LabexMER

"A changing ocean"

LabexMER - Axe 6	Research project 2012-2014	16/02/2012

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1. AXIS 6 : EVOLUTION OF MARINE HABITATS AND ADAPTATION OF POPULATIONS : RETROSPECTIVE APPROACHES AND PREDICTIVE MODELING

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1.1. SCIENTIFIC CONTEXT, SCIENTIFIC QUESTIONS, 1O-YEARS VISION

In the frame of global changes, major disturbances of marine ecosystems result in individual responses (behaviour, physiology, evolution, ontogeny) to environmental stress which therefore affect biological traits (growth, reproduction, fecundity, immunity, etc.), adaptive capacity of living organisms and spatio-temporal dynamics of populations (Feder *et al*., 2000). At a larger scale, physical habitats, distributions of populations and structure of communities are also modified by environmental changes (*e.g*. temperature, contamination by chemicals, eutrophication, hydrodynamics and morphodynamics). Despite the large number of bio-physical interactions involved, most habitat and niche models still keep a low resolution regarding the biological mechanisms (Guisan & Thuiller, 2005). A step forward would consist in fully integrating ecophysiology, evolutionary, macroecology and ecological niche approaches to address issues of biodiversity conservation (Kozak *et al*., 2008 ; Kearney & Porter, 2009). This is why the coupling between population dynamics, models of bioclimatic envelopes, georeferenced environmental data and evolutionary biology is now emerging in terrestrial ecology (Keith *et al*., 2008; Kozak *et al*., 2008). Application of such concepts and tools to marine ecology is certainly innovative and would improve existing methods and models which have shown their limitations (Klok *et al*., 2009).

We propose to adapt this emerging methodological framework to analyse and simulate the changes of marine biodiversity due to environmental and anthropogenic pressures. For this purpose, specific objectives have been identified:

- Assess adaptive and physiological responses through (i) the reconstruction of past evolution by using sclerochronology, sclerochemistry, molecular and physiological proxies, (ii) the quantification of adaptive capacity and evolution by combining experimental approaches, molecular biology and quantitative genetics,

- Characterise habitats and biological communities through analysing and identifying structuring factors (*e.g*. morphosedimentary and hydrodynamics forcing, engineering invasive species, implantation of marine renewable energy technologies, etc.), mapping habitats mosaics and studying species assemblages in different types of environment,

- Formulate and couple interactions to simulate (i) physiological responses, (ii) changes of biotopes, distributions and ecological niches for target species, (iii) benthic and pelagic population dynamics, (iv) distribution of communities,

- Reconstruct past changes, test hypotheses and simulate scenarios of future changes by integrating models at different scales (organism, population, and habitat).

By analysing and coupling marine habitats, ecosystem functioning and adaptive responses, we will more precisely address the following questions:

- At what level and how the interactions between physiological plasticity, adaptation by populations and environmental changes must be formalized?

- What are the consequences of such interactions on ecological niches, and at what scales can they be observed?

- Which mathematical models must be developed to simulate the spatio-temporal evolution of habitats, species and communities?

- What are the effects of conservation and restoration strategies on these biological levels?

The Labex MER partners are already deeply involved in such a multidisciplinary project – *e.g*. habitat mapping, database management, operational modelling, monitoring networks, and functional approaches in ecophysiology, biotic interactions and sclerochronology. The project relies upon existing National and European initiatives on marine monitoring and observatories, evolutionary responses of fishes and bivalves, use of biological archives and paleo-oceanography proxies to reconstruct past environment, habitat mapping and modelling, biogeochemical and operational modelling. LabexMER will provide the necessary incentive to build synergies and address the challenges related to multiple scales interactions and complexity (*e.g*. short term/long term, individuals/population/ecosystem, and mosaics of habitats).

Major outcomes are expected at a scientific level. Results will provide a better understanding of adaptive capacity, population dynamics and interactions between habitats and communities organisation. Our multidisciplinary approach will develop and validate analytical techniques, yield novel mathematical models capable to handle ecosystem complexity and improve the predictions of ecosystem changes. Our findings will also contribute to the improvement of scientific expertise and benefit to public policies regarding the conservation of marine area, the assessment of marine services and the ecological status of coastal zones.

1.2. OBJECTIVES FOR THE NEXT THREE YEARS AND SPECIFIC ACTIONS

Our work plan has been based on the inventory of existing or new projects conducted by the partners, the identification of partner strengths and of the main methodological bottlenecks regarding the effect of environmental changes on species distributions, assemblages and adaptation. This analysis resulted in a proposition of three major topics which are presented below (see also Fig. 1). In a second step, the opportunities offered by the LabexMER regarding capacity and synergies building were considered.
The topics described below go beyond the 3 years plan and correspond to our thematic priorities. The research activities which have been identified have already started or will start during the first 2 years. Specific actions related to this work plan are summarized at the end of section 2 and in section 3 in relation to the Labex funding scheme.

Figure 1. Results of the inventory and analysis conducted in preparatory workshops. Thematic fields are presented in the inner circle (blue). Related research activities are listed in the outer circle (orange). See text for a more complete description of Axis 6 strategy.
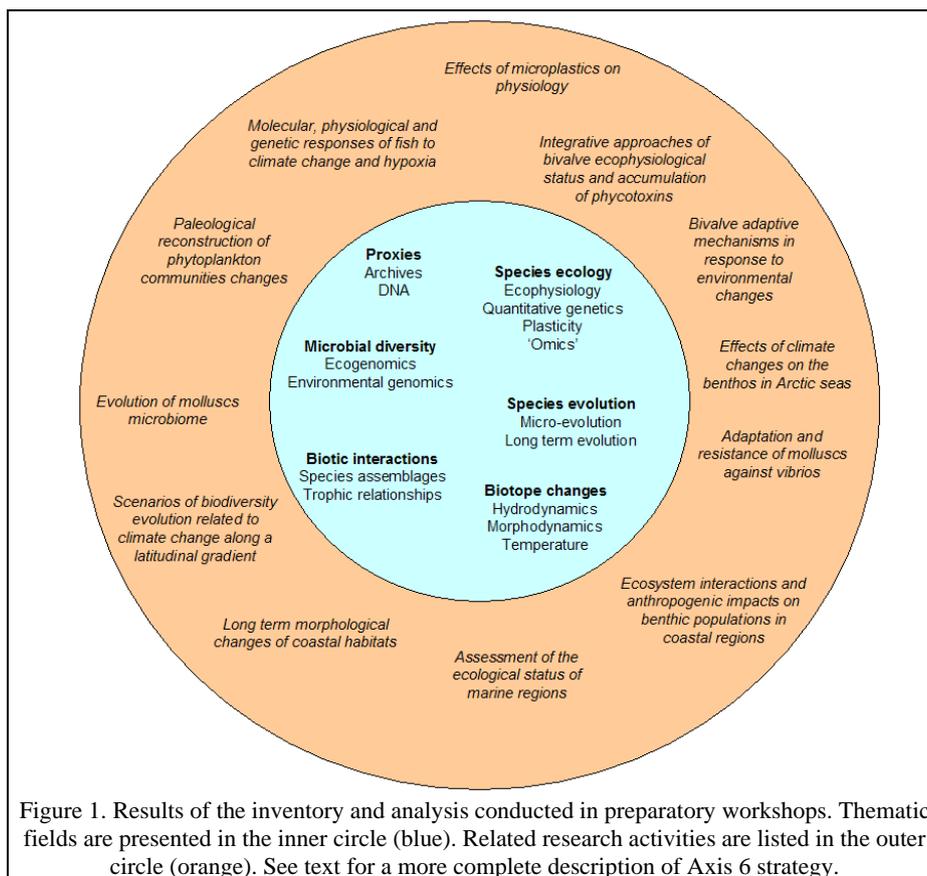
a) Topic 1. Functional microbial and macrobiota biodiversity

Microorganisms (virus, bacteria, and unicellular eukaryote) are spectacularly diverse, both phylogenetically and metabolically. The estimation of the species richness for a given environment is a crucial piece of information. In this area, a major breakthrough comes from the use of 'omics' to analyse the functional biodiversity of microorganisms. Metagenomics is a rapidly growing field of research that has had a dramatic effect on the way we view and study the microbial world. By permitting the direct investigation of bacteria, viruses and fungi irrespective of their cultivability and taxonomic identities, metagenomics has changed microbiological theory and methods and has also challenged the classical concept of species.

We identified the following innovative actions which will build new synergies between teams:

- *Phytoplanktonic and bacterial functional biodiversity.* Microbial biodiversity will be compared in different European sites contrasted in nutrient availability and in sediments displaying different levels of O_2/organic matter/pollutants. The overall objective is to identify species particularly sensitive or resistant to a specific condition that could be used as efficient indicators of good environmental status. Metagenomic approaches will be used and those data will be integrated in trophic and ecosystem models.

- *Paleoecological reconstruction of microbe communities (bacteria and phytoplankton).* Phytoplankton and bacterial genetic materials could accumulate in the sea bottom sediments, and in some abnormal calcified shells. These past phytoplankton and bacterial communities will be used to assess microbial diversity changes over the last century under contrasting conditions (eutrophication versus natural/climate driven changes). Researches on total phytoplankton biodiversity will use metagenomics methods.

- *Microbiome of Mollusc: theory of hologenome.* Zilber-Rosenberg & Rosenberg (2008) define the hologenome as the sum of the genetic information of the host and its microbiota. They

consider the holobiont (animal or plant with all of its associated microorganisms) as a single dynamic entity in which a vast amount of the genetic information and variability is contributed by the microorganisms, eventually leading to an important role of the microbial symbionts in the adaptation and evolution of the holobiont. We propose to assess the role of microbiome in the health but also on disease evolution of molluscs. Monospecific and multispecific biofilms occurring at the epithelium and secretions interfaces will be in particular studied and compared with the environmental microflora. How this microbiome is modulated by a slight increase of temperature. Different genomic methods will be used to characterize the microbiota *e.g.* metagenomic, DGGE, DHPLC.

Regarding macro-biota biodiversity, we plan to work at the level of ecological and biological life history traits (size, trophic resources and trophic level, feeding, substrate selection, habitat…) which are key features to explain the structure and functioning of communities in responses to changes (Archaimbault *et al.*, 2010). Though available data on species communities are often scarce, we can rely upon existing databases which contain information on benthic habitats and associated macrobenthos in a series of study sites along the Brittany coastline. In addition, Dynamic Energy Budget (DEB) theory has recently gain in popularity and been more and more applied at the individual and population levels. DEB theory specifies the processes of substrate (food, nutrients, light) uptake and use (maintenance, development, growth, reproduction) for all organisms (micro-organisms, animals, plants) in a single consistent and coherent framework covering their full life cycle (see also Topic 2 below). It offers a coherent and powerful framework for describing and analysing biological traits. We will therefore develop methods associating statistical approaches with matrices of the main ecological and biological traits of key species and energy-based individual models to build indicators of functional biodiversity. The results will feed Topic 3 on habitat modelling.

b) Topic 2. Physiological and adaptive response to environmental changes

Lavergne *et al.* (2010) stressed that there is evidence of rapid adaptive evolution in response to climate change, but little is known on its effects on population dynamics and shifts of species ranges, which also depend on biotic interactions (competition, predator/prey relationships, positive interactions). A major breakthrough is therefore expected from the combination of species ecophysiology, species micro-evolution (with changes occurring over several generations) and biotic interactions which shape species assemblages and responses to environmental changes.

To address such challenges, Labex teams will work in synergy along the following directions:

- Ecophysiological approaches (experimental and field challenges, individual performance, proxies, biochemical and molecular characterization of adaptation and acclimation systems) and quantitative genetics (QTL approaches, genome scan) on key species (molluscs and fish) will be combined to analyse physiological processes and associated acclimation or adaptive mechanisms.

- The mineralized parts of marine organisms (*e.g.*, mollusc shells, fish otoliths, foraminifera) are known for their ability to faithfully record environmental conditions and life history traits of these animals. We will characterize proxies by ecophysiological and environmental approaches (*e.g.* sclerochronology, sclerochemistry) and develop sequencing of DNA fragments of calcified archive to identify (i) coding systems essential to adapt to fluctuating environments, and (ii) microorganisms controling diseases or abnormal toxicities. Such data will be used to reconstruct past changes and to test and improve populations and habitat models (see Topic 3).

- We will apply these methods to assess the effect of global change (temperature increase, hypoxia, microplastics, toxic phytoplankton, emergence of pathogens...) on physiological, behavioral, cellular and molecular responses, and genetics of various sentinel organisms (bacteria, phytoplankton, algae, invertebrates and fishes).

- We will develop and implement evolutionary traits within the Dynamic Energy Budget modelling framework, one of the cornerstones of the modelling strategy defined in Topic 3.

c) Topic 3. Habitat modelling: a plural and progressive approach

Classical approaches of ecosystem functioning usually address separate scales: statistical habitat and niche models predict the spatial distribution of single species; biogeochemical, food web and food chain models simulate trophic flows and account for biological interactions between functional groups; biologically-structured models consider species bioenergetics and demographic characteristics to assess individual and population responses to environmental changes. These approaches refer to several definitions in the field of ecology (Lavergne *et al*. 2010). Fundamental niche is the full range of environmental conditions defined by species physiological tolerances and can be assessed through statistical methods which are implemented in habitat models. Realized niche is the region of the fundamental niche to which the species is restricted due to interspecific interactions, limited dispersal in relation to ecosystem connectivity, and perturbations. Habitat preferences of a given species are alternatively defined as ecological traits and habitat modelling combines abiotic characters (biotopes) and associated biological communities. More mechanistic population and community models account for the species biological traits which are related to behavioural and physiological features – *e.g.* reproduction strategy, growth, maximum size, maintenance, feeding preferences, life span, development stages, motility. However, as stated by Lavergne *et al*. (2010), most of the models used to predict species ranges and community dynamics generally ignore evolution and assume that the statistical or mechanistic relationship between species abundance and environmental characteristics remains unchanged – though there is more and more evidence that evolution mechanisms can act at a scale of several generations.
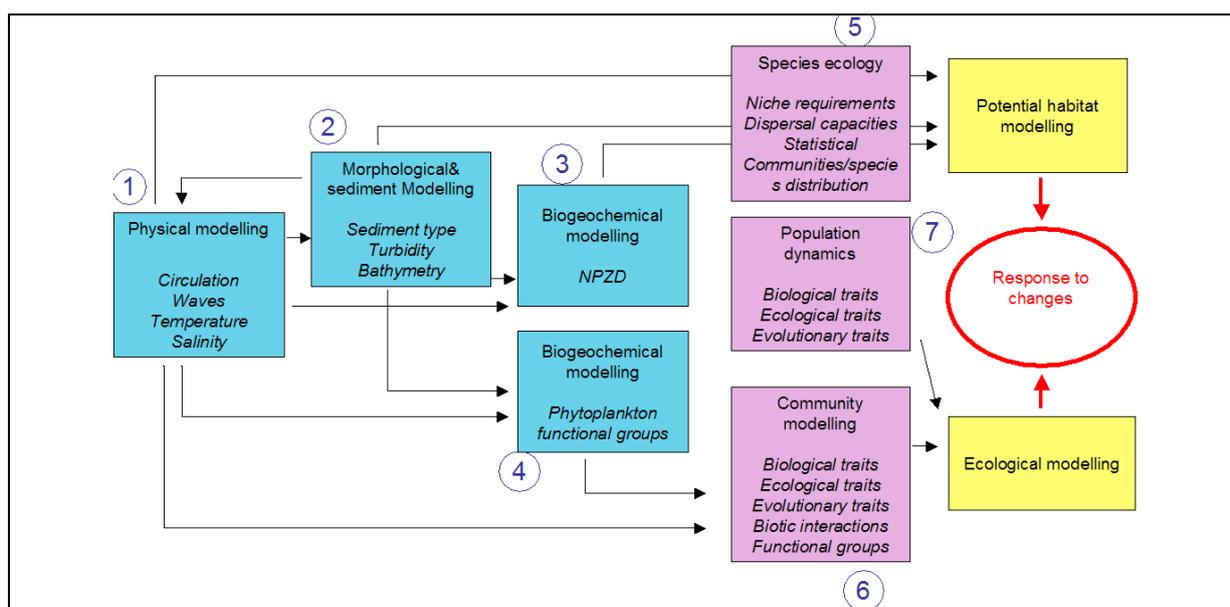
Figure 2. Habitat modelling steps showing types of modelling and relations between modelling approaches. Blue boxes correspond to biotopes. The green box relate to potential habitat modelling which result from the combination between niche modelling and biotope maps or models. Mechanistic ecological models (purple boxes) allow to couple and simulate biological and physical processes. Numbers refer to issues given below and related to habitat evolution under environmental changes or pressures:

1- changes of salinity fields in estuaries related to the variability of river discharge; effects of engineering works or coastal defences on velocity and wave fields;

2- effect of marine wind and tidal farms on sediment types; morphological dynamics of tidal inlets in relation to sea-level variation and storm events;

3- eutrophication due to nutrients inputs from rivers;

4- shift in phytoplankton populations under N/P/Si ratio changes in riverine inputs;

5- potential distribution of a single species – macrophytes, macrozoobenthos;

6- changes in food web flows and community structure due to habitat destruction (dredging), introduction of new species, temperature changes;

7- assessment of ecosystem carrying capacity for exploited species in response to fishing and culture pressure, and environmental changes.

It is clear that the number of interactions, scales and response times of biological and physical components make marine ecosystems complex systems. This makes a complete "end to end" modelling difficult and perilous. Our modelling strategy is therefore based on a step by step approach described in Fig. 2. Key abiotic factors can already be simulated over space and time. They include hydrodynamical features (*e.g.* waves, currents, flushing time, and stratification), hydrological characteristics (*e.g.* temperature, salinity), sediment patterns (*e.g.* sediment types, turbidity). Some of them are likely influenced by biogeochemical processes, so that feedback from biological modelling is expected. Biogeochemical NPZD (Nutrient, Phytoplankton, Zooplankton, and Detritus) models represent a step forward and can be developed further by including functional groups. Habitat modelling consists in assessing the "niche" of a given species or assemblages based on the preferences resulting from environmental constraints (most often physical and hydrological, but possibly biological). Potential habitat modelling will result from the combination of niche requirements and information on physical or biogeochemical parameters collected from existing databases and maps or produced by biotopes models. More advanced process-oriented models are based on mechanistic formulations of biological traits, individual life history and population dynamics and can be fed by the habitat and biotopes models seen above. A major breakthrough will consist in building on recent developments of evolutionary biology and community ecology to improve ecological forecasting as seen in Topic 2.

The afore described modelling architecture will be the basis for our modelling work plan. It will benefit from on-going and future research projects on biogeochemical, habitat and ecological modelling in several areas (some of which have been used to illustrate the step by step approach in Fig. 2).

This strategy will take advantage of Labex funding to further address the following challenges:

- Improve biotope modelling, especially accounting for coupling processes between hydrodynamics, hydrology and sediment transport
- Improve statistical methods for habitat modelling *e.g.* validation, uncertainty, prediction of temporal changes, building of a modelling toolbox.
- Develop multi species and community models, accounting for multiple direct and indirect interactions.
- Combine evolutionary biology and community ecology, which is the major cornerstone in modelling long term ecosystem changes.

d) Summary of specific actions

With respect to this research agenda, we are conducting several types of actions:

- Labeling of national and European projects. A first series of new research proposals have been examined and given full approval by our Steering Committee in January 2012 (ANR white call, ANR Young Scientist call, European call for International Training Network). We expect that the letter of support by Labex Mer will reinforce proposal value. Our Steering Committee will examine other proposals and encourage preparing proposals along the thematic lines which have been defined above.
- We will also proceed to the labeling of *postdocs* and *PhD*s. We will initiate scientific discussions within our partnerships to facilitate and encourage the definition of *PhD* and *postdoc* topics consistent with our research priorities and reinforcing our partnership.
- A call for small projects will be launched in January 2012 and repeated every year. The objective is to give opportunities to scientists to test new ideas (see section 3.5 for an indicative budget).
- Both our axis and axis 2 ("Complexity and efficiency of the biological pump") have submitted a proposition of International Chair of Excellence on Evolutionary Marine Ecology(see section 4.1 for more details). If accepted, it will be opened in 2012 for 3 years duration and it will contribute to objectives defined in topics 2 and 3.

- The same axes will propose a Thematic School on Innovative Modelling Methods to the 2012 Labex Training call for proposal. It will take place in Brest in 2013 and contribute to the implementation of the modeling work plan defined in topic 3 (see section 5 for more details).
- As part of our international collaborative plan, we will open an internal call regarding the funding of short term (few weeks) visiting scientists (see section 3.1 below).

e) Labex Impact

The three topics described above list actions and objectives which require different levels of synergies. They show the breakthroughs which are part of our research agenda – *e.g*. multiscale approaches, analysis of evolutionary traits and genetic markers, intensive use of metagenomic data, progressive and integrated modeling strategy.

Synergies between LEMAR (UBO, CNRS, IFREMER, IRD) and DYNECO (IFREMER) will be created through different mechanisms. For metagenomics, new national and European projects are submitted on phytoplankton diversity, development of methods for the evaluation of the ecological status of marine regions, and microbial diversity hosted by macro-organisms. An international *postdoc* on the analysis of metagenomic data has been given the highest priority for 2012. Regarding ecological modeling, the Thematic School which is proposed for 2013 is also a way to contribute to the interdisciplinary integration of knowledge (actually, this thematic tool is supported by axes 2 and 6, which will increase synergies within the Labex). Evolutionary ecology is a cornerstone in all three topics. The need for more development in this field has led the coordinators of axes 2 and 6 to propose an International Chair in 2012.

International visibility of our activities will be enhanced by the cutting edge research activities described in the three topics which match the international concerns related to the multi-scale ecological responses to environmental changes and pressures. The International Chair, international *postdoc* and Thematic School will have international impacts by attracting leading scientists in the field of ecology. Labex visibility will be reinforced by our strategy of scientific exchange through in- and out-going facilities. A list of foreign scientists potentially interested in visiting the Labex teams has been established in close relationship with the thematic priorities we have identified. Labex will also be visible through and will contribute to international networking. An International Training Network (ITN) named 'From DEB theory to Management: Training researchers for consilience in addressing complex ecological problem' will be submitted in 2012, with one Labex team as a full partner, another as an associated partner.

LabexMER funding will therefore help in increasing critical mass, supporting networking activities and strengthen synergies between the teams. It will also allow exploring new ideas by inviting foreign scientists, facilitating outgoing mobility, organizing Thematic School and testing experimental or computer programming innovative methods for which usual funding schemes are often inadequate or difficult to obtain – see budget breakdown thereafter.

Our strategy will have a leverage effect regarding new funding opportunities. Much is expected from the International Chair in Evolutionary Ecology which corresponds to an emerging research field for which a leadership position will help in contributing to the European Research Area and international initiatives related to the increasing number of biodiversity issues (*e.g*. International Platform on Biodiversity and Ecosystem Services, Marine Strategy Framework Directive). Assessment of habitats changes and species adaptation to environmental changes also require to work on contrasted marine regions (*e.g*. along latitudinal gradient), which result in international collaborative projects.