Project: Effects of restocking on the local adaptation of natural populations of two emblematic molluscs in Brittany

Acronym: README

Laboratory: LEMAR (UMR 6539)

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PROJECT SUMMARY:

Hatchery-raised juveniles are routinely used to support declining marine populations due to overfishing and/or adverse environmental conditions[1]. This approach is of particular interest in Finistère, which has on its territory the only two French hatcheries able to produce spat to repopulate the stocks of two emblematic species, the scallop *Pecten maximus* (Ecloserie du Tinduff) and the European abalone *Haliotis tuberculata* (France Haliotis). For *P. maximus*, the regular seeding of hatchery-raised spat in the Bay of Brest since the years 80[2,3], and in the Normano-Breton Gulf, particularly in the Bay of Granville, constitutes a peculiarity of French fisheries. *For H. tuberculata*, massive mortalities were recorded in northern Brittany and Normandy between 1998 and 2004[5,6], causing the decline of natural populations or even their collapse. Efforts are currently underway to assess the possibility of restocking depleted abalone stocks with hatchery-raised spat.

The enhancement of natural populations with farmed individuals can alter the adaptation of these populations to environmental variability[7], and thus threaten the sustainability of the fisheries concerned. In the case of *P. maximus*, mass seedings of hatchery spat has little effect on the genetic diversity of the natural population of the Bay of Brestt[12], probably due to gene flow from the Iroise Sea[13]. Nevertheless, seeded individuals seem to actively contribute to the reproduction of the local population [12], which raises a major question: to what extent can hybridization between seeded and natural individuals impact the local adaptation of natural populations in the face of environmental variability? This question is all the more significant as the same Brest spat has been used for several years to support various natural beds distributed from the Pertuis Charentais to the Normano-Breton Gulf. However, the monitoring of landings at Granville recently revealed a surprising proportion of scallops with a gonadal maturation pattern abnormally similar to that encountered in the Bay of Brest. This finding thus raised the question of the potential impact of seedings carried out since 2009-10 in Granville using Brest spat on the life traits of the local population of *P. maximus*. This questioning is reinforced by the significant and possibly adaptive genomic differentiation observed between the Bay of Brest and the Normano-Breton Gulf[13]. Concerning *H. tuberculata*, the genetic and adaptive differentiation of wild populations in Brittany and Normandy remains poorly understood. It is therefore crucial to fill this knowledge gap so as not to alter the adaptive potential, and therefore the long-term survival, of the stocks exploited through the planned restocking operations.

The questions posed concerning the effect of restocking on the local adaptation of natural populations are of major interest for the sustainability of fisheries. To answer these questions, the **README** thesis project is articulated around three axes combining genomics of natural populations and a common garden experiment: Axis 1: Study of genomic signatures of local adaptation in natural populations; Axis 2: Assessment of the local adaptation of abalone populations in common garden; Axis 3: Exploration of the possible effect of a genetic introgression between natural scallops and hatchery seedlings

DETAILED PRESENTATION OF THE PROJECT:

1 - Hypothesis and questions asked, state of the art, identification of scientific blocking points

To ensure the sustainability of coastal fisheries, hatchery-raised juveniles are regularly used to support populations that have declined as a result of overfishing and/or adverse environmental conditions[1]. This approach is of particular interest in Finistère, which has on its territory the only two French hatcheries able to produce spat to repopulate the stocks of two emblematic species, the scallop *Pecten maximus* (Ecloserie du Tinduff) and the European abalone *Haliotis tuberculata* (France Haliotis). For *P. maximus*, the regular seedings of hatchery-raised spat in the Bay of Brest since the years 80[2,3], and in the Normano-Breton Gulf, particularly in the Bay of Granville, constitutes a peculiarity of French fisheries. For *H. tuberculata*, massive mortalities were reported in northern Brittany and Normandy between 1998 and 2004[5,6], causing the decline of natural populations or even their collapse (e.g. Chausey). Hatchery-raised juveniles was initiated in 2004[7], and efforts are underway to assess the feasibility of restocking depleted abalone stocks with hatchery-raised spat.

The enhancement of natural populations from farmed individuals can alter the adaptation of populations to environmental variability[7], and thus threaten the sustainability of fisheries. Such a negative impact can result from an erosion of genetic diversity in hatcheries[8] and/or from domestication processes, which can greatly reduce the fitness of individuals born in hatcheries and introduced into the natural environment[9,10,11].

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Concerning *H. tuberculata*, the genetic and adaptive differentiation of wild populations in Brittany and Normandy remains poorly understood. It is therefore crucial to fill this knowledge gap so as not to alter the adaptive potential of stocks, and therefore their long-term survival, through the planned restocking operations.

The questions posed regarding the effect of restocking on the local adaptation of natural populations are of major interest for the sustainability of fisheries. To answer these questions, the **README** project has three objectives: **1/ Clarify the adaptive differentiation of populations of the two species along the coasts of Brittany; 2/ Evaluate whether stock enhancement can induce an introgression of natural populations by hatchery seedlings; 3/ Explore the possible effects of these introgressions on the local adaptation of natural populations**.

2 - Methodological and technical approach

To achieve the objectives described above, the README thesis project is structured around three lines of research. These three axes cover complementary approaches combining 1/ study of populations in their natural environment (Axes 1 and 3) and 2 /experimentation in a controlled environment (Axis 2).

Axis 1: Study of genomic signatures of local adaptation in natural populations

The first stage of the work will consist in evaluating the genetic differentiation of scallop populations distributed from the Bay of Brest to the Normano-Breton Gulf. RADseq genomic data (Restriction Associated DNA sequencing) obtained previously[13] will be re-analyzed using the recently published scallop genome as reference[14]. This analysis will include a large part of bioinformatics work which will be carried out on the DATARMOR platform (Ifremer). Alignment of RADseq data with the reference genome should make it possible to identify possible particular genomic regions involved in the adaptive differentiation of natural scallop populations along the Brittany coast. New high-throughput sequencing data obtained by the RADseq method as part of the collaboration conducted with the SMEL (https://www.smel.fr/) through the FEAMP COGECO project (Axis 3) will also be added to this genomic analysis of natural scallop populations.

Secondly, the genetic structure of natural abalone populations in Brittany and Normandy will be studied using 200 SNP markers (Single Nucleotide Polymorphism) genotyped within the framework of the FEAMP OURMEL project (coord. S. Roussel, UBO LEMAR) . This study will help define the spatial structure of natural abalone populations. Based on the insights from this analysis, RADseq sequencing will be performed to detect any adaptive divergence associated with the population structure previously identified.

Axis 2: Assessment of the local adaptation of abalone populations in common garden

This axis will be centered on a six-month experiment which will be carried out at Océanopolis within the framework of the OCEANOLAB project. Three abalone populations among those detected in Axis 1 will be compared in common garden by comparing their phenotypic performances under environmental conditions (temperature, light, even hydrodynamics) specific to each of the populations. The phenotypic differentiation of populations will be measured through different traits: e.g. shell growth, biometric measurements, energy metabolism, behavioral measurements. This common garden experiment will aim to assess the adaptive value of the phenotypic variability between natural populations. In addition, a hatchery batch will be added to the experiment to estimate the adaptive potential of hatchery-raised individuals.

Axis 3: Exploration of the possible effect of a genetic introgression between natural scallops and hatchery seedlings

This axis will be based on actions carried out on scallops from Granville in close collaboration with the SMEL within the framework of the FEAMP COGECO project. Winter sampling will be carried out in 2022-23 to collect 100 abnormally sexually mature scallops in winter and 100 non-mature scallops over the same period. A batch of 25 individuals will also be taken in the Bay of Brest. The genetic diversity of the samples will be studied with the RADseq method. This analysis will thus make it possible to determine whether the existence of the "abnormal" gonadal maturation patterns observed in certain scallops in Granville could be due to the introgression of the local natural population by hatchery-raised scallop of Brest origin and released in Granville.

3 - Positioning and scientific environment in the regional, national and international context

The README project is based on LEMAR's strong experience in the study of the scallop and European abalone. This experience covers a wide range of approaches addressing ecological, physiological, or genetic aspects. In particular, G. Charrier, co-supervisor of the thesis, has significant experience concerning the genetics of scallop populations[12,15,16,17,18,19].

The thesis will be carried out in a well-structured scientific environment with several funded projects. First of all, within the framework of the OURMEL project (FEAMP) 17k€ are intended for the genotyping/sequencing of abalone populations along the coasts of Brittany in Axis 1. On the other hand, a collaboration with the SMEL through the COGECO project (FEAMP) will finance the genotyping of scallop

samples in Granville described in Axes 1 and 3 (25k € dedicated to this action). Finally, the experimental part (common garden experience) will be carried out with a collaboration with Océanopolis through the OCEANOLAB project (CPER, UBO, Océanopolis). The OCEANOLAB project indeed offers the possibility of providing all the necessary facilities for the experimental part of Axis 2, and will also allow the development of a scientific outreach program in connection with the README project. This outreach activity will focus on the evolution of exploited populations of scallops and abalone in the face of climate change. It should be noted that the experiment described in the README project is scheduled to start in early 2023 in OCEANOLAB.

In addition, the project will be based on a collaboration with Florentine Riquet (INRAE - Sophia Antipolis), who has significant experience in genetics and genomics of populations, experimental ecology and bioinformatics. The collaboration with F. Riquet is part of an interdisciplinary project she is developing to apply for a CNRS position (section 52): "Human activities and environmental conservation: the case of the abalone *Haliotis tuberculata*".

At European level, the project will be based on a collaboration with Ewan Harney (Institute of Evolutionary Biology CSIC-UPF, Barcelona, Spain). E. Harney has significant experience concerning the molecular study of abalone[20,21] and also conducted a common garden experiment to study the basis for the phenotypic diversity of European scallop populations during a post-doc at LEMAR under the direction of G. Charrier (article in prep). The collaboration with E. Harney will therefore be very useful in carrying out the common garden experiment planned in Axis 2.

Finally, an international mobility in Canada will be expected for the doctoral student, in order to allow him to go and work for a few months in the team of Ian Bradbury (Bedford Institute of Oceanography, DFO, Canada). This team has significant experience in the genomic analysis of populations of scallops and in the identification of signatures of adaptive divergence of populations[22,23,24] which should be very profitable to approaches in Axes 1 and 3 of the README project. .

4 - Scientific and partnership context: general elements (ERC, CPER, FEDER, Breizhcop, etc.)

On the one hand, the project will be carried out in close collaboration with various regional socio-economic actors. OThe project will be carried out in collaboration with the SMEL (https://www.smel.fr/) for the two species, whether through the OURMEL or COGECO project. The work on abalone will be also carried out in close collaboration with France Haliotis.

On the other hand, the README project will benefit from the fact that the supervisors are integrated into various high-level scientific networks, whether nationally or internationally. At the national level, the three co-supervisors of the thesis are involved in the GDRi MarCo (Marine Connectivity; https://wwz.ifremer.fr/gdrmarco/). In addition, G. Charrier is a member of two international networks: 1/ CeMEB consortium (Linnaeus Center for Marine Evolutionary Biology, Univ. Göteborg, Sweden; https://www.gu.se/en/cemeb-marine-evolutionary-biology), which is interested in the processes governing the evolution and adaptation of marine organisms; 2/ ICES WGAGFA (ICES Working Group on Application of Genetics in Fisheries and Aquaculture; https://www.ices.dk/community/groups/Pages/WGAGFA.aspx), which focuses on the application of genetic and genomic tools for the conservation and management of exploited marine species. All these networks will provide the doctoral student with a rich and stimulating scientific context, conducive to his progress.

5 – Expected profile and skills of the candidate

The candidate must have a strong experience in population genetics, and must have the necessary skills to conduct the bioinformatics analyzes planned in the project. In addition, a solid background in marine ecology will be greatly appreciated. The candidate should be able both to develop innovative approaches to population genomics, but also to work in close relation with ecologists studying the functioning of scallop

and abalone populations, as well as with non-academic partners involved in the exploitation and management of stocks (hatcheries, fishing industry professionals).

6 – Bibliographic references

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