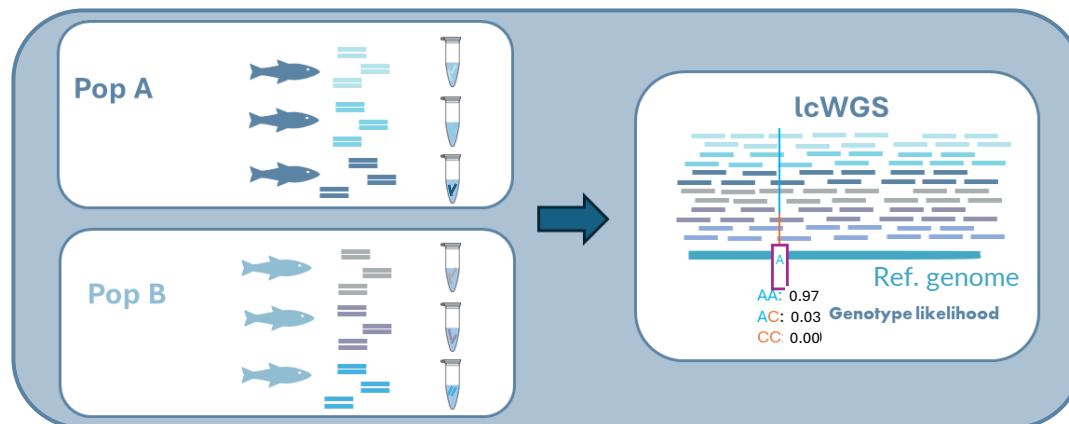
- N = 345 individuals from northern to southern Eastern Atlantic + Mediterranean Sea

North N.Atlantic = 209 ind

South N.Atlantic = 62 ind

Mediterranean Sea = 84 ind

- **lcWGS** = low coverage **Whole Genome Sequencing**  
~ 3X depth of coverage  
High number of SNPs (up to 7M)

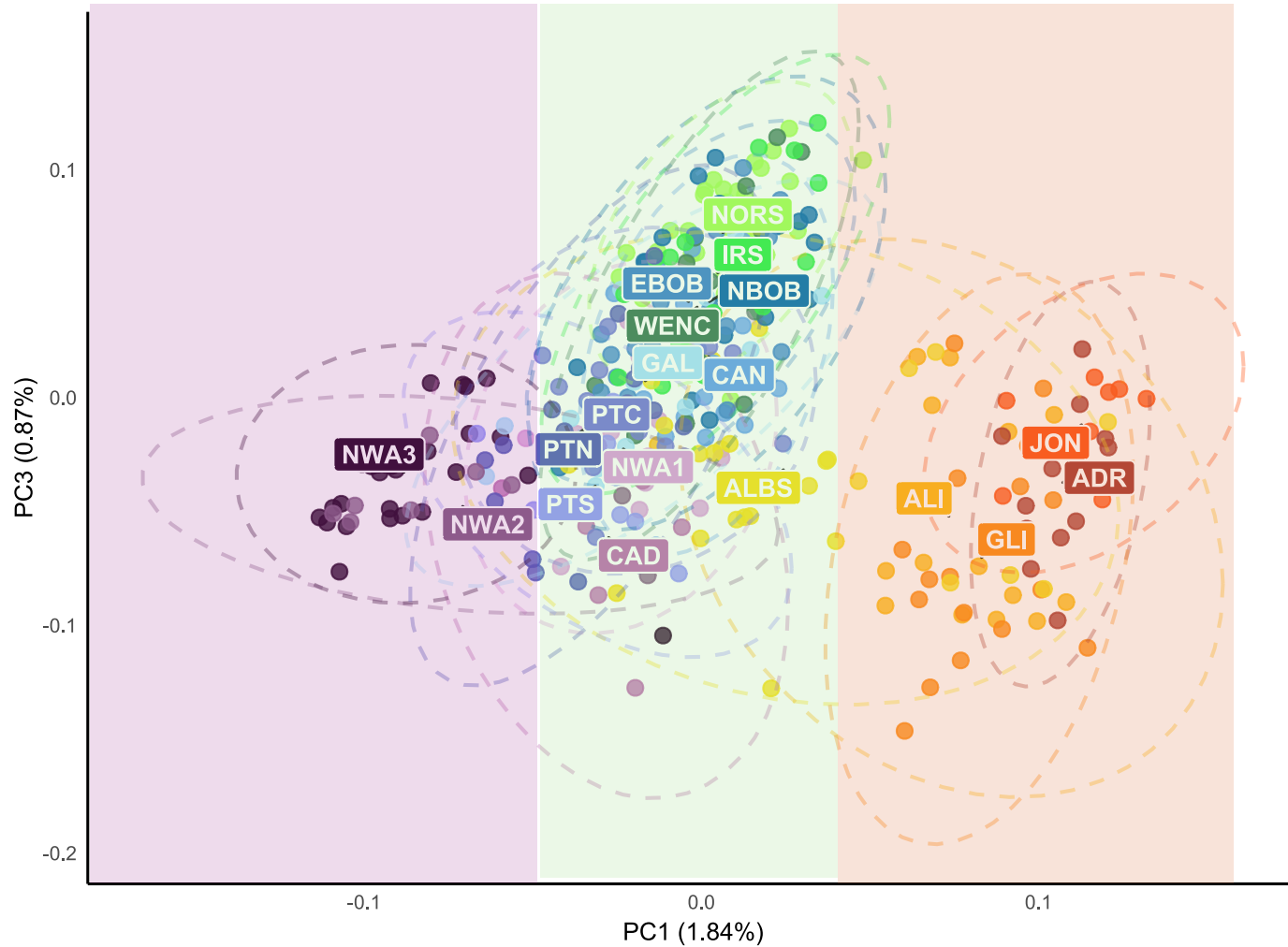




# Results

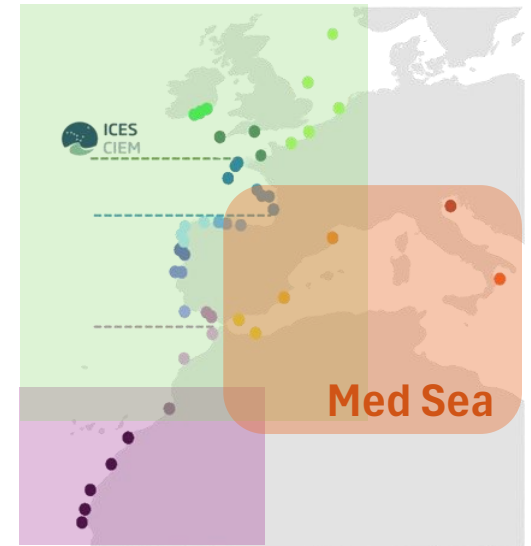
Population structure (7.352.054 SNPs, 345 inds)

PC1-3



N-North Atlantic

S-North Atlantic

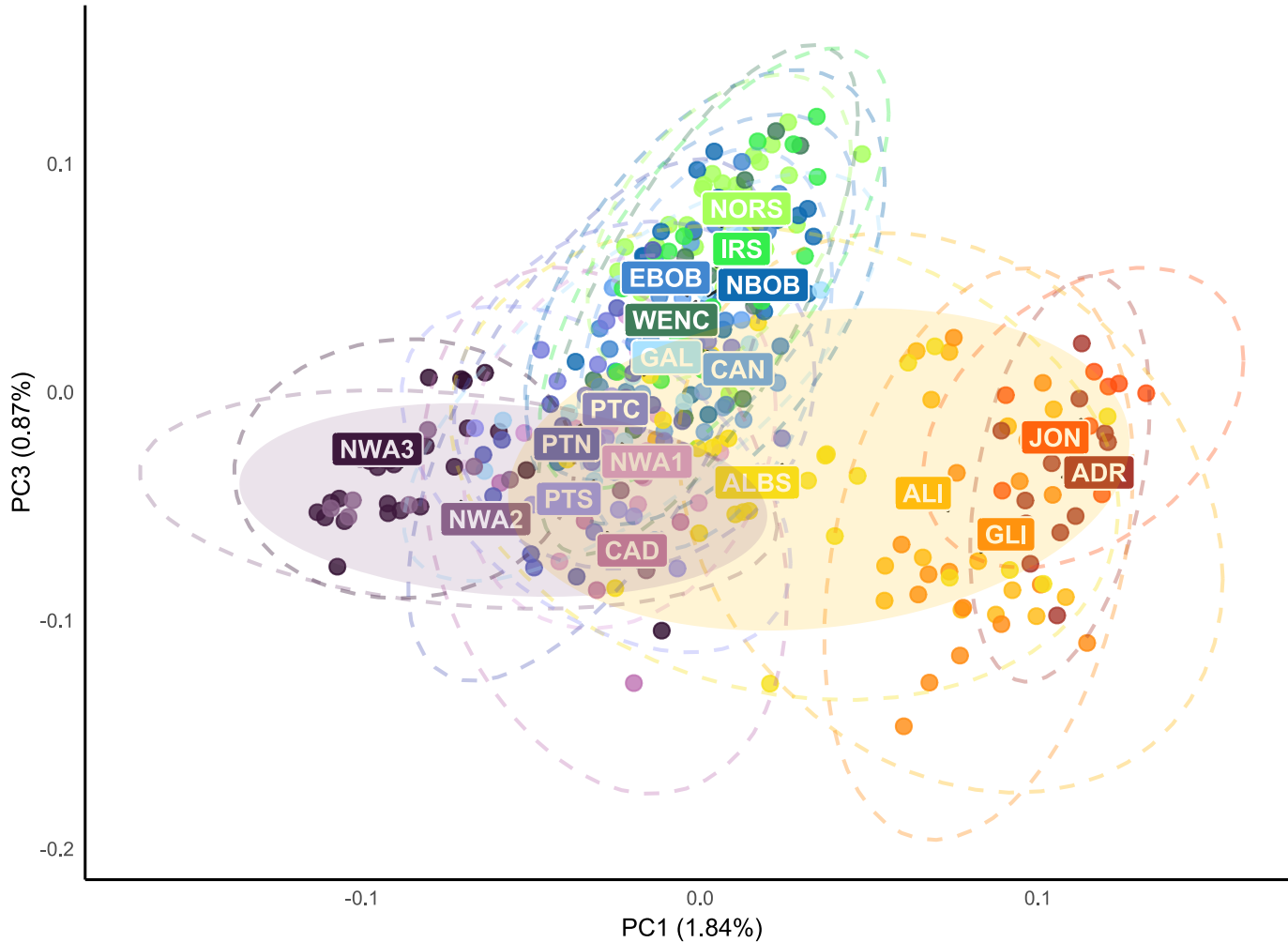


- South N. Atlantic, North N. Atlantic and Mediterranean sardines are genetically distinct populations

# Results

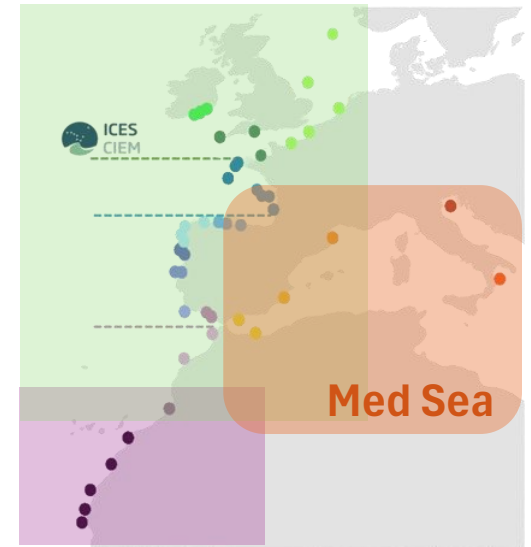
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N-North Atlantic

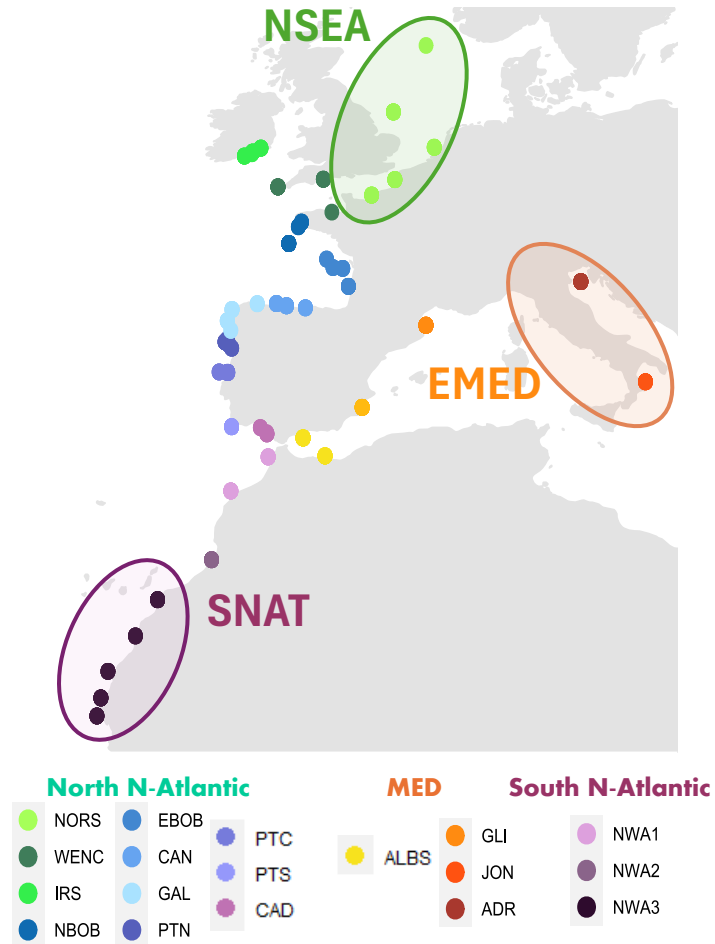
S-North Atlantic



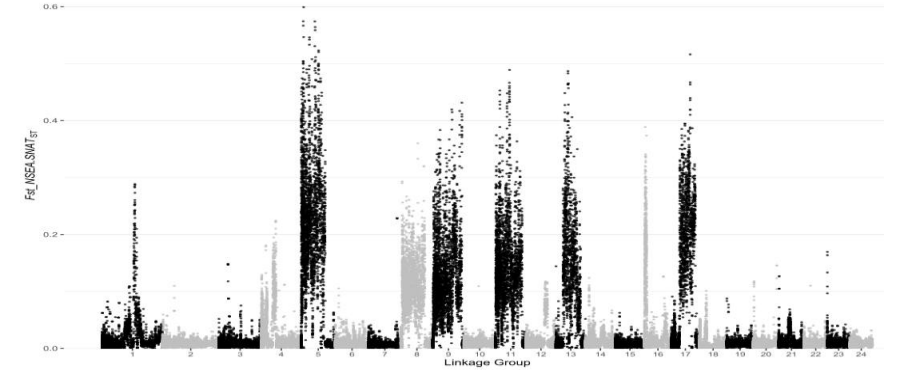
- South N. Atlantic, North N. Atlantic and Mediterranean sardines are genetically distinct populations
- Alboran Sea and NWA2 = transition zone

# Results

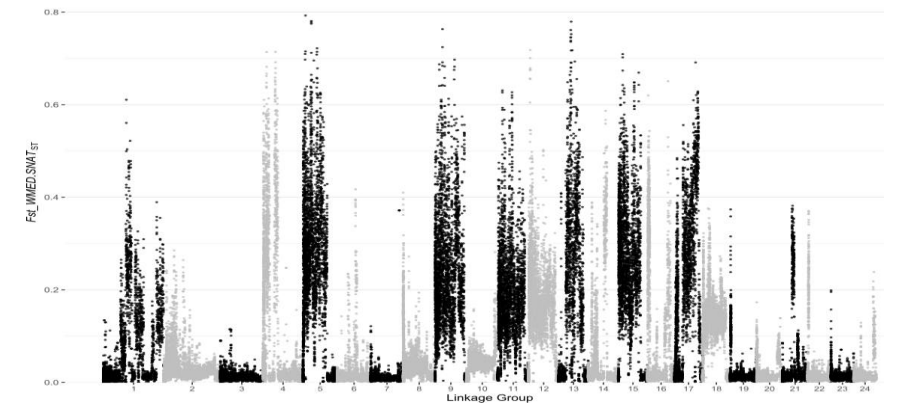
Genetic differentiation ( $F_{ST}$ ) among **distant locations** is **heterogeneous** along the chromosomes



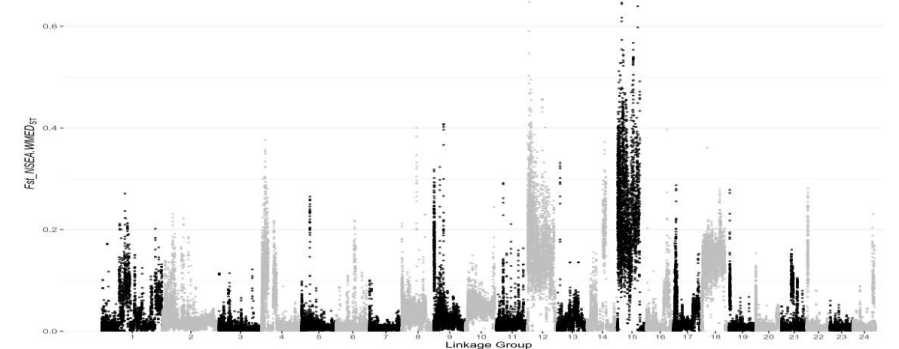
## NSEA vs SNAT



## EMED vs SNAT

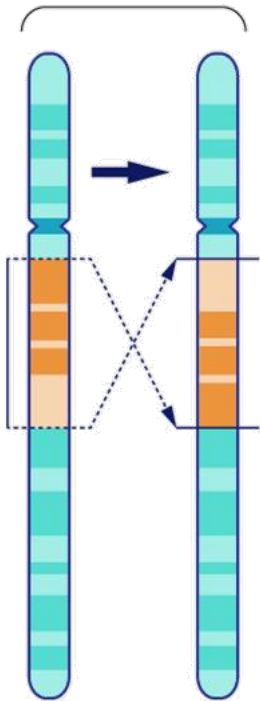


## NSEA vs EMED



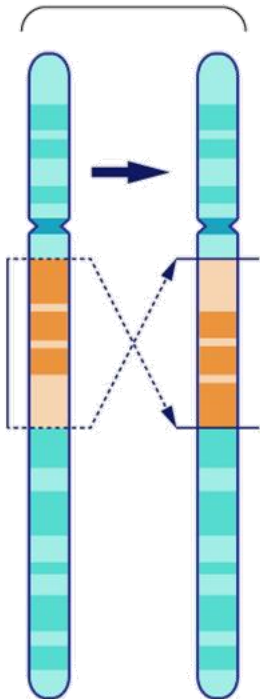
## Why do we see such high peaks of differentiation across the genome?

### **Inversion**



## Why do we see such high peaks of differentiation across the genome?

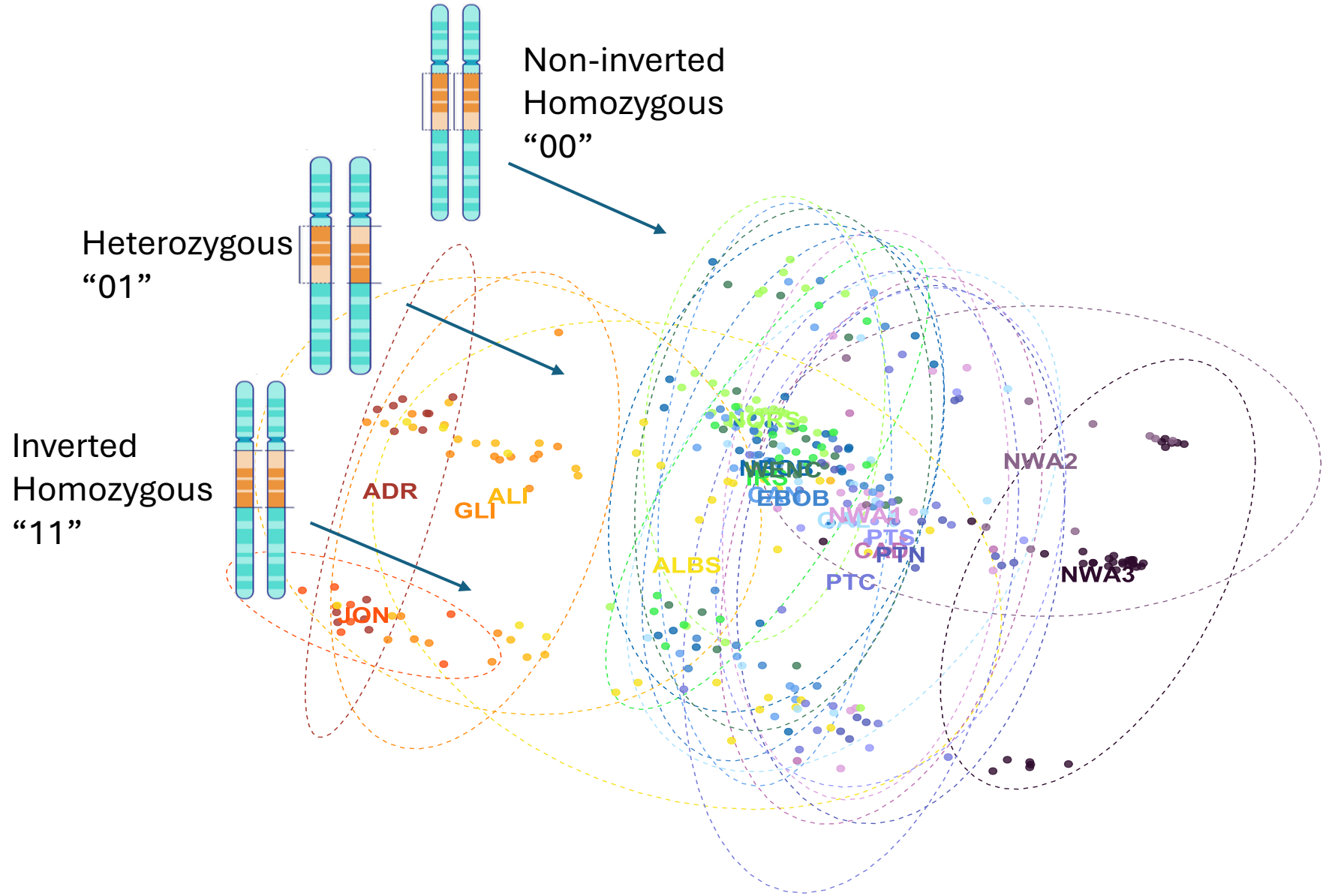
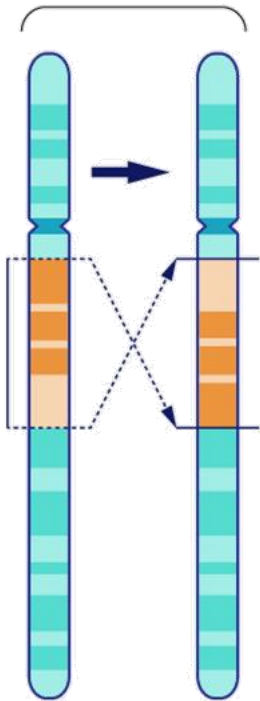
### Inversion



- **A flipped DNA fragment:** structural mutations, in which a segment of the chromosome is reversed
- **Suppressed recombination:** creation of new DNA combinations at reproduction (recombination) between non-inverted and inverted fragments is suppressed due to improper line up of the two types.
- **Strong linkage:** genetic markers within the flipped not-recombining regions are inherited as a block. Variations are carried together.

# Inversions in European sardines

## Inversion



# Results

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*How many inversions?*

Previously reported with the ref. genome

- 5 large (>10 MB) chromosomal inversions

Identified in this study:

- 19 new putative inversions of different sizes (0.55 - 24 MB)

# Results

## How many inversions?

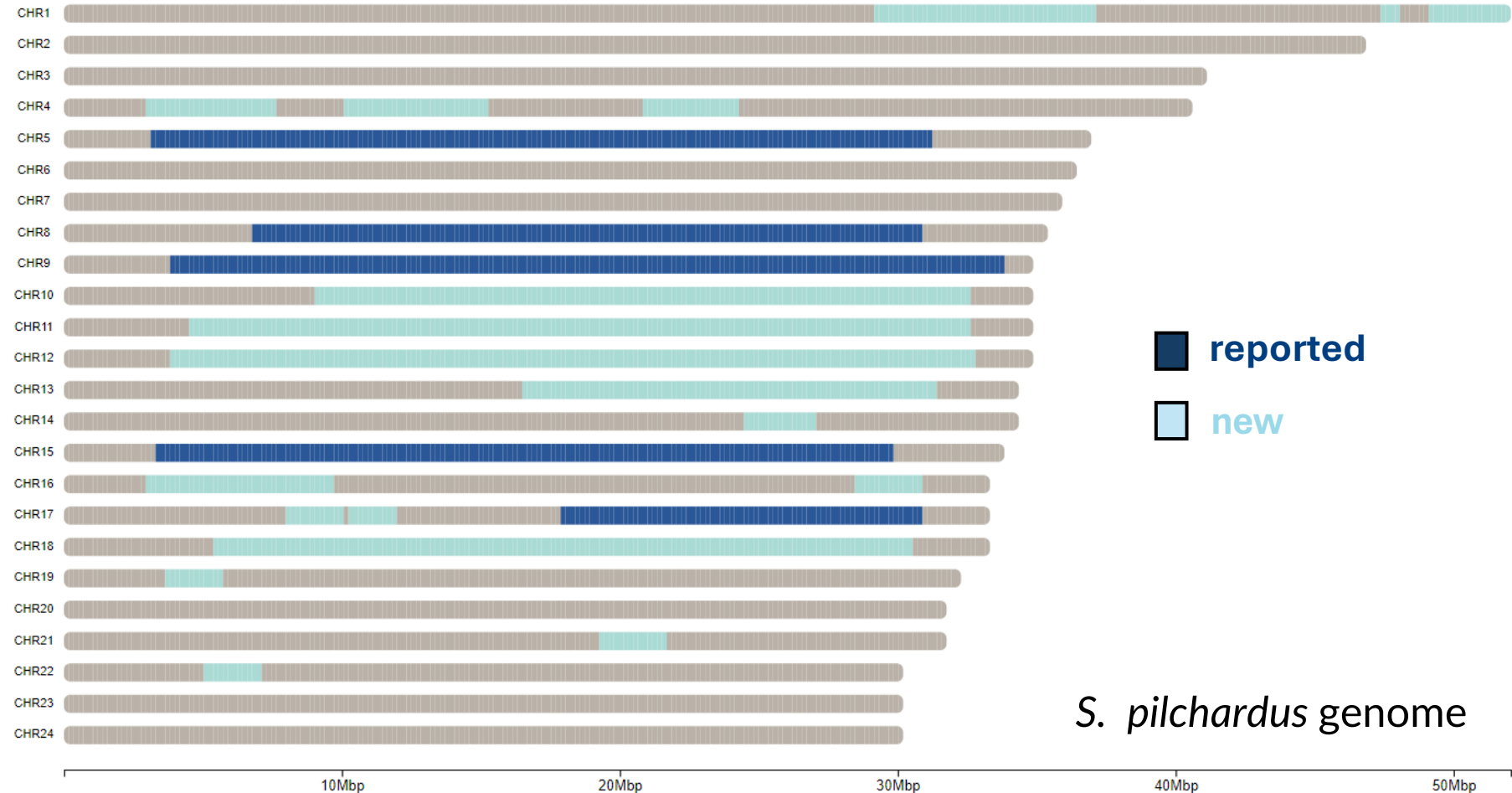
- 24 putative inversions identified, delimited and genotyped
- Resulting genotypes: “00,01,11” => “*invertypes*”
- They cover 34% of the genome.
- Located on 17 chromosomes out of 24
- Some chromosomes carry **more than one** inversion

## Previously reported with the ref. genome

- 5 large (>10 MB) chromosomal inversions

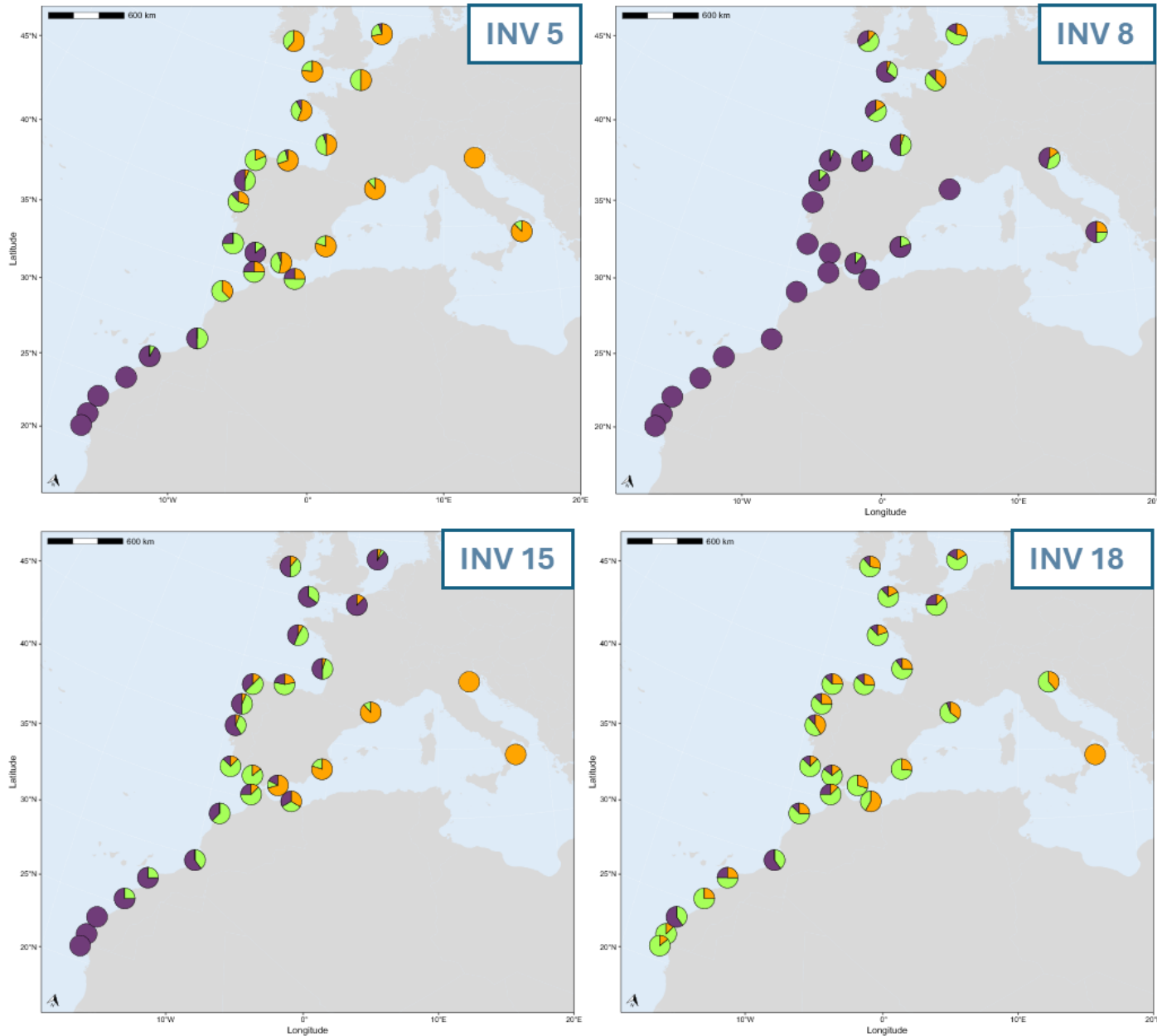
## Identified in this study:

- 19 new putative inversions of different sizes (0.55 - 24 MB)



*S. pilchardus* genome

# Results

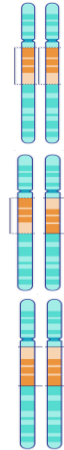


Geographical distribution of *invertypes* (inverted/non-inverted/mix of both types) varies across the different putative inversions detected.

■ Homozygous “00” / “11”

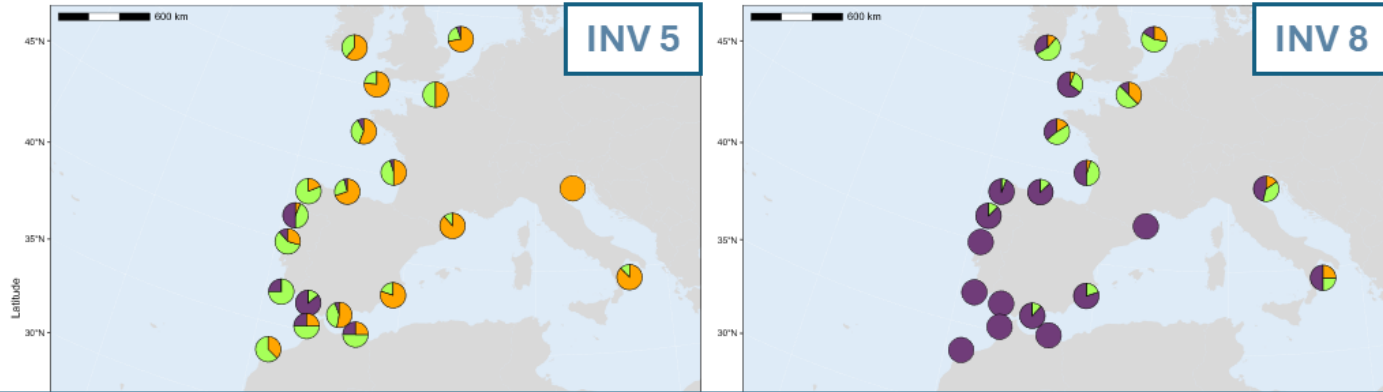
■ Heterozygous “01”

■ Homozygous “11” / “00”



**Homozygous *invertypes*** at the extremes of our distribution (SNAT and EMED) while **heterozygous** are found at NNAT.

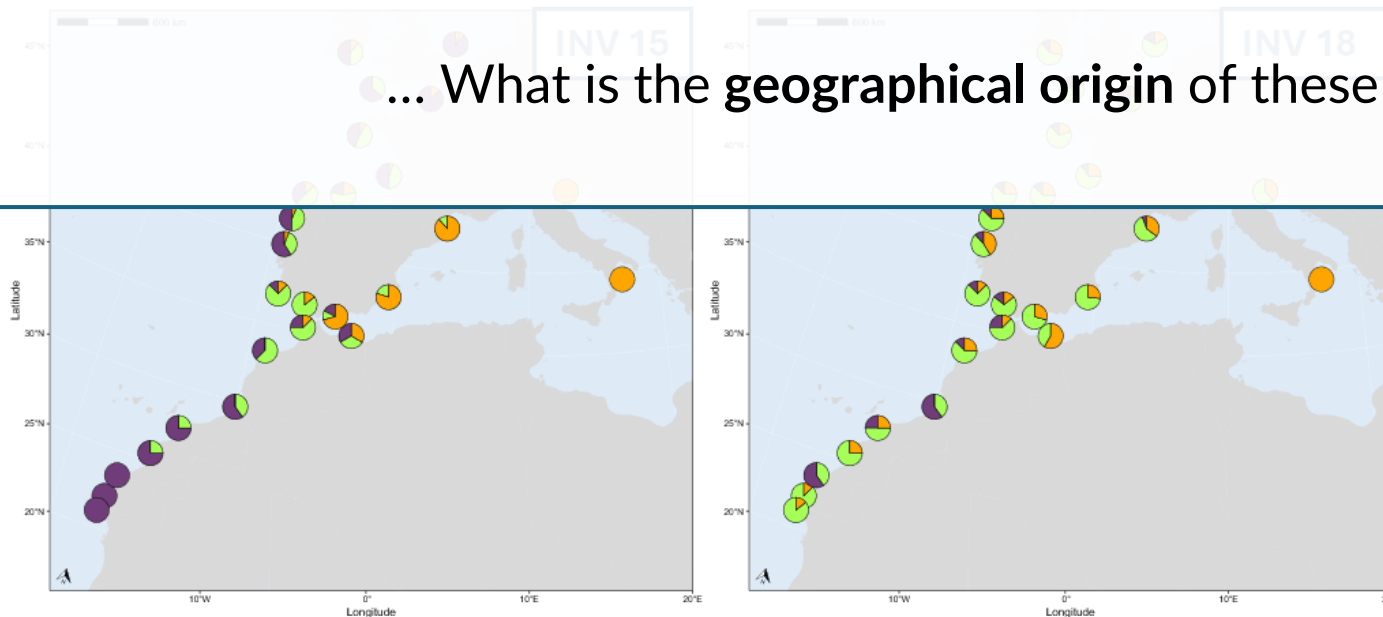
# Results



Geographical distribution of *invertypes* (inverted/non-inverted/mix of both types) varies across the different putative inversions detected.

Why are we seeing this **spatial pattern**?  
Why such a **big number** of chromosomal inversions?

... What is the **geographical origin** of these chromosomal inversions?



*Homozygous invertypes* at the extremes of our distribution (SNAT and EMED) while *heterozygous* are found at NNAT.

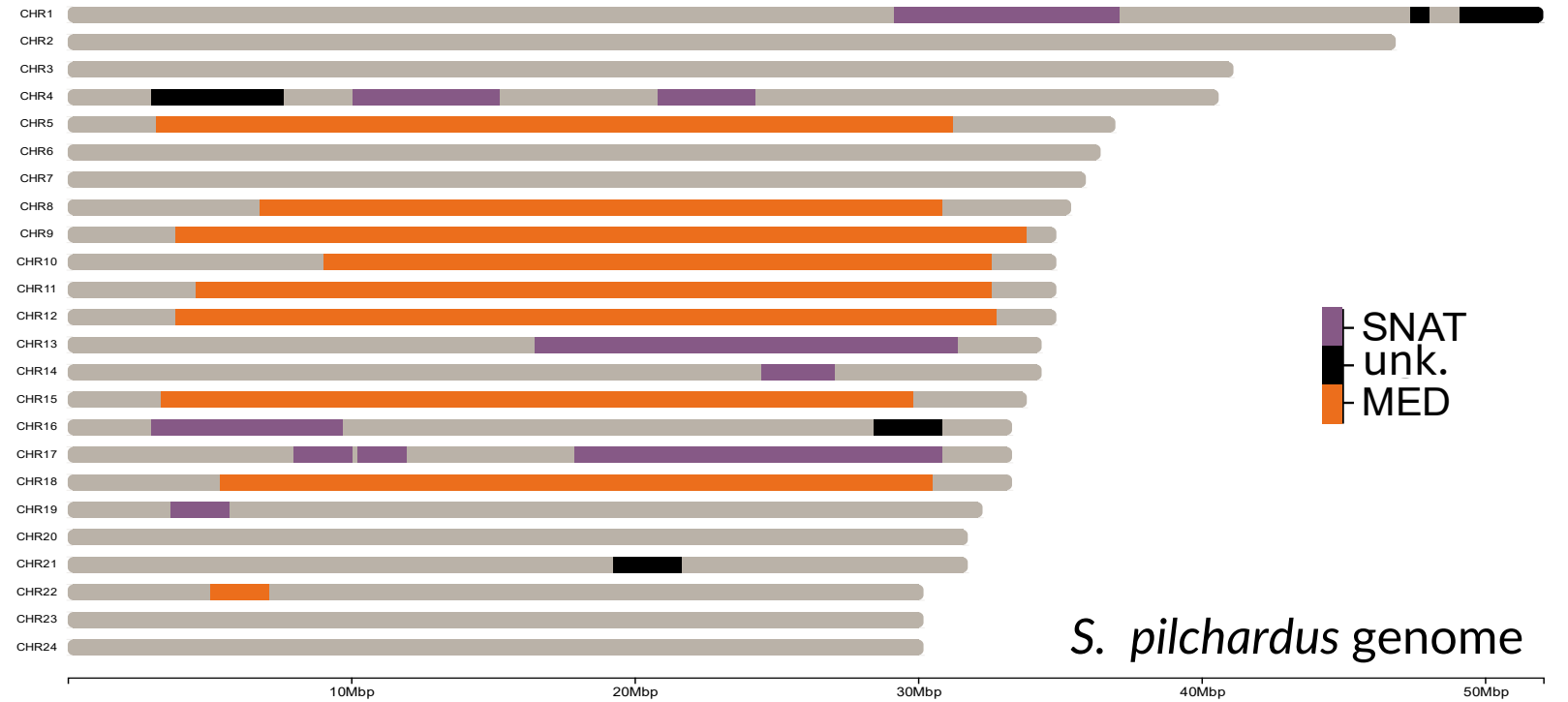
# Results

Where do inversions come from?

## Origin of inversions

- Inverted SNAT: 10
- Inverted MED: 9
- Unknown: 5

50/50 



*S. pilchardus* genome

Given the presence of so many chromosomal inversions in European sardine, which is their (evolutionary) history?

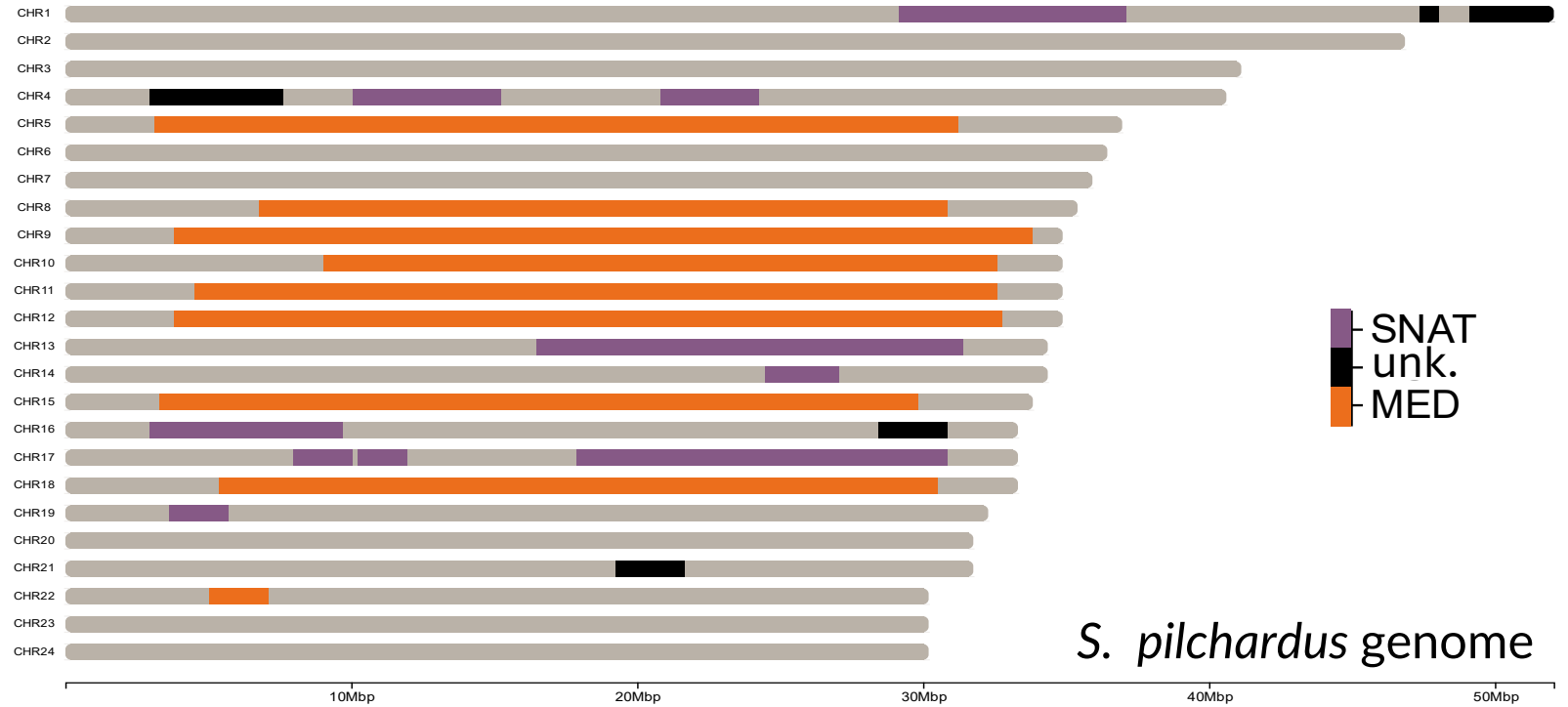
# Results

Where do inversions come from?

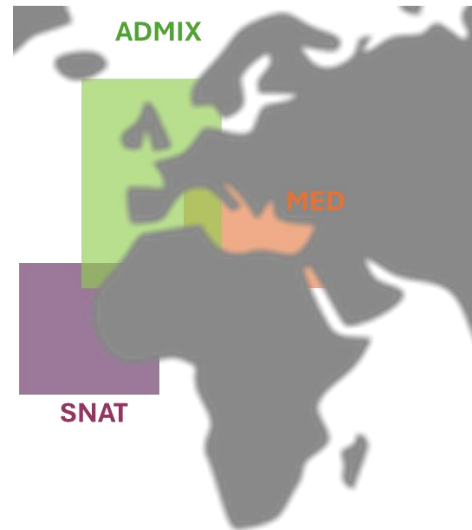
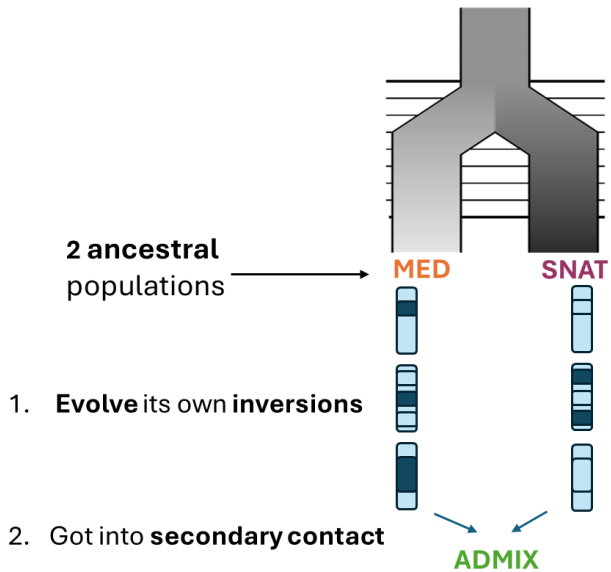
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- Unknown: 5

50/50 



Common origin



Given the presence of so many chromosomal inversions in European sardine, which is their (evolutionary) history?

- 2 ancestral populations + ADMIX zone
- Differences between lineages are **spread evenly across the genome**

# Results

## Population Structure – Neutral vs. *Invertypes*

79.267 SNPs, 345 inds

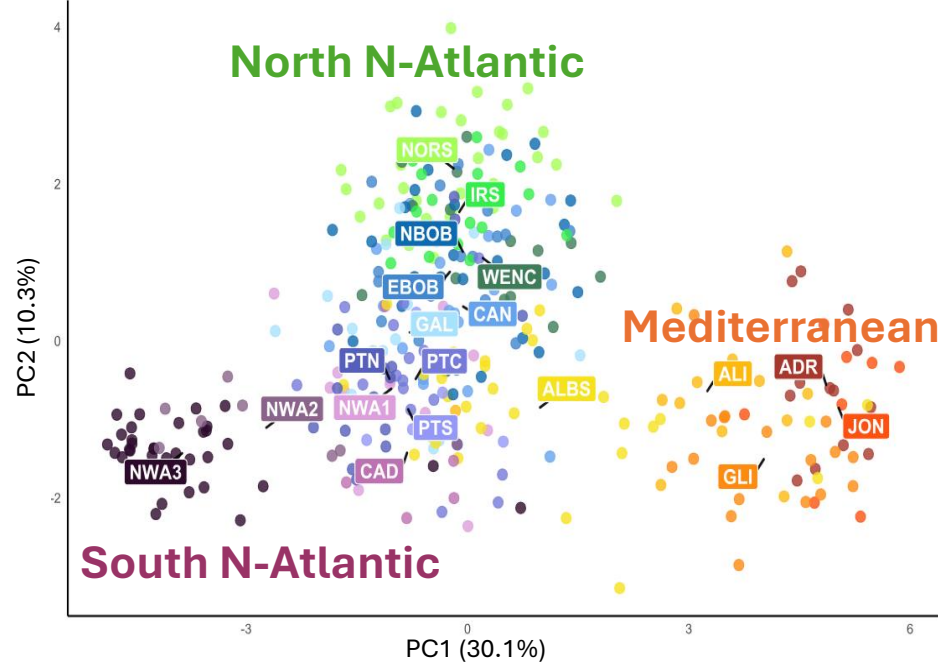
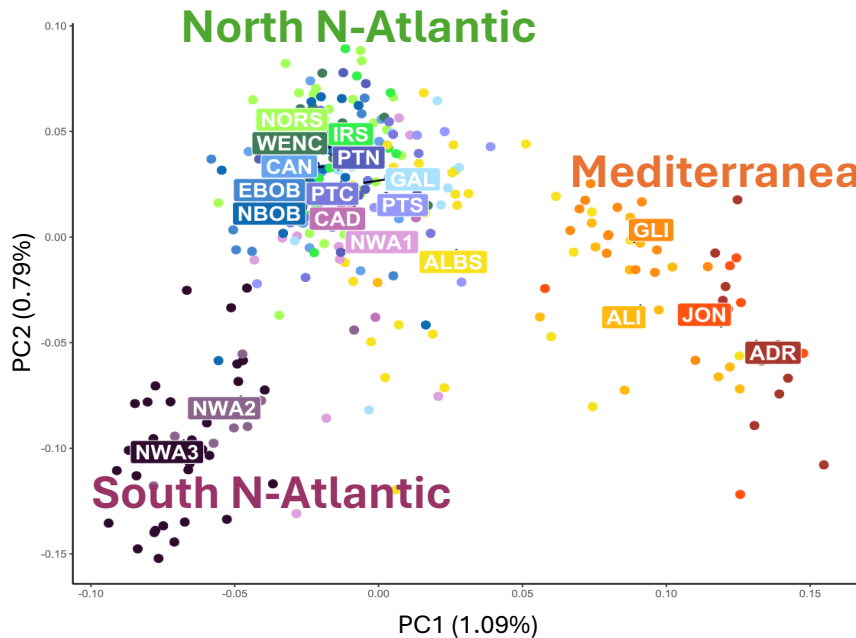
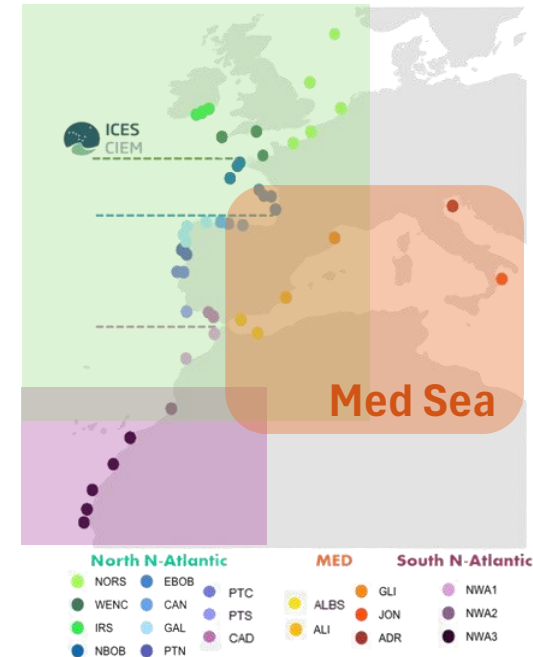
Neutral SNPs (no inversions, no physical linkage)  
 → Recover 3 main clusters  
 → But lose the latitudinal gradient in the North N-Atlantic

24 *invertypes*, 345 inds

*Invertypes* “00,01,11” only:  
 → Fully recover the population structure seen with all markers (7 M)  
 → Including the North N-Atlantic gradient

N-North Atlantic

S-North Atlantic



Most of the genome rehomogenize in NNAT, but inversions behaved differently from the rest of the genome and retain the historical signal of the basin where they originated.

# Take-home message:

## POPULATION STRUCTURE and CONNECTIVITY:

- Three genetic clusters connected by two transition zones
- Highly admixed North Atlantic, but inversions reveal subtle structure
- Inversions play a major role in shaping the observed population structure, explaining inconsistencies in previous studies using fewer or neutral-only markers.
- Inversions retain the historical signal of the basin where they originated and helped us understand the evolutionary history of the European sardine.

## IMPLICATIONS and FUTURE WORK

- Although their adaptive significance is not yet clear, understanding and monitoring these inversions is likely important for conservation
- E.g.; previous studies have linked inversions to large phenotypic effects or adaptive traits



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# Thank you for listening!



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