

# COMPARATIVE POPULATION GENOMICS ILLUMINATES SPECIES BOUNDARIES IN EUNICELLA AND ALCYONIUM OCTOCORALS

## SUMMARY:

The process of speciation is a central topic in evolutionary biology due to its role in shaping biodiversity patterns. Yet, the study of speciation is challenging particularly in recently diverged species, in which reproductive isolation is not complete and gene flow and hybridization can still occur.

The main objective of the PhD thesis will be to investigate species boundaries in two octocoral genus representing six accepted octocoral species: *Eunicella verrucosa* (Pallas, 1766), *E. cavolini* (Koch, 1887), and *E. singularis* (Esper, 1791), *Alcyonium digitatum*, *A. acaule* and *A. coralloides*. The six species are considered as habitat-forming species supporting biodiversity rich communities and show contrasted distribution range in the Atlantic and/or in the Mediterranean. Noteworthy, some of these species are under strong conservation concerns owing to recurrent mass mortality events linked to anthropogenic climate change.

Preliminary works conducted by our team using Kmer analyses and whole genome resequencing show potential for on-going hybridization between *E. singularis* and *E. cavolini* while the high divergence among Atlantic vs. Mediterranean populations of *A. coralloides* suggest the occurrence of two different species. In this context, the PhD student will: i) follow the characterization of the genetic relationships within and among the six different species; ii) infer their demographic history; iii) look for the genomic landscapes of differentiation and genes/genomic regions potentially involved in speciation process. To reach these objectives, the PhD student will implement state of the art bioinformatics and population genetics analyses to analyze a whole genome resequencing and a RNAseq dataset.

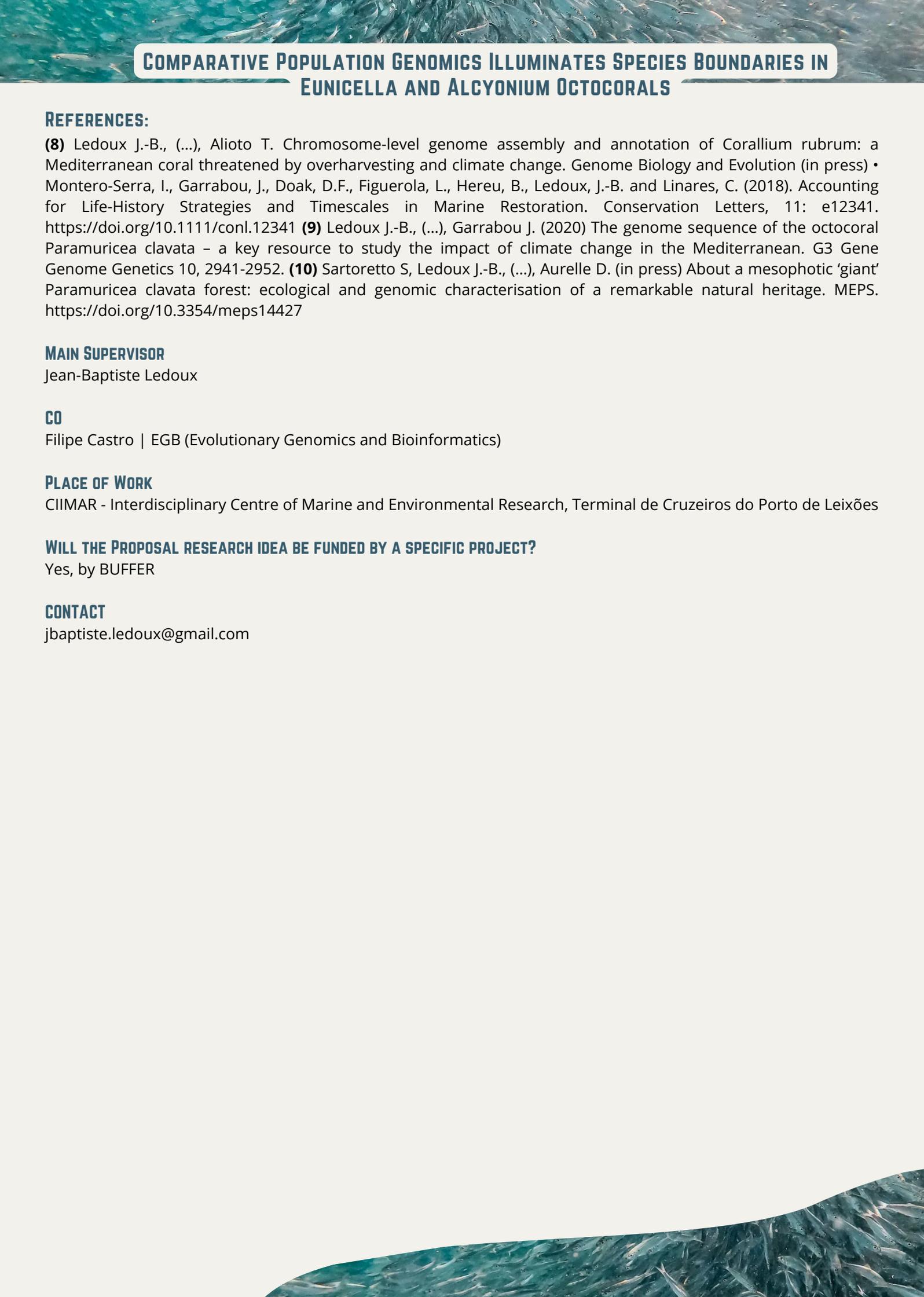
Overall, this thesis will improve our basic knowledge regarding speciation in the marine species providing support to refine biodiversity estimation in octocorals.

## MAIN METODOLOGIES:

Using whole genome re-sequencing data from approx. 60 individuals coming from 13 localities in the six species, the PhD student will i) characterize the full spectrum of genetic diversity and structure, including admixture within and among the six species; ii) infer the species demographic history using approximate Bayesian computation in a coalescent framework, iii) explore the genomic architecture and landscape of differentiation among species (e.g. islands of differentiation, large structural variants). These results will be complemented by an in-depth analysis of RNAseq dataset on the same species to further refine the identification of genetic regions potentially involved in speciation process.

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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 BUFFER

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