

# SNPfish: Genomic tools for fisheries management

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## Introduction

There is a growing need in Europe for a legally enforceable traceability system to tackle Illegal, Unreported and Unregulated (IUU) fishing, and support consumer protection both at species and population levels.

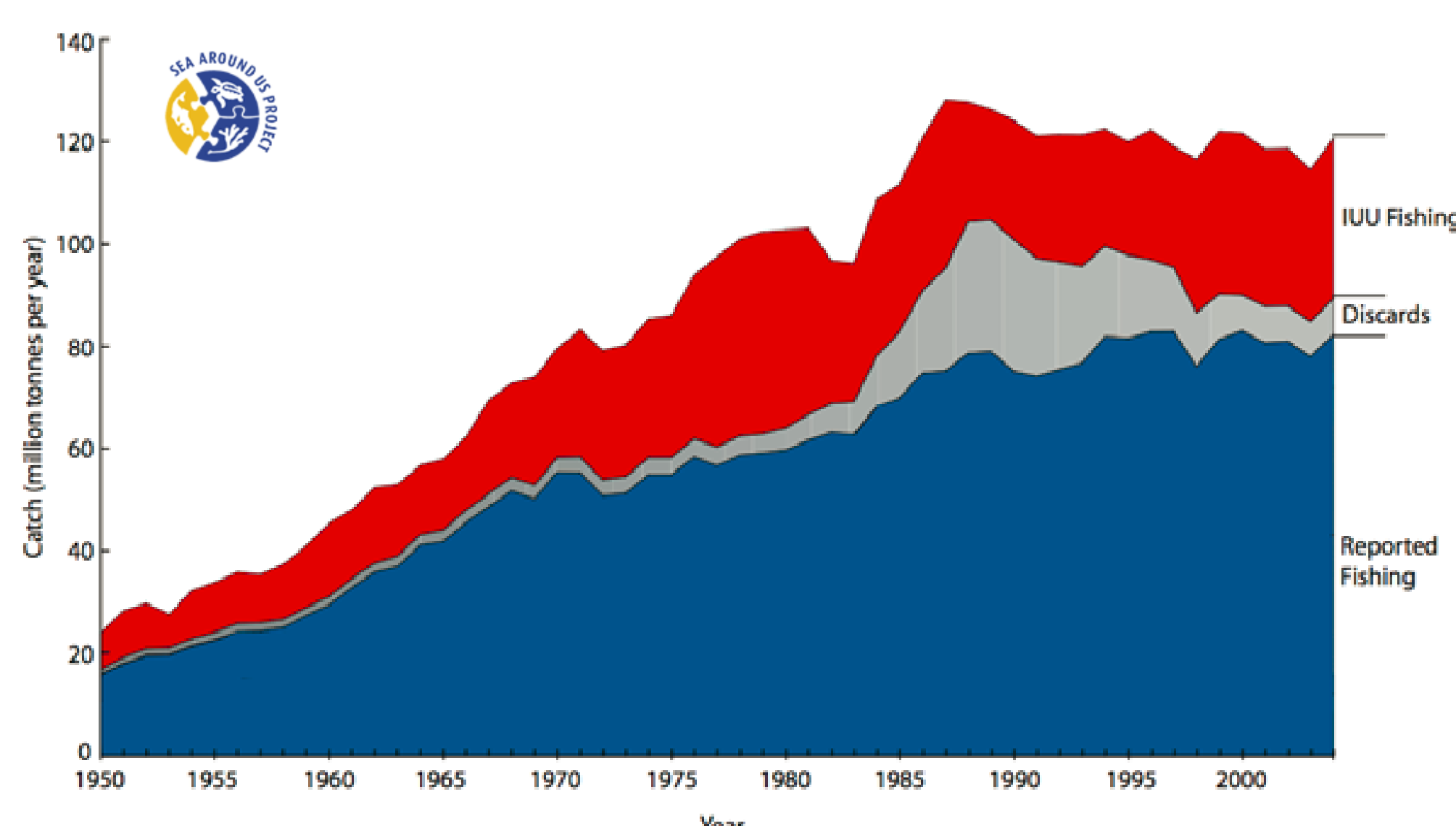


Fig. 1: Illegal, Unreported and Unregulated (IUU) fishing constitutes a significant proportion of fish landings and are a threat to the both the marine ecosystem, and the viability of honest fishing companies.

The FAO and independent scientists estimate that 80% of marine fish stocks are fully or over-exploited worldwide. In this context the fight against IUU fishing is a high priority, due to the severe threat it poses to global marine ecosystems and sustainability of world fisheries. The losses for Europe attributed to IUU fishing have been valued at €385 million per year (Fig 1).

Genomic tools for authenticity testing of fish and fish products are increasingly forming a key element within this traceability system. This project is developing genetic markers to provide population level assignment for three commercially important species (mackerel, herring and blue whiting; Fig. 2).

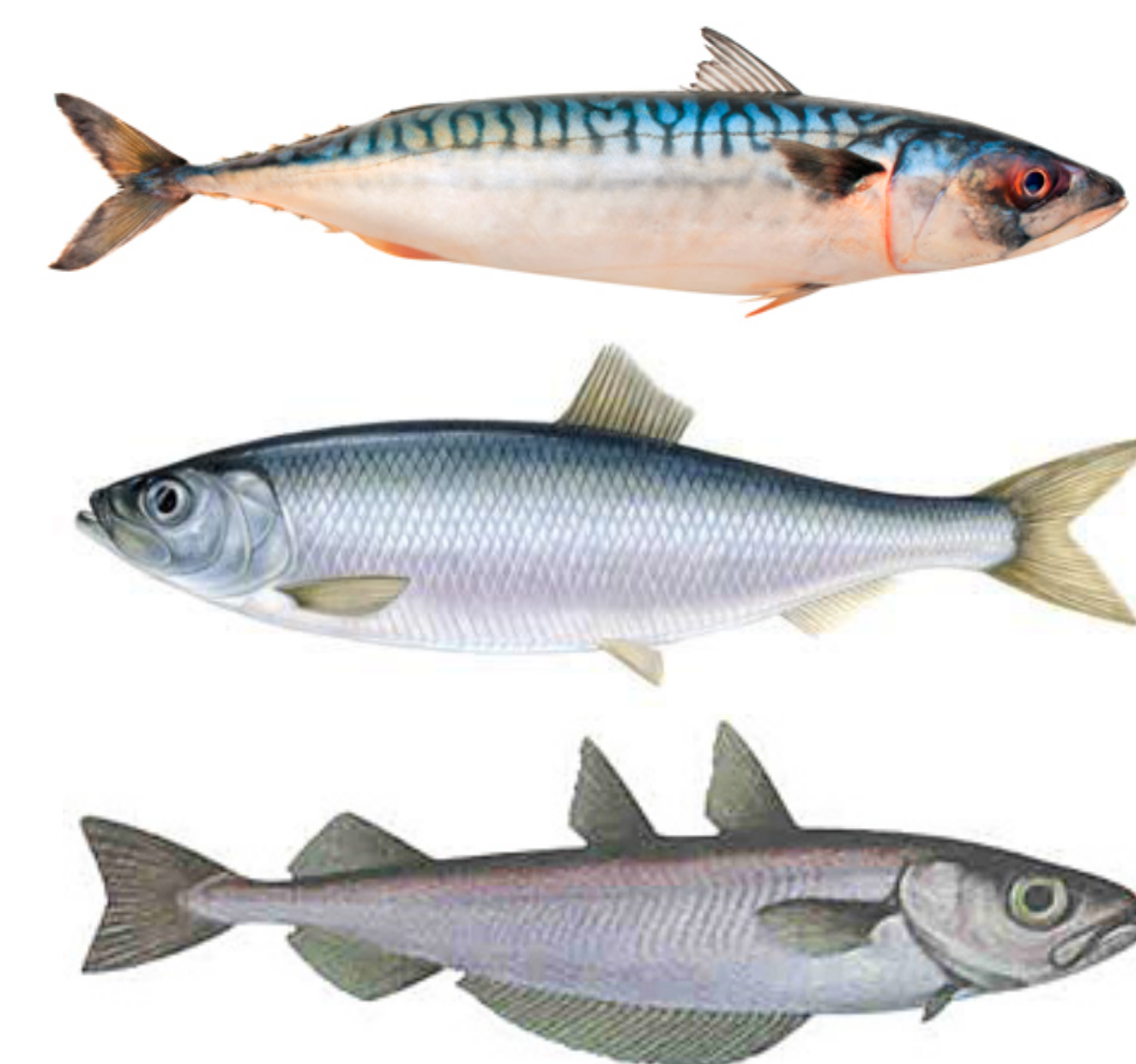


Fig. 2: Key fisheries species focussed on in the project, from the top: mackerel, herring and blue whiting.

## Methods

Samples for each of the three species were collected across the Atlantic (see Fig 3). Genetic markers were developed using RAD sequencing for the samples of spawning fish. Additional samples were then genotyped at a smaller panel of loci using the Biomark Fluidigm. Bioinformatics was carried out in Stacks and SAMtools. Data filtering and population genetic analyses were carried out in Plink and R (Adegene).

## Results

Thousands of markers were produced using the RAD sequencing. The data was filtered for sequence quality, genotyping rate, and MAF. This reduced the data set to approximately 10,000 loci per species, of which 96 are carried forward to be genotyped on the Fluidigm for each of the three species.

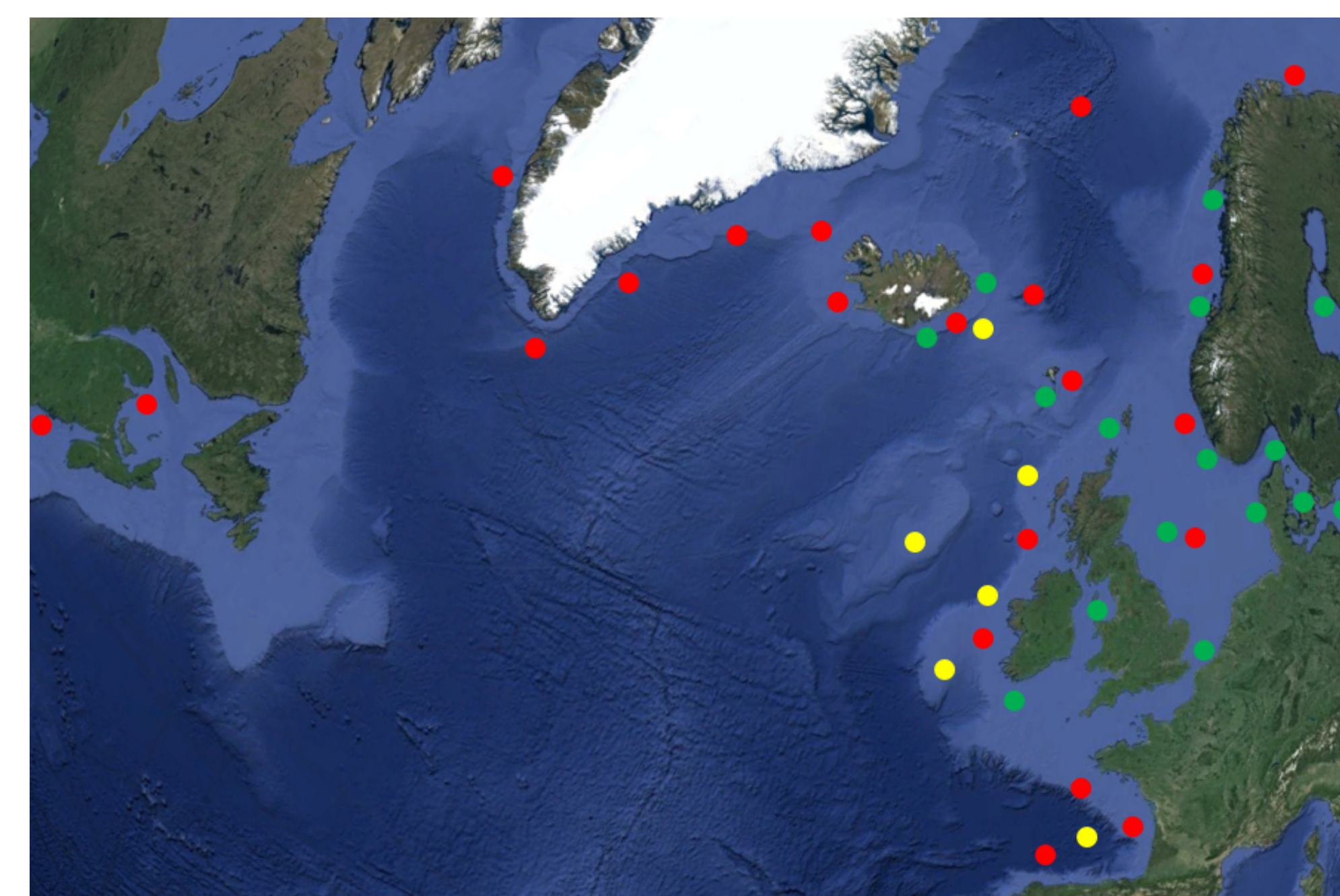


Fig. 3: Sampling map for the three species; mackerel (red), herring (green) and blue whiting (yellow).

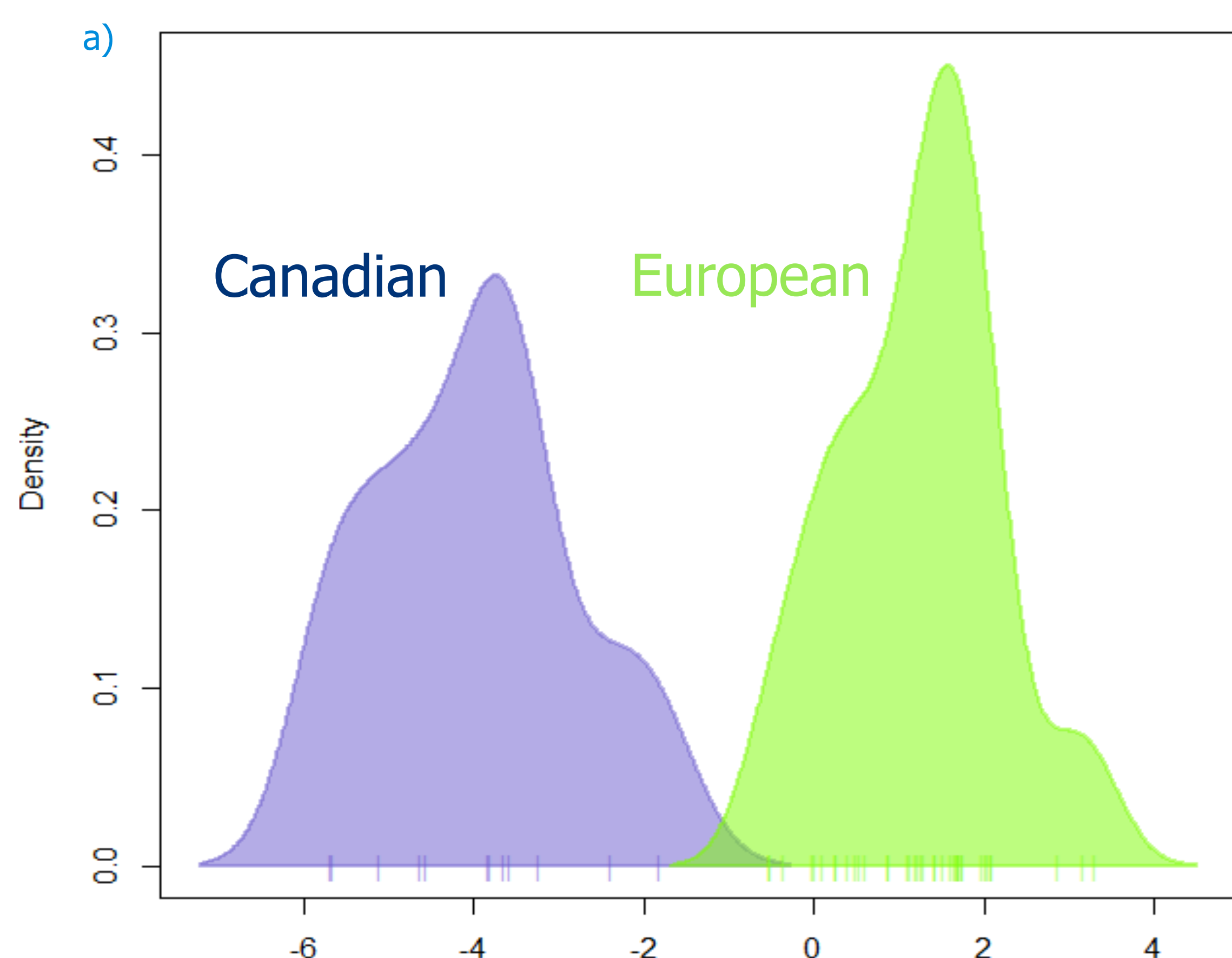
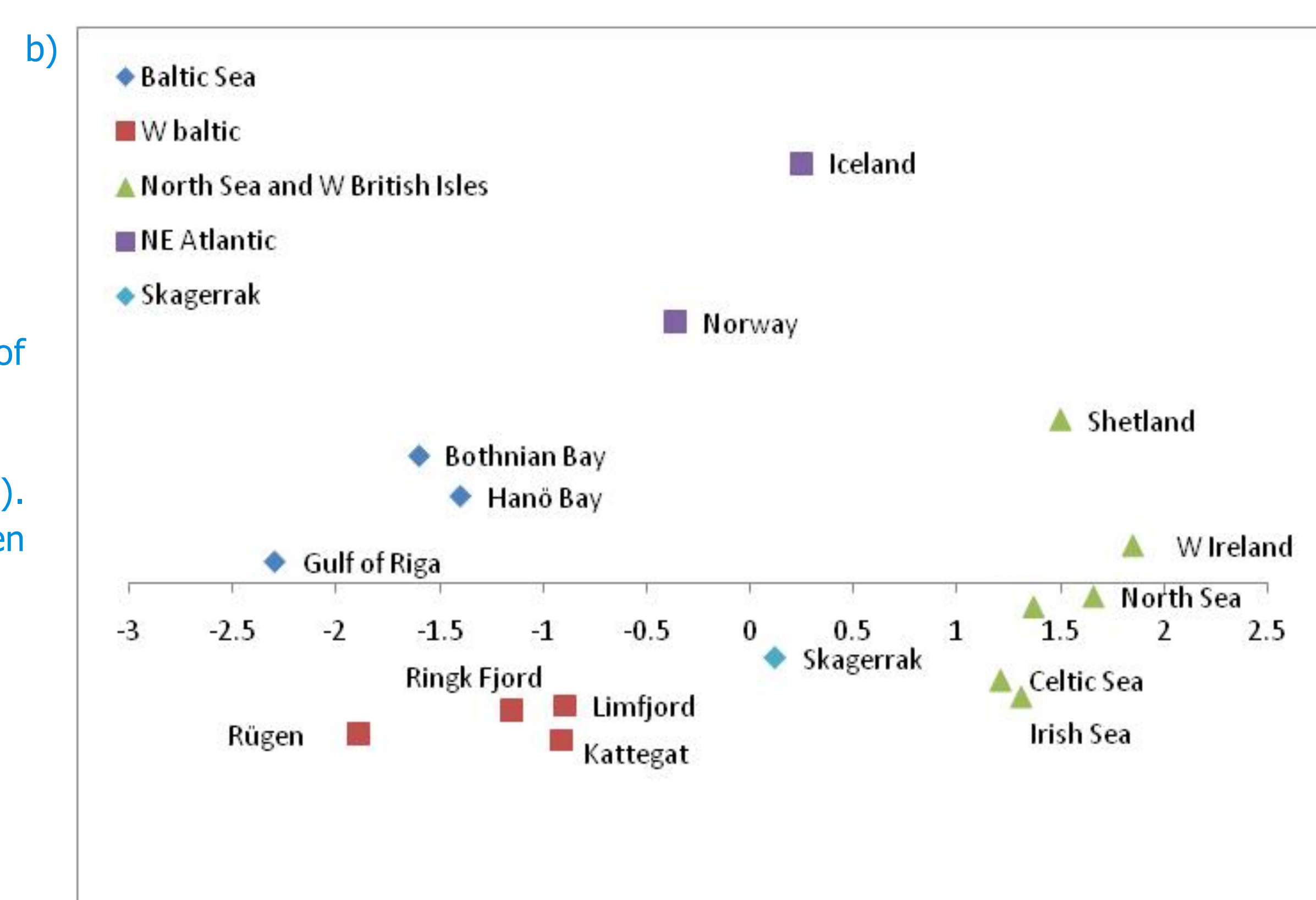


Fig. 4: Initial results for

a) mackerel (Discriminant analysis of principle components)

b) herring (Multidimensional scaling). Results show the differentiation between populations.



## Conclusions

The work so far has demonstrated that these markers give us greater detail of the population structure of these fishes than has been possible before. In addition, the quick processing time of these analyses mean that these new genomic methods could be useful tools in the fight against IUU fishing and in promoting consumer confidence in eco-certification.

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