

# LIFE PINNARCA

LIFE NAT/ES/001265



## DELIVERABLE DC5.1

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Report with the results of genotyping 200 individuals

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## Preamble

When submitting the project and proposing the deliverables linked to the genetic part and in particular the C5 deliverable, we had agreed to genotype 200 individuals from open sea and lagoons in order to be able to compare these populations at a genetic level and to obtain information on the genetic structure of the remaining populations, including hybrids (*P. nobilis* x *P. rudis*). This analysis could have helped us to understand, if genetic-based, the reasons why fan mussels survive in the reservoirs and to improve the genetic diversity of the restocking population, if need be. Unfortunately, after the C2 and C3 censuses, it turned out that there were not enough individuals left alive in the open sea to complete the sequencing of 200 individuals.

However, during the first phase of the Pinnarca Life project, a sampling effort has been achieved by the partners UAEGEAN, CIMAR UA, IEO CSIC, IRTA, IMEDMAR-UCV, UNINA-DB and IOPR, on resistant, sensitive (*i.e.* morbid then dead) and hybrid individuals for both genetic analysis and pathogen detection. Therefore we had to change our route from genotyping 200 individuals and we used the available tissues and other samplings (such as haemolymph) for various pathogen detection purposes in the sanctuary populations and to provide the first clues for the resistance at the genetic and microbiota levels.

## 1. Detection of pathogens through transcriptomic and genomic

### 1.1. Occurrence of *Haplosporidium pinnae* in the sanctuary area of Thau Lagoon (Occitany, France)

Since the beginning of the MME in Spain in 2016, nearly one hundred percent of monitored open sea water populations have been decimated around the Mediterranean Sea. The only refuge areas with living *P. nobilis* populations were found in coastal lagoons. As mentioned in the DA.1 for France, the Thau lagoon is home to a vitally important population of *P. nobilis* and was thought to be safe from the parasite *Haplosporidium pinnae*.

However, following a field survey with tissue sample collection during summer and fall 2020, molecular infection with *H. pinnae* could be detected for the first time individuals from Thau lagoon.

Tissue biopsies using a non-lethal method described elsewhere (Bunet *et al.*, 2021) were conducted on 6 *P. nobilis* (Table 1): 4 healthy individuals from Meze plagette and two moribund individuals from the Lafarge site exhibiting symptoms of the disease during summer 2020 (Fig. 1).

