



# Genomics of Mediterranean invaders

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## Introduction

The spread of invasive species, from the Red Sea into the Mediterranean Sea (Lessepsian alien species), is one important driver of biodiversity loss in this basin [5]. Currently available literature on Lessepsian species mainly focuses on ecological data and the few genomic studies carried out so far have not thoroughly investigated the role and impact of adaptive and deleterious variability in the colonisation of the Mediterranean [1, 2, 3].

Among more than 900 invasive marine species we decided to focus on *Siganus rivulatus* and *Pterois miles*.

The first one is an herbivorous species that entered the Mediterranean approximately around 1930 and has since spreaded throughout the eastern basin.

*P. miles* started its rapid expansion in the Mediterranean around 10 years ago and since then it rapidly spreaded all over the Levantine basin.

## Materials & Methods

We sample 10 individuals of both *S. rivulatus* and *P. miles* from each sampling location: Red Sea (1), Cyprus (2), Crete (3) and the Ionian Island (4) in Figure 1.

The sampling was designed to have individuals from equidistant location along the invasion route.

We collected tissues from which we extracted DNA for genomic analyses.

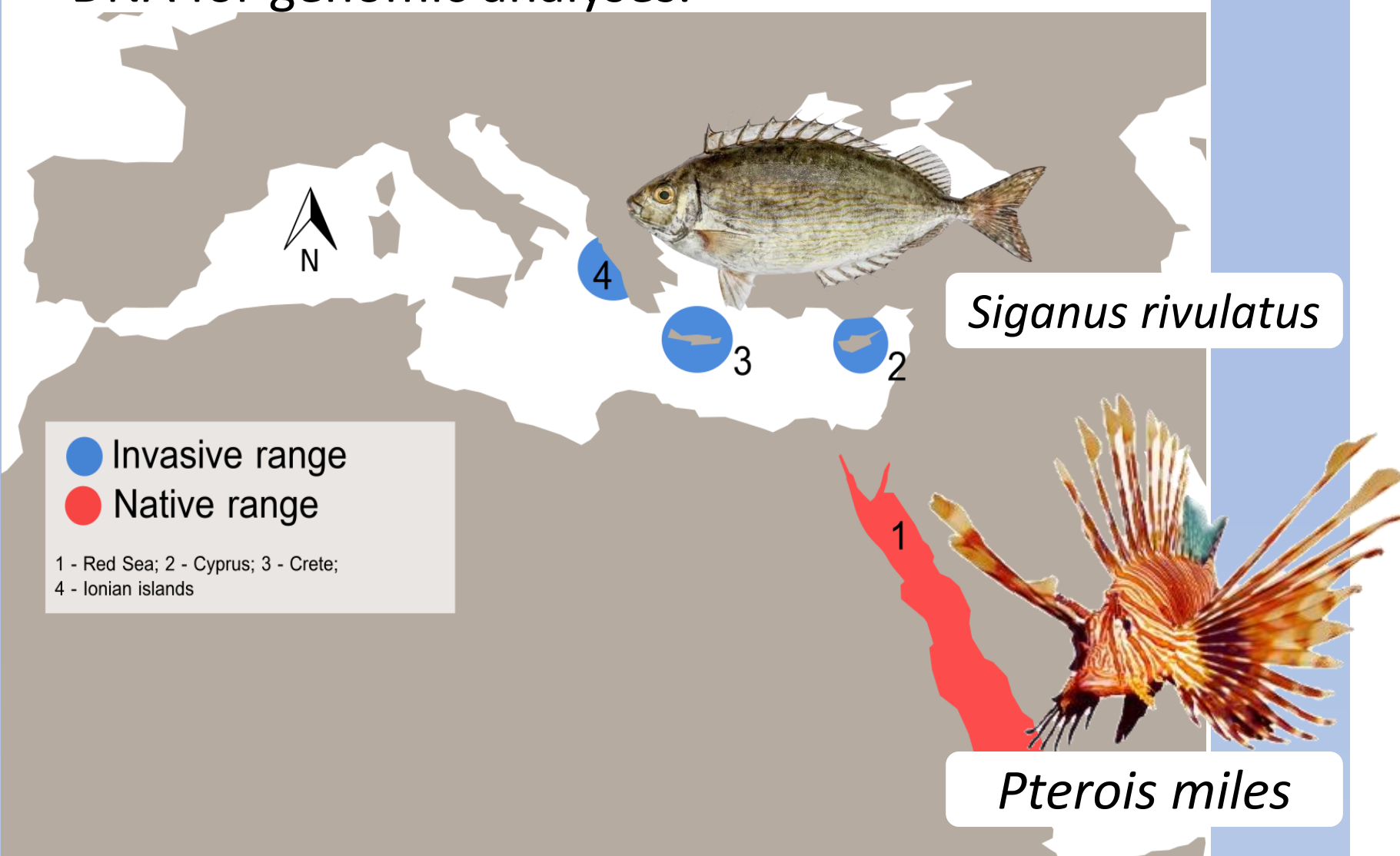


Figure 1. Sampling map

## Aims & Results

### Reconstructing invasion dynamics

#### Aim

- Investigate how different invasion speeds and patterns have shaped genetic diversity distribution and genetic load accumulation in two invasive marine species.

#### Results

- The results obtained so far on *P. miles* show that the rapid invasion of this species has resulted in a significant decrease in genetic diversity (Figure 2, measured as heterozygosity) moving from the source population to the northern limit of the invasion.

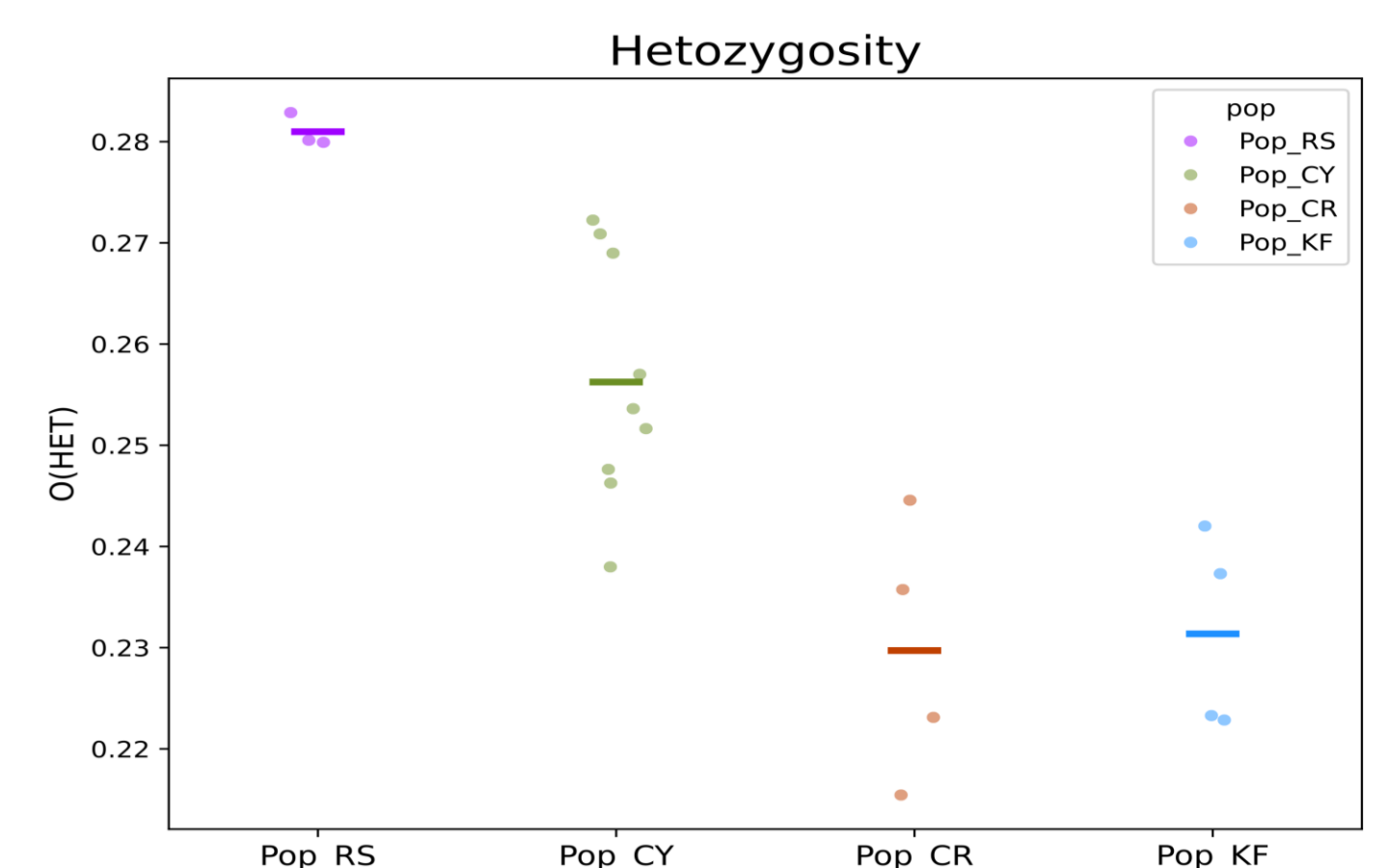


Figure 2. Heterozygosity values for Red Sea (RS), Cyprus (CY), Crete (CR) and Ionian islands (KF) populations

### Genomic adaptation

#### Aim

- Understand if the two species are using the same combinations of genes to adapt to the new environment

#### Results

- We found that 11.3% of the variable sites in our dataset (*P. Miles*) fall on evolutionary conserved positions of the genome. These regions need to be explored further to understand their role in adaptation to the new environment and whether these regions are under selection in both species.

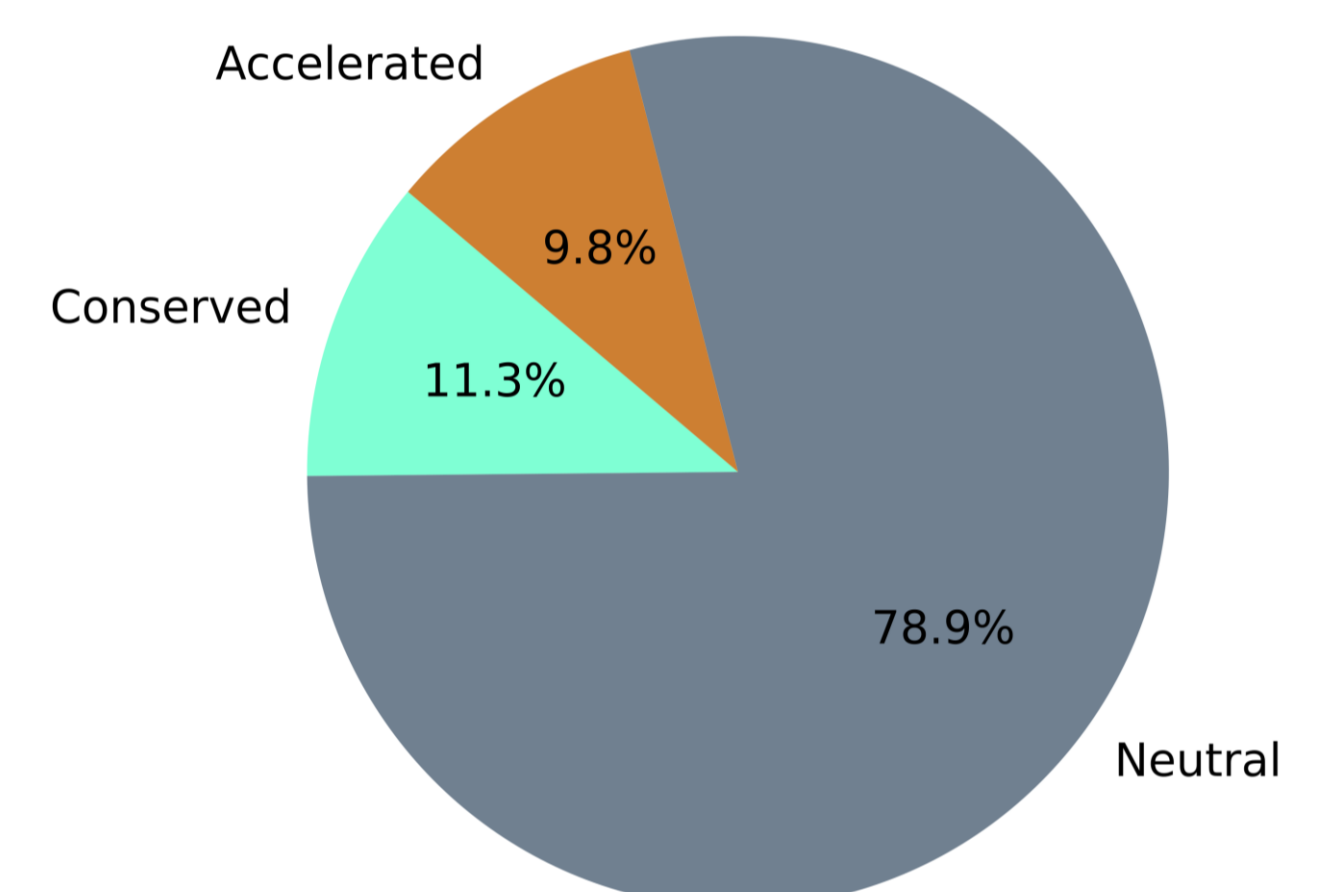


Figure 3. Proportion of conserved, accelerated and neutral variant position in the *P. miles* dataset

### Future scenarios

#### Aim

- Considering several possible scenarios, involving climate change, oceanographic currents and passive transport via ballast waters, create realistic predictive simulation models using SLiM [4] to understand how the invasion of new environments by the two species may occur and how non-neutral diversity might influence the invasive potential of these species.

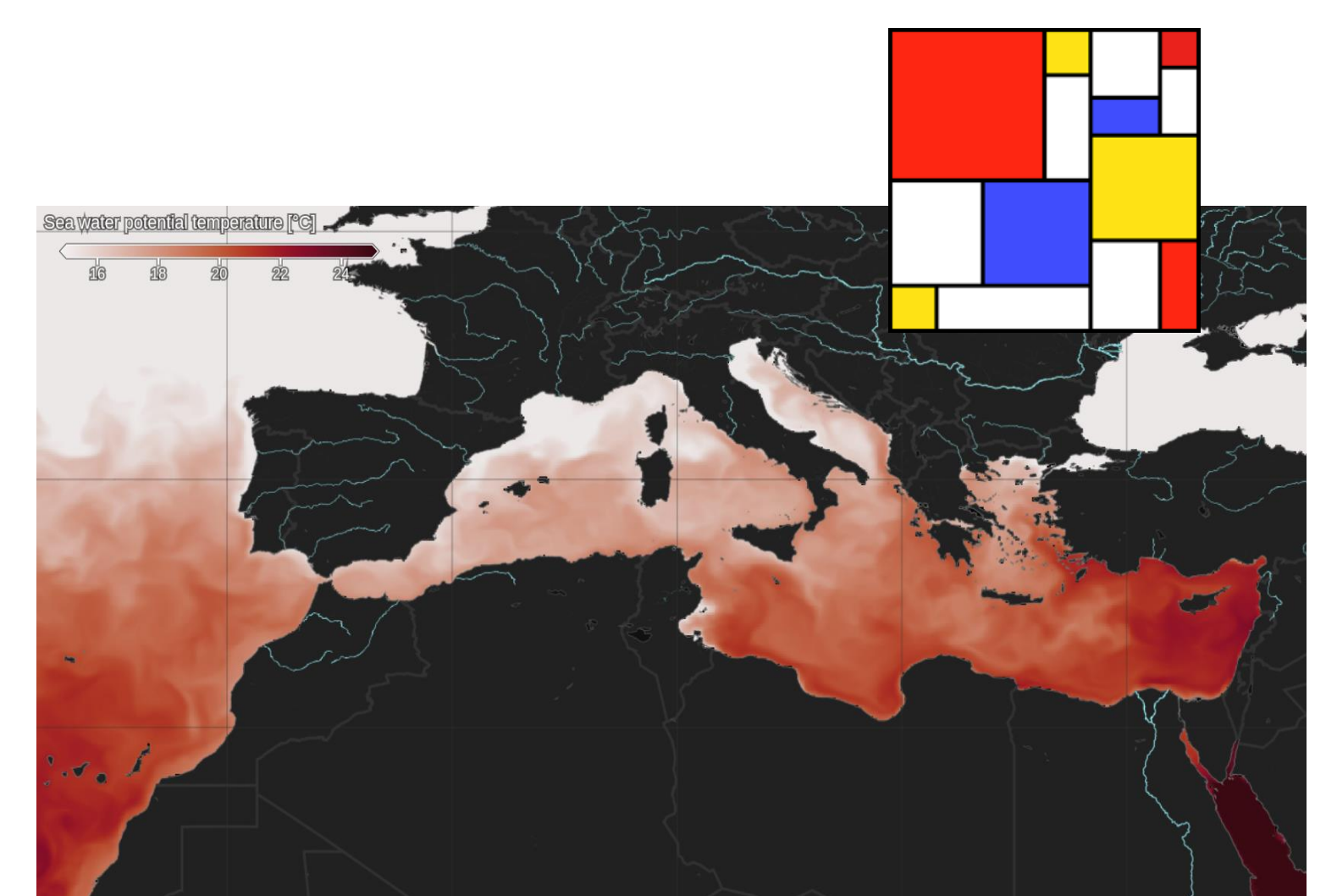


Figure 4. Sea water potential temperature map of the Mediterranean Sea and SLiM logo (top right corner)

## References

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