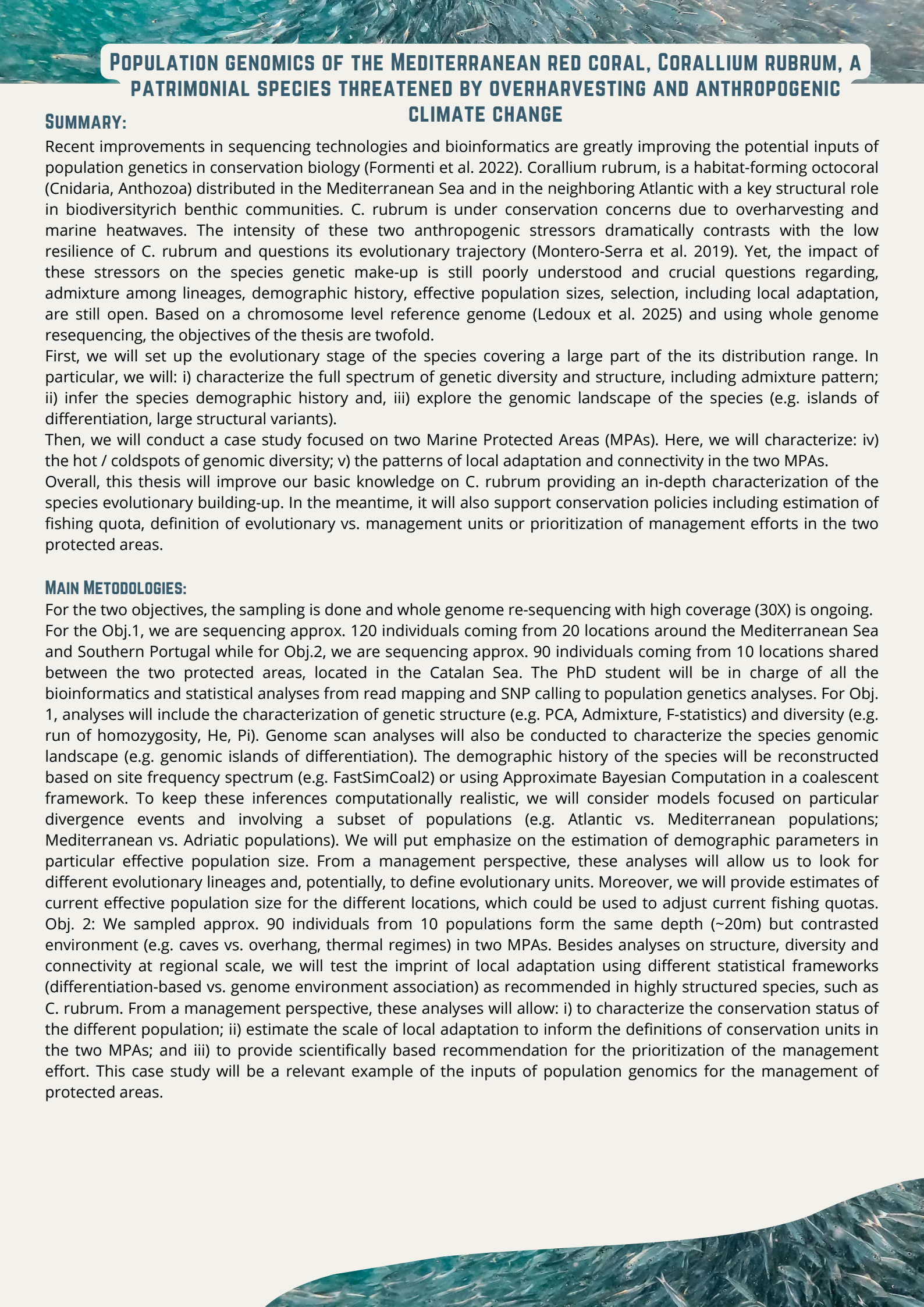




POPULATION GENOMICS OF THE MEDITERRANEAN RED CORAL, *CORALLIUM RUBRUM*, A PATRIMONIAL SPECIES THREATENED BY OVERHARVESTING AND ANTHROPOGENIC CLIMATE CHANGE

SUMMARY:

Recent improvements in sequencing technologies and bioinformatics are greatly improving the potential inputs of population genetics in conservation biology (Formenti et al. 2022). *Corallium rubrum*, is a habitat-forming octocoral (Cnidaria, Anthozoa) distributed in the Mediterranean Sea and in the neighboring Atlantic with a key structural role in biodiversity-rich benthic communities. *C. rubrum* is under conservation concerns due to overharvesting and marine heatwaves. The intensity of these two anthropogenic stressors dramatically contrasts with the low resilience of *C. rubrum* and questions its evolutionary trajectory (Montero-Serra et al. 2019). Yet, the impact of these stressors on the species genetic make-up is still poorly understood and crucial questions regarding, admixture among lineages, demographic history, effective population sizes, selection, including local adaptation, are still open. Based on a chromosome level reference genome (Ledoux et al. 2025) and using whole genome resequencing, the objectives of the thesis are twofold.

First, we will set up the evolutionary stage of the species covering a large part of its distribution range. In particular, we will: i) characterize the full spectrum of genetic diversity and structure, including admixture pattern; ii) infer the species demographic history and, iii) explore the genomic landscape of the species (e.g. islands of differentiation, large structural variants).

Then, we will conduct a case study focused on two Marine Protected Areas (MPAs). Here, we will characterize: iv) the hot / coldspots of genomic diversity; v) the patterns of local adaptation and connectivity in the two MPAs.

Overall, this thesis will improve our basic knowledge on *C. rubrum* providing an in-depth characterization of the species evolutionary building-up. In the meantime, it will also support conservation policies including estimation of fishing quota, definition of evolutionary vs. management units or prioritization of management efforts in the two protected areas.

MAIN METODOLOGIES:

For the two objectives, the sampling is done and whole genome re-sequencing with high coverage (30X) is ongoing. For the Obj.1, we are sequencing approx. 120 individuals coming from 20 locations around the Mediterranean Sea and Southern Portugal while for Obj.2, we are sequencing approx. 90 individuals coming from 10 locations shared between the two protected areas, located in the Catalan Sea. The PhD student will be in charge of all the bioinformatics and statistical analyses from read mapping and SNP calling to population genetics analyses. For Obj. 1, analyses will include the characterization of genetic structure (e.g. PCA, Admixture, F-statistics) and diversity (e.g. run of homozygosity, H_e , P_i). Genome scan analyses will also be conducted to characterize the species genomic landscape (e.g. genomic islands of differentiation). The demographic history of the species will be reconstructed based on site frequency spectrum (e.g. FastSimCoal2) or using Approximate Bayesian Computation in a coalescent framework. To keep these inferences computationally realistic, we will consider models focused on particular divergence events and involving a subset of populations (e.g. Atlantic vs. Mediterranean populations; Mediterranean vs. Adriatic populations). We will put emphasis on the estimation of demographic parameters in particular effective population size. From a management perspective, these analyses will allow us to look for different evolutionary lineages and, potentially, to define evolutionary units. Moreover, we will provide estimates of current effective population size for the different locations, which could be used to adjust current fishing quotas. Obj. 2: We sampled approx. 90 individuals from 10 populations from the same depth (~20m) but contrasted environment (e.g. caves vs. overhang, thermal regimes) in two MPAs. Besides analyses on structure, diversity and connectivity at regional scale, we will test the imprint of local adaptation using different statistical frameworks (differentiation-based vs. genome environment association) as recommended in highly structured species, such as *C. rubrum*. From a management perspective, these analyses will allow: i) to characterize the conservation status of the different population; ii) estimate the scale of local adaptation to inform the definitions of conservation units in the two MPAs; and iii) to provide scientifically based recommendation for the prioritization of the management effort. This case study will be a relevant example of the inputs of population genomics for the management of protected areas.

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PLACE OF WORK

CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, Terminal de Cruzeiros do Porto de Leixões

WILL THE PROPOSAL RESEARCH IDEA BE FUNDED BY A SPECIFIC PROJECT?

Yes, by REDCOR-BGE

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