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### Introduction

In recent years increasing human activities are threatening the biodiversity of the Mediterranean Sea, making it one of the most impacted seas in the world [1].

The spread of invasive species, from the Red Sea into the Mediterranean, (Lessepsian alien species) is one important driver of biodiversity loss, as invasive species are negatively interfering with native species[1].

Available literature on invasive 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 Sea [2-4].

### Aim of the project

Study the impact of adaptive and deleterious genetic variation of successful Lessepsian species in the invasion of the Mediterranean Sea:

1. Test whether they share genomic characteristics that predispose a population to easily spread in a new environment
2. Understand the consequences of the invasive processes on the genetic variability of these species.

## Methods

The chosen species for the investigation will be sampled in

- Native range: Red Sea
- First invasive range: Cyprus
- Secondary invasive range: Greece



### GENOMIC DATA PRODUCTION

- Assembly of a reference genome
- Re-sequencing of representative samples from both the invasive and the native range

Analyses for the identification of target regions:

- RNAseq for highly expressed regions
- Atacseq for accessible regions

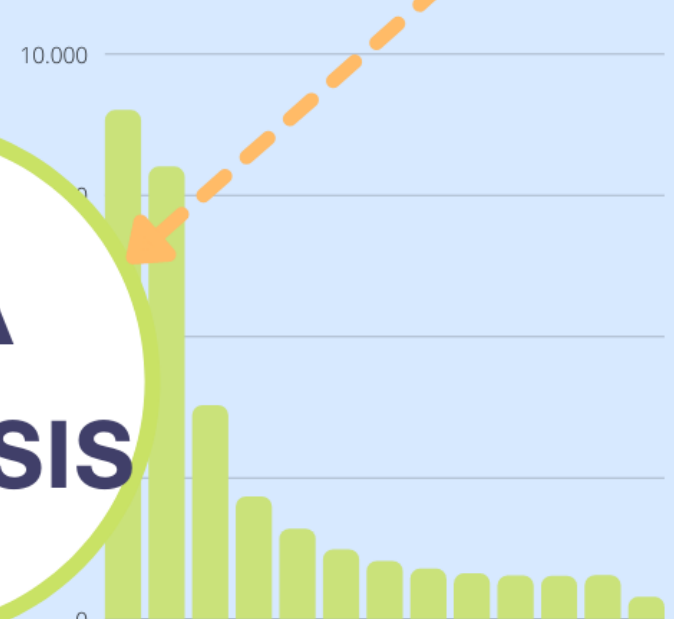
### TARGET GENOMIC REGIONS



### DATA ANALYSIS

Analyses of:

- Demographic reconstruction of the invasion process
- Genetic load
- Genomic regions under selection



### First year activities

The first year of the PhD project is mainly focused on the identification and sampling of species of interests among Lessepsian invaders. For that purpose, we collected data and literature regarding invasive fishes in the Mediterranean Sea, focusing on species that have been studied more and with a larger distribution area in the Mediterranean basin.

SPECIES	ECOLOGY	FIRST RECORD IN THE MEDITERRANEAN	DISTRIBUTION AREA
STEPHANOLEPIS DIASPROS	IT LIVES IN COASTAL WATERS ON ROCKY BOTTOMS AND FEEDS ON BENTHIC INVERTEBRATES.	1927	
PTEROIS MILES	INHABITS STONY BOTTOMS UP TO 150MT DEPTH. FEEDS ON FISH AND SMALL CRUSTACEANS	1991	
LAGOCEPHALUS SCELERATUS	BENTHIC, IT LIVES ON SANDY BOTTOMS. FEEDS ON BENTHIC INVERTEBRATES.	2003	
SIGANUS RIVULATUS/ LURIDUS	IT LIVES IN SHALLOW COASTAL WATERS. HERBIVOROUS DIET	1924 1931	
FISTULARIA COMMERSONII	LIVES IN SHALLOW WATERS FROM 5 TO 25 M IN ROCKY AREAS. FEEDS ON FISH, OCTOPUS AND CRUSTACEANS.	2000	

These species will be sampled in the invasive range (Cyprus and Greece) and in the native range (Red Sea) to obtain DNA and RNA sequences to analyse.

### Expected Results

We expect to detect significant signs of neutral and selective processes happening in the invasive population:

- Some of the genetic variants under selection in the new environment could be present in the source population of the Red Sea, allowing us to estimate the importance of pre-adaptations in the colonisation of a new environment.
- The demographic reconstruction of the invasive process will allow us to infer the dynamics that characterised the invasive event and its consequences.

### Citations

1. Templado, J. (2014). Future trends of Mediterranean biodiversity. In The Mediterranean Sea (pp. 479-498). Springer, Dordrecht.
2. Azzurro, E., Nourigat, M., Cohn, F., Ben Souissi, J., & Bernardi, G. (2022). Right out of the gate: the genomics of Lessepsian invaders in the vicinity of the Suez Canal. Biological Invasions, 24(4), 1117-1130.
3. Bernardi, G., Azzurro, E., Golani, D., & Miller, M. R. (2016). Genomic signatures of rapid adaptive evolution in the bluespotted cornetfish, a Mediterranean Lessepsian invader. Molecular ecology, 25(14), 3384-3396.
4. Chiesa, S., Azzurro, E., & Bernardi, G. (2019). The genetics and genomics of marine fish invasions: a global review. Reviews in Fish Biology and Fisheries, 29(4), 837-859.