

# Evidence of local adaptation in European anchovy (*Engraulis encrasicolus*, L) from the Bay of Biscay

Iratxe Montes<sup>1\*</sup>, Iratxe Zarronaindia<sup>1,2</sup>, Aitor Albaina<sup>1</sup>, Mikel Iriando<sup>1</sup>, Carmen Manzano<sup>1</sup>, Darrell Conklin<sup>2,3</sup>, Unai Cotano<sup>4</sup>, W. Stewart Grant<sup>5</sup>, Xabier Irigoien<sup>6</sup>, Andone Estonba<sup>1</sup>

1 Department of Genetics, Physical Anthropology and Animal Physiology, University of the Basque Country UPV/EHU, Leioa-Bilbao, Spain. \* [iratxe.montes@ehu.es](mailto:iratxe.montes@ehu.es)

2 IKERBASQUE, Basque Foundation for Science, Bilbao, Spain.

3 Department of Computer Science and Artificial Intelligence, University of the Basque Country UPV/EHU, Donostia-San Sebastian, Spain.

4 AZTI Tecnalia, Marine Research Unit, Pasaia, Spain.

5 Commercial Fisheries Division, Alaska Department of Fish and Game, Anchorage, AK, USA.

6 Red Sea Research Center, King Abdullah University of Science and Technology, Thuwal, Saudi Arabia.

**Abstract:** European anchovy is a small teleost with major socio-economic importance that fuels research efforts. Its population genetic structure has been much studied and previous studies, using molecular markers and otolith microstructure and chemistry, have suggested genetic heterogeneity for the Bay of Biscay anchovy; however, the extent of differentiation and mechanisms producing and maintaining it are still not understood.

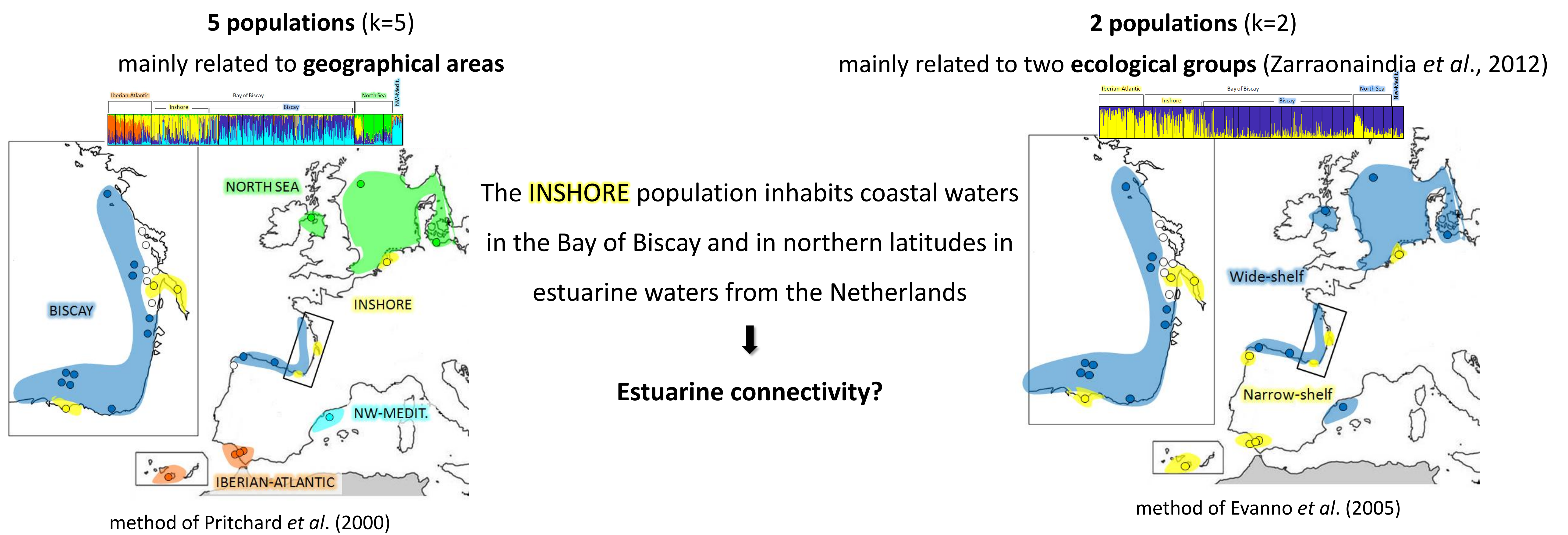
This study has assessed the population genetic structure of European anchovy, with a particular focus on the fine-spatial scale of the Bay of Biscay, analyzing 482 transcriptome-derived SNPs. Two populations with differentiated ecological properties and distributions were identified in the Bay of Biscay, which are in concordance with the two anchovy ecotypes previously proposed for the species. These two populations in the Bay of Biscay have shown local adaptation signatures including a strong allele-frequency association with salinity. Even both populations show high genetic differentiation, suggesting reproductive isolation, they spend life stages together in a trans-boundary region where fresh and saline waters mix: the Gironde plume. All these results combined with the fact that both populations have an overlapping spawning period and place might reflect an early stage process of ecological speciation.

**Keywords:** SNP, population genetics, divergent selection, salinity, ecotypes, ecological speciation.

## 1. Population genetic structure of the European anchovy

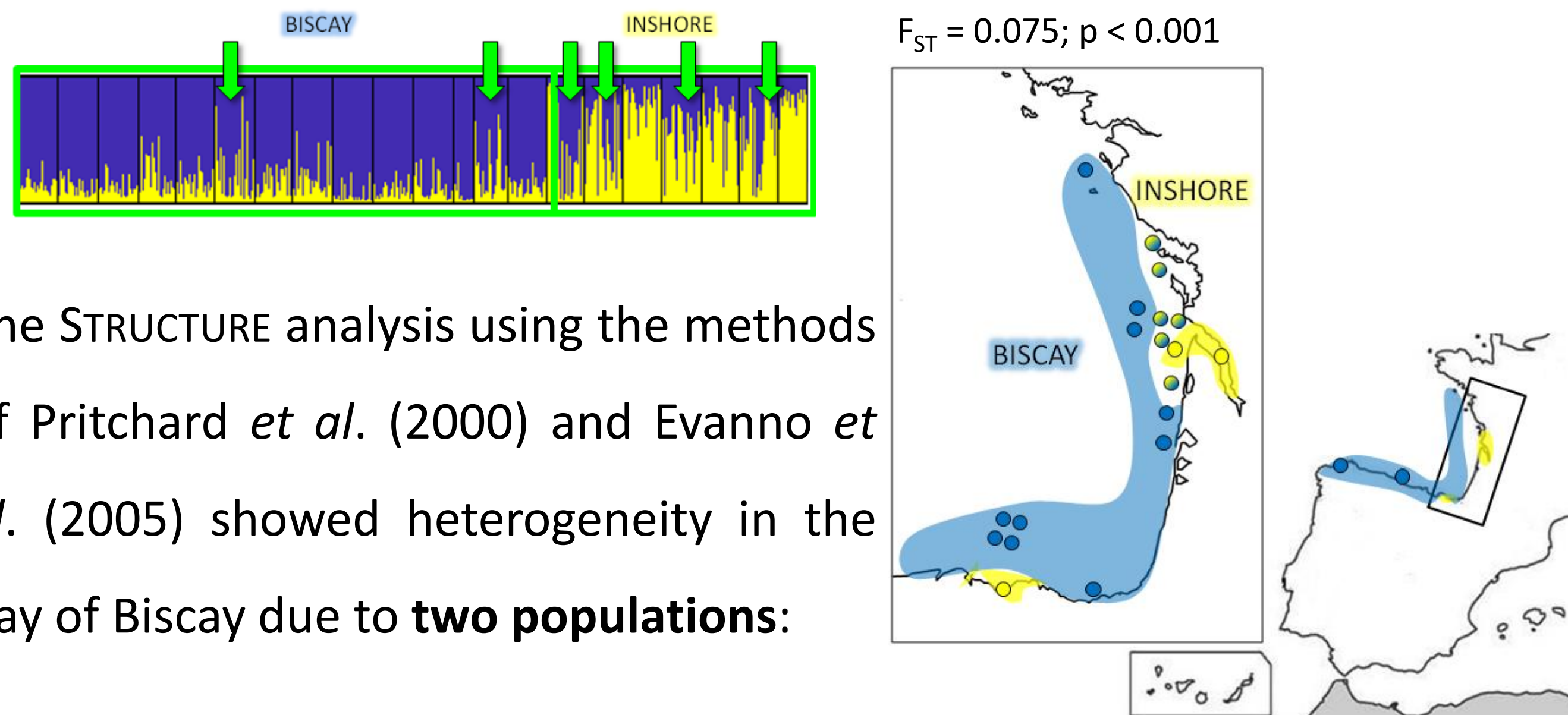
851 samples from 31 locations (4 geographical regions) analyzed with 482 SNPs discovered and validated from Montes *et al.* (2013)

2 levels of population genetic structure are revealed by STRUCTURE v2.3.4 software (Pritchard *et al.*, 2000):



## 2. The Bay of Biscay anchovy

### 2.1. Population genetic structure



The STRUCTURE analysis using the methods of Pritchard *et al.* (2000) and Evanno *et al.* (2005) showed heterogeneity in the Bay of Biscay due to **two populations**:

- Major population inhabiting offshore/oceanic waters = **BISCAY**
- Minor population inhabiting estuaries and river plumes = **INSHORE**

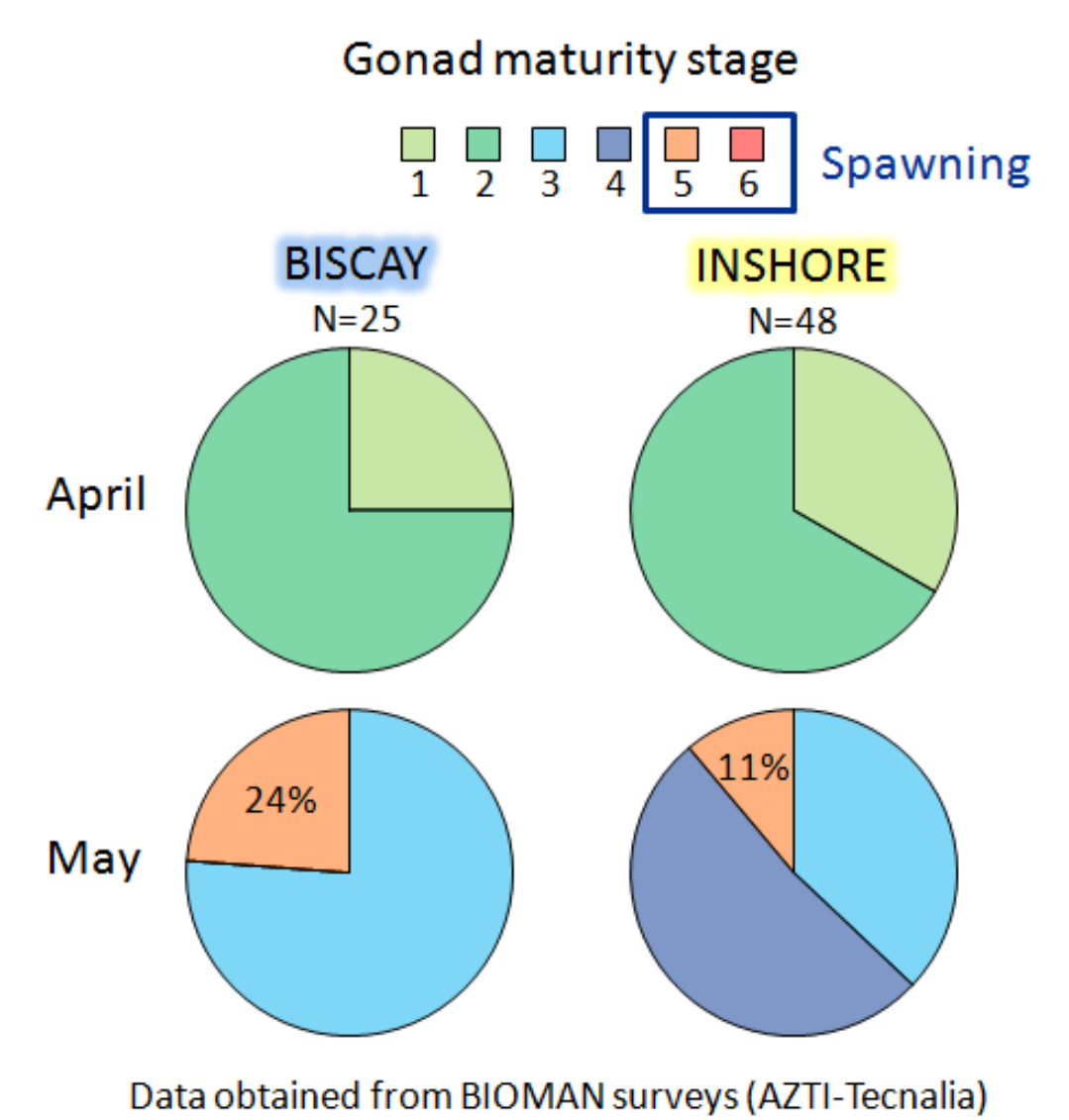
Additionally, some locations (●) include individuals from both populations (see green arrows, ↓, in the STRUCTURE analysis).

2 populations of anchovy in the Bay of Biscay cohabit in the Gironde plume: a trans-boundary region where fresh and saline waters mix.

### 2.2. A barrier to gene flow

2 populations cohabiting  
+  
no geographical barriers  
=  
barrier to gene flow

The gonad maturity stage data analysis for 73 individuals from mixed samples/hauls (●) indicated that **both populations mature together** and individuals from both populations **spawn in May in the same area**.



The two populations in the Bay of Biscay have an overlapping spawning period and place.

The mechanism for reproductive isolation between **BISCAY** and **INSHORE** populations might have a genetic component.

### 2.3. Adaptation to salinity

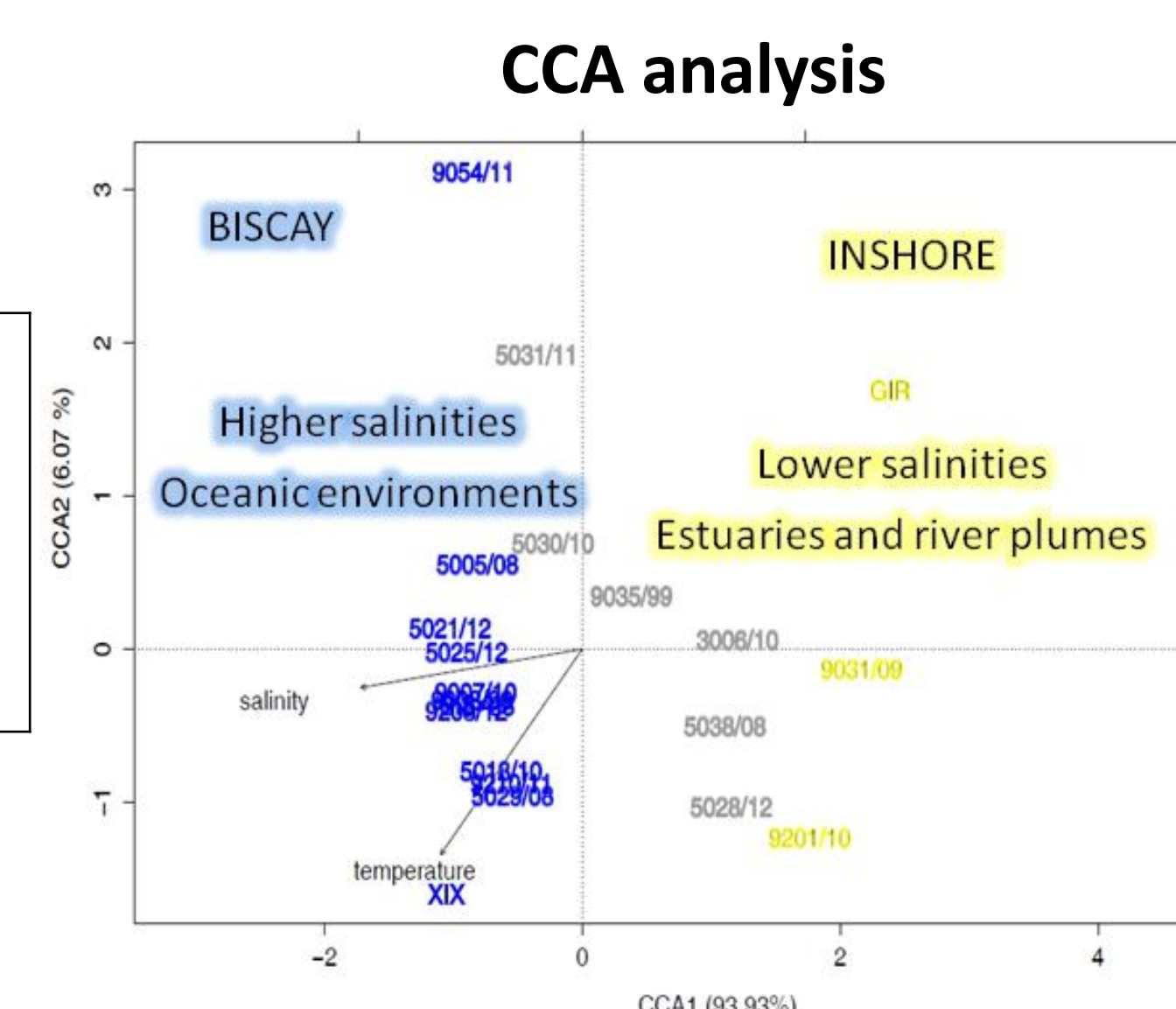
The CCA analysis and the Mantel test suggest that genetic differences between **BISCAY** and **INSHORE** populations are correlated with salinity → the two populations are differentially adapted to salinity.

Adaptation to different salinities might explain genetic differences between **BISCAY** and **INSHORE** populations

**Mantel test**

Association	Mantel R
D – Ds	0.8293*
	<b>Partial-mantel R</b>
D – Ds [Dg]	0.8315*
D – Ds [Dt]	0.7432*

\* p < 0.001



## References

- Evanno G, Regnaut S, Goudet J (2005). *Mol Ecol*, 14:2611-2620.
- Montes I, Conklin D, Albaina A, Creer S, Carvalho GR, Santos M, Estonba A (2013). *PLoS ONE*, 8(8): e70051.
- Pritchard JK, Stephens M, Donnelly P (2000). *Genetics*, 155: 945-959.
- Zarronaindia I, Iriando M, Albaina A, Pardo MA, Manzano C, Grant SW, Irigoien X, Estonba A (2012). *Plos ONE*, 7 (7): e42201.