

Role of local adaptation, phylogeographic history and connectivity in the structuring and functioning of great scallop populations (*Pecten maximus*)

PhD Supervisor: Pierre BOUDRY (Ifremer, LEMAR; pierre.boudry@ifremer.fr)

Co-supervisor: Grégory Charrier (UBO, LEMAR; gregory.charrier@univ-brest.fr)

1. Scientific and economic background

Understanding the impact of climate change on modern biodiversity is currently a central question in ecology and a major concern for the management of natural living resources. Yet it is highly challenging to predict how species will respond to new environmental conditions, since their resilience potential is tightly linked to their evolutionary history and to the range of intra-specific adaptive variation existing among populations (e.g. Sandford & Kelly 2011). In this context, **species distributed over a large latitudinal gradient may be the most appropriate models for investigating the evolutionary dynamics of species facing environmental change**, since they are generally structured into populations that may be locally adapted to a broad range of latitude-dependent pressures.

The great scallop (*Pecten maximus*) is a marine bivalve distributed along the North-East Atlantic coasts, from Morocco to Norway. The great scallop records daily environmental variations in its calcified shell throughout its life, by depositing daily growth increments on the outer edge the shell (Chauvaud *et al.* 1998). Growth in scallops is strongly influenced by environmental factors, such as temperature (Heilmayer *et al.* 2004). Thus, **the shell of *P. maximus* can act as a high-frequency archive and proxy for reconstruction of climatic conditions** experienced by individuals during their life span, and shells from archeological sites can be used to assess paleoenvironmental changes (Chauvaud *et al.* 2005). A large variation in size and growth has been observed along the latitudinal gradient, between northern (Scotland – Norway) and southern (Galicia – Bay of Biscay) populations, suggesting the possibility of plastic and/or adaptive responses to environmental variability (Chauvaud *et al.* 2012).

Moreover, the great scallop is of high economical interest for European fisheries, and is mostly exploited in France and UK (Beaumont & Gjedrem 2007). Most of landings stem from the English Channel, where management units are only based on geographical and political bases. However, the sustainability of scallop fisheries is possible only if these management units are defined according to the biological differentiation of exploited stocks. Therefore, it is crucial to get a good knowledge about: 1/ the population structure and connectivity, and 2/ the resilience capacities of these populations in the face of environmental changes.

2. Hypotheses and scientific questions

Recent microsatellite-based studies have shown a clear (presumably) neutral genetic differentiation between two groups of populations, *i.e.* Norwegian and Atlantic (*i.e.* from Galicia to British Isles), which may reflect phylogeographic divergence of these populations (Hold 2012, Morvezen *et al.* 2016). Interestingly, this phylogeographic structure corresponds with phenotypic differentiation in size and growth along the latitudinal gradient (Chauvaud *et al.* 2012), raising the possibility that latitudinal variation in growth may also be under genetic control, possibly reflecting adaptive processes (Stillwell 2010). Variation in shell growth along the latitudinal gradient may be linked, at least partly, to **neutral evolution of traits resulting from distinct phylogeographical histories (Hypothesis 1)**. Moreover, this phenotypic differentiation may also result from **local adaptation processes associated with latitudinally varying selective pressures (Hypothesis 2)**.

To the opposite, at a smaller geographic scale between Galicia and northern British Islands (Scotland), results from Chauvaud *et al.* (2012) show still a high variation in size and growth, while genetic markers suggest a lack of population structure a high connectivity (Hold 2012, Morvezen *et al.* 2016). These opposed results may suggest that the latitudinal variation in growth observed in *P. maximus* (Chauvaud *et al.* 2012) might reflect **phenotypic plasticity in response to variable environments (Hypothesis 3)**. Indeed, growth rate of individuals translocated between populations is clearly plastic in response to environmental variability (Buestel *et al.* 1987).

Results obtained so far do not allow to test thoroughly the likelihood of each of the three alternative and not mutually exclusive hypotheses. Understanding the extent of genetic control is crucial for the development of scallop shells as proxies of environmental change. Therefore, the PhD project proposes to study the respective role of local adaptation, phylogeographic history and connectivity on the phenotypic differentiation of great scallop populations along a latitudinal gradient extending from Norway to Galicia.

3. Methodology

The project will consist in a population genomics study of great scallop populations along a latitudinal gradient, using a RAD-Seq approach (Restriction Site Associated DNA Sequencing). This Next Generation Sequencing method allows the simultaneous analysis of thousands of SNPs (Single Nucleotide Polymorphisms) using the Illumina technology (Baird *et al.* 2008). The first objective of this study will be to thoroughly analyze the **phylogeographic** structure of natural great scallop populations and evaluate the level of **neutral evolutionary divergence**. The second goal will be to conduct a genome scan analysis to detect **genomic signatures resulting from differential selective pressures, and outlier loci** that significantly differ between populations, reflecting local selective forces.

4. Profile and skills of the candidate

The candidate must have a strong experience in population genetics. He also must have a solid background in marine ecology. The candidate must be able not only to develop new population genomics approaches, but also to work in tight collaboration with ecologists focusing on the functioning of scallop populations, as well as fisheries biologists interested in the management of scallop populations.

5. References

- Artigaud *et al.* (2014a) *J Proteomics* **105**, 164-173
Artigaud *et al.* (2014b) *Marine Genomics* **15**, 3-4
Baird *et al.* (2008) *PLoS ONE* **3**(10): e3376
Beaumont & Gjedrem (2007) *Genimpact final scientific report*, 83-90
Buestel *et al.* (1987) *Haliotis* **16**, 463-477
Chauvaud *et al.* (1998) *J Exp Mar Biol Ecol* **227**, 83-111
Chauvaud *et al.* (2005) *Geochem Geophys Geosyst* **6**, Q08001
Charrier *et al.* (2012) *Conserv Genet Resour* **4**, 931-934
Chauvaud *et al.* (2012) *PLoS ONE* **7**, 1-10
Heilmayer *et al.* (2004) *Funct Ecol* **18**, 641-647
Hold (2012) PhD dissertation, Bangor University
Morvezen *et al.* (2016) *Cons Gen* **17**, 57-67
Sanford & Kelly (2011) *Annu Rev Mar Sci* **3**, 509-535
Stillwell (2010) *Oikos* **119**, 1387-1390
Thébault *et al.* (2009) *Limnol Oceanog* **54**, 1002-1014