Vague D
Campagne d'évaluation 2017 – 2018
ADAPTATION ET DIVERSITE EN MILIEU MARIN
Unité de recherche
UMR 7144 AD2M
Dossier d'autoévaluation

Informations générales

Nom de l'unité :	**Adaptation et Diversité en Milieu Marin**
Acronyme :	**AD2M**
Champ de recherche de rattachement :	**Ecologie Marine**
Nom du directeur pour le contrat en cours :	**LALLIER François**
Nom du directeur pour le contrat à venir :	**NOT Fabrice**

Type de demande :

Renouvellement à l'identique X Restructuration ☐ Création ex nihilo ☐

Établissements et organismes de rattachement :

Liste des établissements et organismes tutelles de l'unité de recherche **pour le contrat en cours** et **pour le prochain contrat** (tutelles).

Contrat en cours :	Prochain contrat :
- UPMC	- UPMC
- CNRS	- CNRS

Choix de l'évaluation interdisciplinaire de l'unité de recherche ou de l'équipe interne :

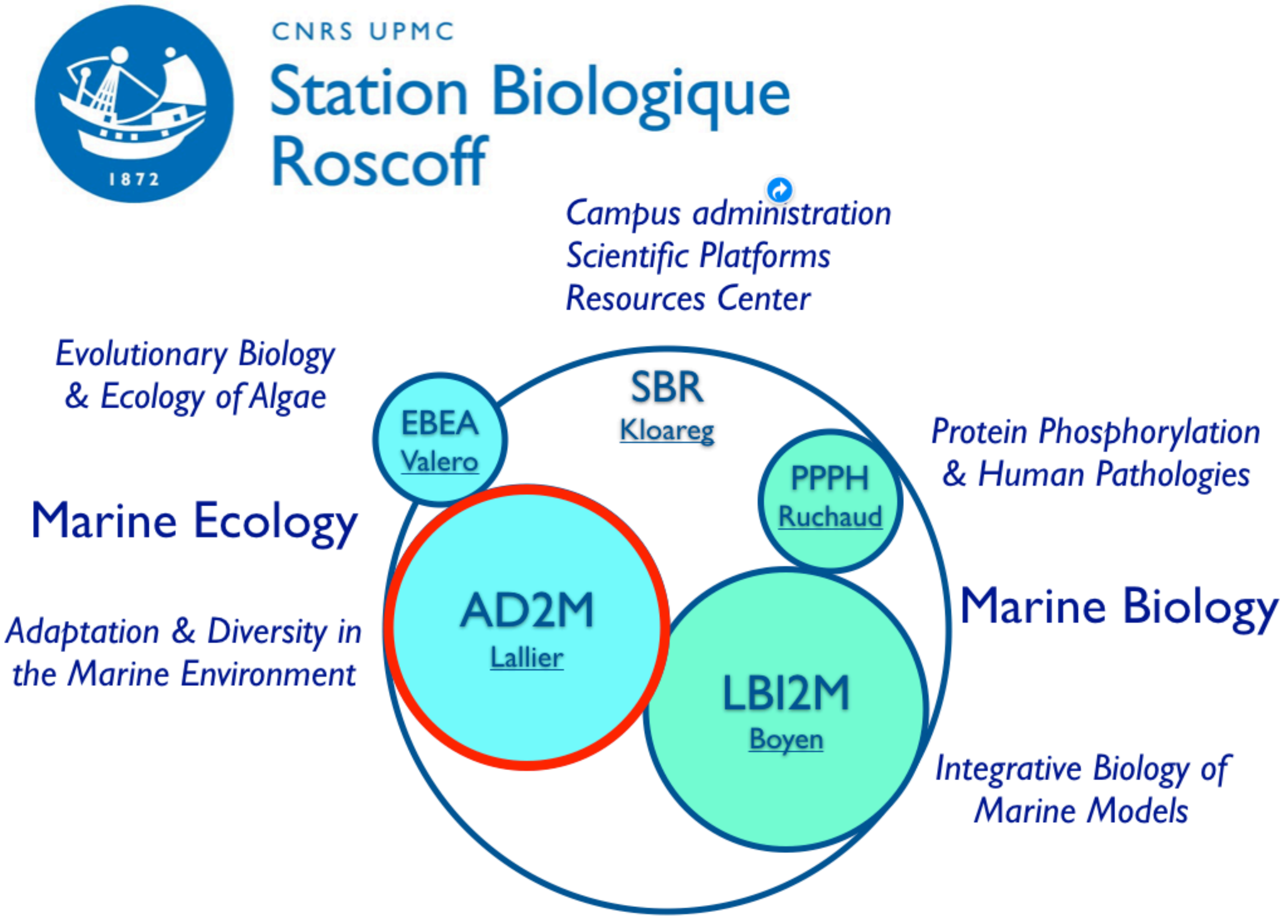
Oui ☐ Non X

DOSSIER D'AUTOÉVALUATION

1. AD2M laboratory presentation

Introduction

Since 2001, the Station Biologique de Roscoff (SBR) is organized as a "Fédération de Recherche" (FR 2424) comprising support services, research facilities and several Research Units. Our laboratory forms one of these research units, named "Adaptation et Diversité en Milieu Marin" (AD2M, UMR 7144): founded in 2005 it has been successfully renewed twice, in 2009, and in 2013 for the ongoing contract (2014-2018). The simplified diagram below shows that our laboratory deals with most of the research being conducted in marine ecology at the SBR, with the notable exception of the EBEA lab (UMI 3614), formerly a team of our lab.



The AD2M lab develop its research in the broad domain of descriptive, functional and evolutionary ecology, specifically applied to marine organisms and ecosystems. The marine environment is undoubtedly home to the widest diversity of organisms. It is therefore not surprising that the different teams of AD2M address their questioning to organisms that are spread over the whole tree of life: from photosynthetic prokaryotes to all unicellular eukaryotes (protists) in the plankton, and from macroalgae to various marine, mostly benthic, invertebrates - annelids, mollusks, crustaceans and chordates.

The marine environment displays compelling physico-chemical characteristics that shape the way these organisms are living and interacting with eachother. Of course, littoral and coastal ecosystems are foremost in our activities - and specially those of the English Channel - but our work encompass the whole oceanic domain, relying on oceanographic cruises to explore remote locations from the pelagic realm to the deep ocean. We deploy mechanistic as well as integrative approaches, based on the most recent developments in modern biology (e.g. -omics), aiming at a comprehensive understanding of the functional and evolutive processes that govern marine biodiversity.

As part of SBR our lab benefits from the support services and research facilities operated locally by the FR 2424. Our lab is a major user of the services providing access to marine ecosystems and ressources (SMO, RCC, RAS... see section 8.1 in FR2424 report). In terms of technological platforms these include genomic and metabolic facilities, microscopy, and bioinformatics (see section 8.2 in FR2424 report). Members of our lab actively participate in the development of these platforms (and, for some of them, initiated their activity).

We also acquire and develop our own specific equipments such as in situ sensors and analytical tools (respirometers, phytoPAM,...), flow cytometry and additional microscopy,... including ad hoc experimental devices for in vivo acclimatation of marine organisms.

During the present contract our lab was organized in 7 research teams and a small management team (Table 3.1) as follows

- Marine Chemistry (CHIM) , headed by Yann Bozec (CR, CNRS)
- Benthic Ecosystems Ecogeochemistry and Functionning (EFEB) heded by Dominique Davoult (PR, UPMC)
- Diversity and Connectivity in the coastal marine landscape (DIVCO) headed by Frédérique Viard (DR, CNRS)
- Adaptation and Biology of Invertebrates in Extreme Environments (ABICE) headed by Stéphane Hourdez (CR, CNRS)
- DIversity and Interactions in Oceanic Plankton (DIPO) headed by Laure Guillou (DR, CNRS)
- Marine Phtotrophic Prokaryotes (MaPP) headed by Laurence Graczarek (DR, CNRS)
- Protists and Pelagic Ecosystems Evolution (EPEP) headed by Colomban de Vargas (DR, CNRS)

Evolution of human ressources (Table 3.2, 3.3, 3.4)

As of June 30 2017, the AD2M lab comprises 82 members including 44 permanent members (16 CNRS researchers + 14 professors + 16 engineers and technicians) and 38 temporary members (24 PhDs + 10 post-docs + 3 engineers).

Temporary members are de facto variable in numbers, depending on ongoing projects, and the total number of members of AD2M has fluctuated between 80 and 96 during the present contract. For example 28 PhD students have defended their thesis during the reference period (2012-june 2017).

We have had no recruitment (nor retirements) of researchers at CNRS since 2012; 2 recuitments of professors, one at UPMC (C. Lejeusne in 2014) and one from ENSTA Brest who formally joined our lab for her research activity (A. Nicolle in 2015). Total flux for researchers and professors: +2

Sadly, during the present contract we suffered the loss of two technicians in 2015 due to fatal illness (R. Michel and D. Le Guen). The CNRS has very efficiently fulfilled these positions through mobility (O. Bohner in 2015 and S. Ruault in 2016), and 3 new CNRS engineers have joined our lab in 2012, 2014 and 2016 (J. Coudret, E. Bigeard, S. Loisel). Total flux: +3 (not including the recent departure of 1 engineer S. Audic in July 2017)

The fluxes of temporary staff are detailed for each team in a table introducing their report (see below).

Evolution of funding (Table 4)

The recurrent, yearly credit attributed by CNRS and UPMC to our lab has been slightly but steadily decreasing from 2012 to 2016, from 228 to 209 k€ (8% decrease in 5 years). It represents about 11% of our functionning budget. This is unfortunate but not surprising since most research money (with the notable exception of permamnet members' salaries) has to be found through application to european, national or regional proposals nowadays.

Overall, all teams included, we have raised between 1500 and 2000 k€ each year on top of the recurrent funding during the reference period. From 2012 to 2016, European and international projects have yielded around 13% of these funds, regional projects accounted for 12% and national ones (mostly through ANR) represented more than half our income (55%). The detail of each contract obtained by the different teams can be found in each team report (see below) and in Annex 4.

NB: In Table 4, the 2016 columns, although technically correct, are misleading due the mode of funds attribution : starting from 2016 grant money managed by CNRS is fully allocated the year you earn the grant, no matter how long the contract lasts. Before that date it was spread over the duration of the contract.

Scientific Policy

Our research activity is essentially fundamental research in descriptive, functional, and evolutionnary ecology. Our projects and results are often related to social and economical concerns : global and climate change, marine resources exploitation (algae, mollusc aquaculture, deep-sea mining...). Our expertise in sustainable development or biological conservation is often useful to various stakeholders at regional, national or international levels (e.g. AMP protected marine areas; expertise reports for ministeries and national agencies, IPBES,...).

Diffusion of our knowledge to students and the general public is a strong commitment for all of our staff. We have a large proportion of professors in our lab, involved in bachelor and master degrees in Roscoff and Paris, and we have promoted numerous outreach actions (books, movies, conferences and hands on exhibitions).

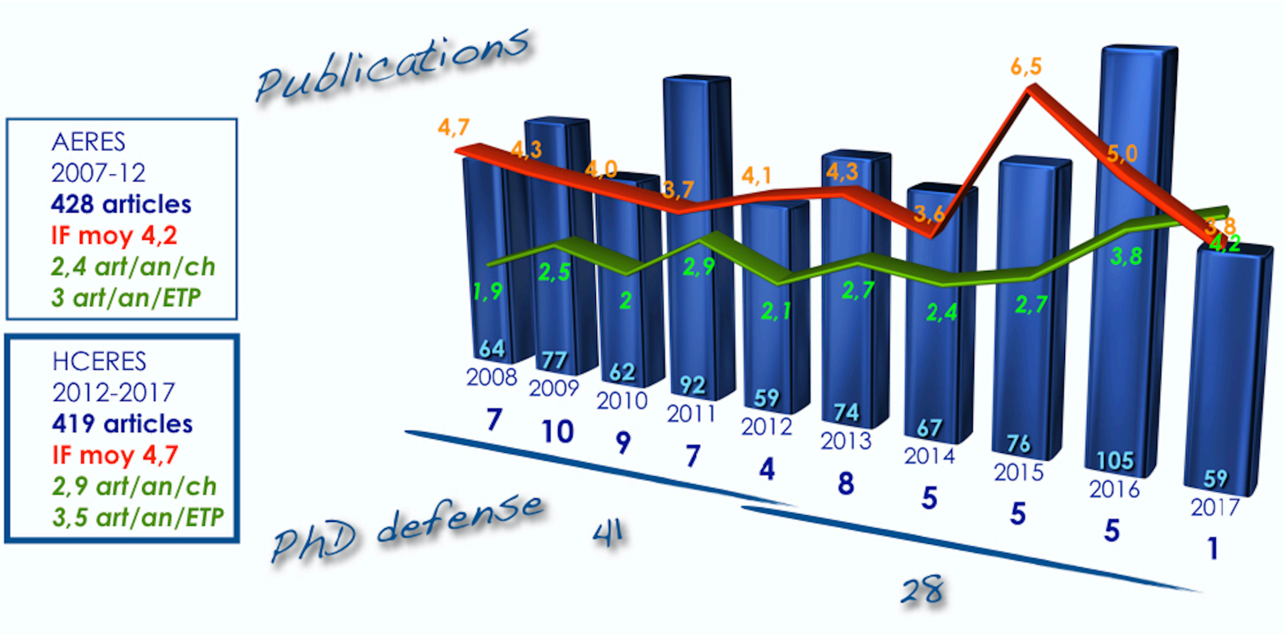
2. Research products and activities

Scientific report

Each team propose a summary of their activity and achievements in the following pages in relation to their selection of production and research activites (Annexe 4). For the whole laboratory, we propose a global analysis of article publications and present an account of major achievements during the period, illustrated by 18 publications (listed in Annex 4) covering represnentative activities of the different teams.

Global publication analysis

The production of the lab in terms of publication is very satisfying with 419 articles and a mean Impact Factor (2016) of 4,7. This is roughly equal in numbers to the amount of publications reported in 2012 for the previous 5-year period (422) with a significant increase in mean IF (4,2), despite the departure of one team to form UMI 3614 (EBEA, M. Valero). The mean ratio of papers/researcher has increased (2,4 to 2,9) amounting to 3,5 articles per year per research ETP when taking into account the teaching activity of professors. Of course this mean number varies individually with an order of magnitude in the number of published papers by each researcher (from 6 to 62 during the period). Evolution of number and IF over the course of these two periods is illustrated on the graphic below, together with the number of defended PhDs (for 2017 3-4 thesis will be defended in the coming months).

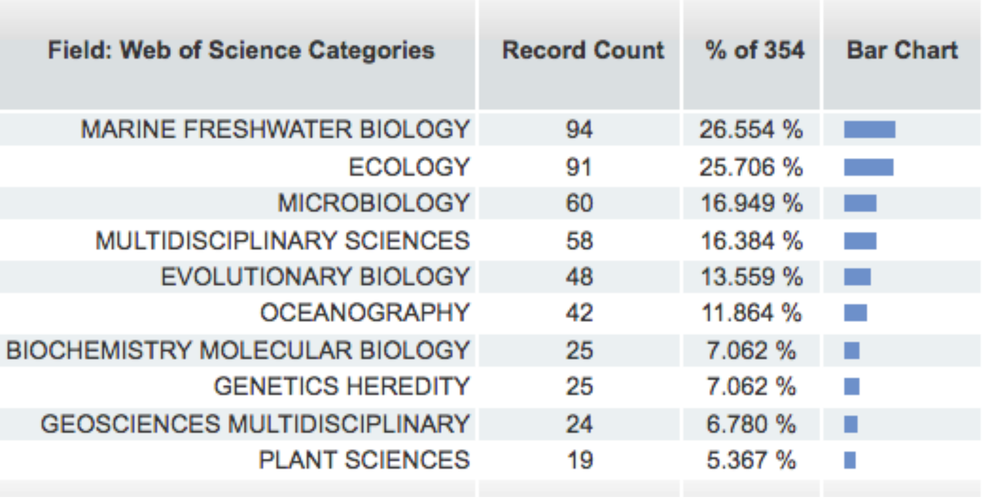


Brief bibliometric analysis

Mean IF factor over the whole period (or even for each year) does not convey much information. The median IF of 2,8 tells us that the mean IF (4,7) is increased by a fair number of high impact journals, as can be seen in the table below. The second column shows the journals we publish in most frequently, telling a little more about the most productive areas (microbiology...), and the third column indicate the journals that contribute the most to the mean IF. Not surprisingly, *Science* comes out on top with the series of 2015 papers relating the first results of the Tara Oceans expedition. But although some "marine" journals come out in the most frequent, they are not present among the most significant, indicating that our research is spread well beyond the marine community.

TOP 10 BEST	IF (2016)	TOP 10 MOST FREQUENT		TOP 10 BEST IF*FR	
Nature	40,1	PLoS ONE	33	Science	260
Science	37,2	ISME J	19	ISME J	184
Nature Comm	12,1	Biogeosc.	15	Nature	161
NAR	10,2	Protist	13	PLoS ONE	93
Plos Biology	9,8	Mar Biol	13	PNAS	68
PNAS	9,7	Envir Microbio	12	Mol Ecol	67
ISME J	9,7	Mol Ecol	11	Envir Microbio	65
Ecology Lett.	9,4	J Phycol	10	Biogeosc.	58
Syst. Biol.	8,9	Est Coast Sh Sc	10	Nature Comm	36
Curr. Biol.	8,9	Scientific Rep	8	Protist	36

This is also illustrated when our published papers are distibuted across Web of Sciences categories (Table below). Of course we are a marine lab and "Marine Freshwater Biology" comes out first with "Oceanography" in hte middle, together comprising 38% of our articles. But our publications in Ecology, Microbiology or Evolutionary biology amount to more than 56% with a very significant 16% in Multidisciplinary journals.



Field: Web of Science Categories	Record Count	% of 354	Bar Chart
MARINE FRESHWATER BIOLOGY	94	26.554 %	▬
ECOLOGY	91	25.706 %	▬
MICROBIOLOGY	60	16.949 %	▬
MULTIDISCIPLINARY SCIENCES	58	16.384 %	▬
EVOLUTIONARY BIOLOGY	48	13.559 %	▬
OCEANOGRAPHY	42	11.864 %	▬
BIOCHEMISTRY MOLECULAR BIOLOGY	25	7.062 %	▪
GENETICS HEREDITY	25	7.062 %	▪
GEOSCIENCES MULTIDISCIPLINARY	24	6.780 %	▪
PLANT SCIENCES	19	5.367 %	▪

Selection of production and research activites

The list of selected papers can be found in Annex 4 with a two-part selection of publications for the whole laboratory, and a more detailed report of publications, communications and activities for each team. Table 5 summarize numerical figures for all the items mentionned in Annex 4.

A full list of publications is also provided in annexes, in two files where publications are sorted according to the present (7 teams) or future (3 teams) structure of the lab. Three summary tables can also be found in annexes for convenience: PhD students, Attractivity, Socio-economical implication.

Outstanding achievements

The **Marine Chemistry** team has developed ferry boxes installed on Brittany Ferries ships sailing from Plymouth to Roscoff to obtain high spatial resolution mesurements of surface pCO2 and air-sea CO2 fluxes all year round. Pierre Marrec thesis and associated papers (e.g. **Marrec et al 2015**) revealed that on an annual scale the northern, seasonally stratified part acted as a CO2 sink whereas the southern, well mixed part acted a source of CO2. Models and extrapolation to adjacent areas and over a decade resulted in an annual average uptake of -1.11 ± 0.32 Tg C yr^{-1} . A similar approach based on high temporal resolution using instrumented buoys allows predictions on complex coastal areas such as the Bay of Brest (**Salt et al 2016**). Increasing the precision of such global estimations is of foremost importance for C fluxes balance.

The **Ecogeochemistry and Functioning of Benthic Ecosystems** team has set up long term (6 month) acclimatation experiments to acidified and/or heated sea water to test global change effect on coastal species. **Noisette et al (2015)** reports that the slipper shell can tolerate ocean acidification, particularly in the intermediate $p\mathrm{CO}_2$ scenario (750 µatm), and even better under moderate temperature increase. The team is also a leader for intertidal and coastal rocky shores community functionning. During the last 5 years important results on kelp forest functionning have been published linking complex community structure with their seasonal functioning (e.g. **Leclerc et al 2013**). Their contributions, together with those of the DIVCO team and UMI EBEA in Roscoff, significantly contribute to the european effort, highlighting major threats for these ecosystems but also opportunities for conservation (**Araujo et al 2016**).

The **Diversity and Connectivity** team focus on eco-evolutionary studies of marine species dispersal and diversity that shape marine landscapes. They develop new technological approaches together with theoretical modeling to disentangle fine-scale processes that govern species diversity and dispersal. By developing a post-genomic SNPs panel, combined with extensive field surveys and experimental work (laboratory crosses), they showed that two closely related *Ciona* species are not hybridizing in the wild: apparent hybridization patterns are in fact the outcome of ancient introgression between the two taxa (**Bouchemousse et al. 2016**). Developing empirical studies using *Crepidula fornicata* as a case study, they showed relationships between size and reproductive success and that sperm storage might be a key parameter of sex-change in this protandrous and gregarious species (**Broquet et al 2015**), illustrating previous theoretical and simulation studies.

The **Adaptation and Biology of Invertebrates in Extreme Conditions** team has devoted much time and resources over the last 8 years to gather a large set of genomic and transcriptomic data on selected deep-sea hydrothermal and polar species. These data are used in phylogenetically-constrained approaches of species evolution as well as differential transcriptomic approaches of species acclimatation to biotic (e.g. symbiosis) or abiotic (e.g. temperature, metals) stresses. For example they have served to unravel adaptation processes driving thermophily in vent polychaetes (**Fontanillas et al. 2017**) or to identify key factors involved in host-symbiont relationships in deep-sea mussels (**Détrée et al 2016**).

The **Marine Phototrophic Prokaryotes** team back up their work on their in depth knowledge of the genome structure and function of Cyanobacteria (*Synechococcus*). These genomic data were used to better understand the factors responsible for the ecological distribution of the main *Synechococcus* clades and pigment types (**Farrant et al., 2016**) or to study adaptive thermostability of light harvesting complexes (**Pittera et al. 2017**). In close collaboration with the EPEP team and Tara Oceans consortium they also contributed to the study of plankton dynamics in the Agulhas rings (**Villar et al. 2015**).

The **Divesity and Interacations in Oceanic Plankton** team has led work to establish (and maintain) a most valuable Protist Ribosomal Reference database (**Guillou et al. 2013**) allowing better studies of the diversity and distribution of various groups of planktonic protists (e.g. Parmales, **Ichinomiya et al. 2016**). Besides, focus on various biotic interactions have evidenced phototrophic symbioses in Rhizaria, an overlooked group of giant protists (**Biard et al. 2016**), highly complex genetic diversity of algal blooms (**Dia et al. 2014**) with consequences for their control through parasites, and the impact of clade-specific viral infection for the ecology and evolution of a prominent phytoplankter, Micromonas (**Baudoux et al. 2015**).

Finally, last but not least, the **Evolution of Protists and Pelagic Ecosystems** team has produced an impressive amount of outstanding papers based on the analysis of the Tara Oceans collection of samples. In perhaps the most emblematic and representative paper, **de Vargas et al. (2015)** showed that, on a global planetary scale, Eukaryotic ribosomal diversity saturated at ~150,000 operational taxonomic units, about one-third of which could not be assigned to known eukaryotic groups.

3. Laboratory organisation

Management, animation, organisation of the lab

The management team is composed of the Director (F. Lallier) and the Deputy Director (F. Viard) with the assistance of one administrative staff (C. Manceau). The management team is also assisted by Liaison staff for Health and Safety matters (Agent de Prévention, AP, D. Marie) and for Training (Correspondante Formation, CoFo, C. Daguin-Thébaut). The management team relies on two committees to help managing ressources and promote its scientific policy:

- a Scientific Committee (CS) composed of the team leaders meets 5-6 times a year to examine strategic choices, often linked to the opening of funding opportunities at international, national or regional levels. Lab CS is coordinated with SBR CST where team leaders also participate to inform and coordinate our lab actions at local level.

- a Laboratory Council (CdL) composed of elected and appointed members representing staff categories (researchers, technical staff and students) meets twice a year. They give advice on the strategic choices of the lab and examine matters regarding human resources, training and health and security. Again, this is done in close coordination with the Federation Council (CF) of SBR.

All laboratory staff are informed of CS and CdL meetings and agendas in advance, and reports are distributed rapidly and remain available on the Intranet pages of the lab for future reference.

In terms of scientific animation our lab organizes a yearly Lab Day (Journée UMR) where posters presented during the past year are presented and serve as a focal point to discuss ongoing research projects. We participate in weekly seminar meetings organized at the SBR level, often proposing external visitors to present ther research. Our PhD students and post-docs are also very active within the AJC-SBR association of early career researchers. In addition to assistance and information on scientific and technical aspects, AJC organises a “Early Career Researcher Day” each year for ECRs to present their work in English as talks or posters in front of other lab members and usually two top scientist guest stars.

However there is a lack of thematic / topical or technological meetings dedicated to share and improve our ideas and practices. This was originally planned for the present contract but has not been implemented formally: budget priorities have not permitted to secure funding for these events but there was also a lack of volunteers to seize their organization.

Parity

Although no specific measures are set up to ensure parity at our level we give equal opportunity when recruiting temporary staff, either PhD or post-docs, focusing on competences and not taking gender into account. A posteriori we observe a small bias towards males both for lab members and PhD students (see below). The bias is stronger for researchers, compared to technical staff, recruitment being made at the University of CNRS level. Team leadership in our lab is almost equally shared with 3 female for 7 teams.

Lab members (Table 3.2) : 21 F for 49 total yields 43% F / 57% M

Researchers (Table 3.2) : 10 F for 30 total yields 33% F / 67% M

Technical staff (Table 3.2) : 11 F for 18 total yields 61% F / 39% M

PhD students (Table 3.3) : 24 F for 52 total yields 46% F / 54% M

Health and safety

In terms of safety and security our lab conforms to CNRS and UPMC regulations under the umbrella of the SBR as a whole: there is one lab member officialy appointed to supervise health and safety matters at lab level (AP D. Marie, IR CNRS), acting in coordination with the other SBR labs within a joint "Health and Safety Committee" (CLHS) at the SBR level (also headed by D. Marie).

Health and safety matters are regularly examined during Laboratory Council (twice a year) and several Health and Safety meetings at SBR. The "Document Unique" reporting recognized problems is updated at least once a year, identifying actions to be taken to resolve apparent problems. Both permanent and temporary staff are duly informed of laboratory regulations and safety procedures, people being regularly trained for fire instruction and first aid.

The major problem identified in 2013 for an healthy working environment was crowded office and lab space : some answers have (slowly) been found, notably for office space. There is often a lack of funding to enforce regulations since grant funding cannot usually be used for this matter. Specifically in Roscoff, the lab (UMR 7144) has no "infrastructure" budget from CNRS or UPMC because this is distributed at the SBR / FR 2424 level.

In the next pages, a detailed report is presented for each of the seven teams of the lab, including a specific SWOT analysis.

A global SWOT analysis for the lab follows, just before the presentation of the 5-year project for the next contract.

Vague D
Campagne d'évaluation 2017 – 2018
UMR 7144 Adaptation et Diversité en Milieu Marin
Chimie Marine (CHIM)
Bilan 2012-2017

Composition durant le contrat actuel

Personnel Permanent	mouvement	Personnel Temporaire	période
BOZEC Yann (CR1)		MARREC Pierre (DOC)	Oct 11 – Dec 14
MACE Eric (AI)		SALT Lesley (CRC)	Oct 13 – Sep 15
MORIN Pascal (DR2, HDR)	→ Mar 13		
SEVIN Laure (IE)			
VERNET Marc (T)			

Marine Chemistry Team Presentation

The Marine Chemistry Unit focuses its research on the biogeochemistry of coastal ecosystems with particular emphasis on the carbon cycle and air-sea exchange of Greenhouse Gases (GHGs). After the departure of Pascal Morin (DR2) for IPEV (French Polar institute) at the beginning of the reference period (early 2013), the team decided to redefine its activities based on 3 themes:
Theme 1 : GHGs cycles and exchange at air-sea interface
Theme 2 : Observation of Coastal ecosystems
Theme 3: Development and deployment of novel *in-situ* sensors

These research were supported by CNRS/UPMC and by responding successfully to various financial calls such as Region Bretagne and CD29 (*1 PhD, 1 Post-doc*), LEFE/CYBER (*project CHANNEL, collaboration with IUEM*), MISTRALS/MERMEX (*project CARBORHONE, collaboration MIO*), NERC UK (*project CANDYFLOSS, collaboration PML, NOCS*), Europe FP7 and H2020 (*JERICO, Marinexus and JERICO-Next, collaborations PML, NOCS*). Within these projects the team carried out 90 crossings onboard Ferries between Roscoff and Plymouth/Cork, 2 cruises in the North Atlantic (Outer Hebrides and Extended Ellet Line), 4 cruises in the Mediterranean Sea (Gulf of Lions) and 120 campaigns off Roscoff for the national observing network SOMLIT. This low frequency dataset were completed by more than 500000 data points of pCO_2 and ancillary data collected on various platforms (FerryBox, automated buoys ASTAN/MAREL-Iroise), constituting a comprehensive dataset for our research, from which the main results are summarized below.

Theme 1: GHGs cycles and exchange at air-sea interface

Over the past decade, the coastal oceans have been the focus of several studies highlighting the key role of these ecosystems in the global budget of air-sea CO_2 fluxes (Borges et al., 2005; Cai et al., 2006; Thomas et al., 2004). In these extremely heterogeneous and dynamic coastal ecosystems the direction and magnitude of these fluxes present much larger gradients than in the open ocean, which make coastal ecosystems relevant for global estimates of air-sea CO_2 fluxes despite their relatively small surface area (7% of the total ocean surface area). The spatial variability in air-sea CO_2 fluxes is large from one ecosystem to the other and the constraint of air–sea CO_2 fluxes and their variability at various time and spatial levels remain a central task in global carbon and climate studies. Moreover, these ecosystems are particularly sensitive to ocean acidification (OA) and climate change. International projects such as IMBER and SOLAS support research focusing on the current carbon cycle in coastal ecosystem and its response to rising atmospheric CO_2. In this context, our team carried its research with 2 main objectives:

1) Assess by multi-scale approaches the CO_2 air-sea fluxes in coastal ecosystems.
2) Evaluate the impact of natural (NEP, NAO) vs anthropogenic (SST warming, eutrophication, OA) processes on carbonate chemistry of coastal ecosystems.

1) In the framework of the JERICO and CHANNEL projects, we investigated partial pressure of CO_2 (pCO_2) dynamics on the coastal margin of north-western Europe using a comprehensive dataset of pCO_2 and ancillary data. This dataset was collected on 2 Voluntary Observing Ships operating between Roscoff/Plymouth (*Armorique*) and Roscoff/Cork (*Pont-Aven*) from 2013 to 2015. In **Marrec et al. (2013)** we solved the discrepancies observed in previous studies that investigated the air-sea CO_2 fluxes in the Western English Channel: We demonstrated the importance of the thermal front located approximatively at 49.5°C, which separates the northern stratified WEC, a sink of atmospheric CO_2 of -0.4 ± 0.1 mol C m^{-2} yr^{-1}, from the southern homogenous WEC, a source of CO_2 for the atmosphere at $+0.5 \pm 0.2$ mol C m^{-2} yr^{-1}. **Marrec et al. (2014)** showed that high-frequency measurements are necessary to accurately assess air-sea CO_2 fluxes in very dynamic coastal ecosystems. For example, we estimated that a short bloom of 10 days, which resulted in very large and sudden seawater pCO_2 drawdown accounted for 29% of the CO_2 sink during the productive period (from May to-mid September). In **Marrec et al. (2015)** we combined the high frequency datasets recorded in the WEC with satellite observations from the adjacent Celtic and Irish Seas (collaboration PML, UK). Based on the resulting Multilinear Regressions (MLRs) we estimated air-sea CO_2 fluxes on the entire shelf for the period 2003-2013. Our results were validated against *in-situ* data from the SOCAT and LDEO databases and discrete samples collected on our VOS. We scaled the mean annual fluxes over the 3 provinces for the last decade and obtained the first annual average uptake of 1.11 ± 0.32 Tg C yr^{-1}.

In the framework of the CANDYFLOSS project, in collaboration with S. Painter (NOC, UK) and V. Kitidis (PML, UK), our postdoc L. Salt extended the reach of the data collected during the CHANNEL project in the Celtic Sea onboard the RRS Discovery (DY017) and undertook carbon measurements in the Outer Hebrides. The offshore transport of inorganic carbon in this region is thought to be significant in the region and has never been quantified. A total of 520 samples for A_T (Total Alkalinity) and DIC (Dissolved Inorganic Carbon) were collected and analyzed onboard, from 6 transects. **Painter et al. (2016)** demonstrated that the downslope flux of POC from the Hebrides Shelf is approximately 3-to-5-fold larger per unit length/area than the global mean. To reach this conclusion we quantified the offshore transport of particulate and dissolved carbon fractions via the “Ekman Drain”, a strong downwelling feature of the NW European Shelf circulation, and subsequently compared these fluxes to simultaneous regional air-sea CO_2 fluxes and on-shore wind-driven Ekman fluxes to constrain the carbon dynamics of this shelf.

Finally, in the framework of the MERMEX/CARBORHONE project, we carried out 4 cruises in the Gulf of Lions onboard *RV Téthys 2*, which revealed a strong decreasing gradient of air-sea CO_2 influxes from the coast to offshore waters. This gradient is mainly driven by biological (summer) and thermodynamic (winter) processes in the near-shore region and meso-scale eddies (fall) in the offshore surface waters (collaboration P. Hosegood, University of Plymouth). The main results of these cruises still need to be published but the pCO_2 data, similarly as for the CHANNEL and JERICO projects were regularly submitted in the international database SOCAT and thus contribute to the global synthesis of CO_2 air-sea fluxes of the international community. The team co-signed 3 “community” papers based on these datasets (**Bakker et al.**, 2014, **2016**; Le Quéré et al., 2015).

2) To evaluate the current state of the carbonate chemistry in coastal ecosystems and its potential alteration under climate change and OA, in 2003 we initiated time series of A_T and DIC at 2 coastal sites (Bay of Brest and ASTAN off Roscoff) from the national coastal observatory SOMLIT (See below Theme 2). Based on this dataset **Salt et al. (2016)** computed that annually, the Bay of Brest generally behaves as a source of CO_2 to the atmosphere (0.14 ± 0.20 mol C m^{-2} yr^{-1}), showing inter-annual variability significantly linked to annual net community production (NCP). The presence of a large community of benthic filter feeders, sensitive to OA, leads to high levels of particulate organic matter (POM) and opal deposition during the spring diatom bloom. Over the following few months, benthic POM remineralisation reduces the spring CO_2 deficit relative to the atmosphere, and remineralisation of biogenic silica supplies further late spring primary production. The result is an inverse spring NCP - air-sea CO_2 flux relationship, whereby greater NCP in early spring results in lower fluxes of CO_2 into the Bay in late spring. This recycling mechanism, or silicic acid pump, also links the spring and summer NCP values, which are both determined by the peak wintertime nutrient concentrations. The carbonate system is further affected by the benthic community in winter, when $CaCO_3$

dissolution is evident from notable deviations in the ΔAT:ΔDIC ratio. This study highlights the necessity of individual study of coastal, temperate ecosystems and contributes and the sensitiveness of these ecosystems to OA (**Salt et al., 2016**)

In a long-time continued collaboration with H. de Baar (NIOZ, Netherlands) and H. Thomas (University of Halifax) we exploited the dataset collected in the North Sea subsequently by Y. Bozec, H. Thomas and L. Salt from 2002 to 2005 to assess the internal consistency of the North Sea carbonate system. We showed that for most of the year, there was a similar level of internal consistency, with A_T being calculated to within ±6 μmol kg^{-1} using DIC and pH, DIC to ±6 μmol kg^{-1} using AT and pH, pH to ±0.008 using A_T and pCO_2, and pCO_2 to ±8 μatm using DIC and pH, with the dissociation constants of Millero et al. (2006). In spring, however, we observe a significant decline in the ability to accurately calculate the carbonate system. Lower consistency is observed with an increasing fraction of Baltic Sea water, caused by the high contribution of organic alkalinity in this water mass, not accounted for in the carbonate system calculations.

Finally, and still in collaboration with NIOZ and the University of Halifax, our postdoc L. Salt evaluated the variability of North Sea pH and CO_2 response to NAO forcing. High biological activity causes a distinct seasonality of surface water pH in the North Sea, which is a strong sink for atmospheric CO_2 via an effective shelf pump. The intimate connection between the North Sea and the North Atlantic Ocean suggests that the variability of the CO_2 system of the North Atlantic Ocean may, in part, be responsible for the observed variability of pH and CO_2 in the North Sea. In this work; based on three extensive observational records covering the relevant levels of the NAO index, we provide evidence that the North Sea pH and CO_2 system strongly responds to external and internal expressions of the NAO. Under positive NAO, the higher rates of inflow of water from the North Atlantic Ocean and the Baltic outflow lead to a strengthened north-south biogeochemical divide. The limited mixing between the north and south leads to a steeper gradient in pH and partial pressure of CO_2 (pCO_2) between the two regions in the productive period. This is exacerbated further when coinciding with higher sea surface temperature, which concentrates the net community production in the north through shallower stratification. These effects can be obscured by changing properties of the constituent North Sea water masses, which are also influenced by NAO. Our results highlight the importance of examining interannual trends in the North Sea CO_2 system with consideration of the NAO state (Salt et al., 2013).

Theme 2: Observation of Coastal Ecosystems

The Marine Chemistry unit has been involved with the national SOMLIT network for the past 15 years. The team is responsible for the bi-monthly sampling at the SOMLIT-site off Roscoff and performing the subsequent chemical analysis of the SOMLIT parameters. In addition, our team has initiated additional sampling of A_T and DIC samples for the past 10 years at the SOMLIT-Brest and SOMLIT-Roscoff sites. This comprehensive dataset has been deconstructed, with the collaboration of colleagues at IFREMER Brest, to determine the drivers of seasonal and inter-annual variability in the carbonate system in the Bay of Brest by our post-doc Lesley Salt as mentioned above.

In Tréguer et al. (2014), we focused on the winter months of the 15 years dataset at the Roscoff and Brest Somlit-sited and we characterize the physical and chemical variability of these coastal waters and document changes in both precipitation and river runoffs. Our study reveals that variability in coastal waters is connected to the large-scale North Atlantic atmospheric circulation but is also partly explained by local river influences. Indeed, while the NAO is strongly related to changes in sea surface temperature at the Brest and Roscoff sites, the Esta Atlantic Pattern (EAP) and the Atlantic Ridge (AR) have a major influence on precipitations, which in turn modulate river discharges that impact sea surface salinity at the scale of the two coastal stations.

To extend these 2 regional studies, we exploited at a larger scale the SOMLIT dataset to identify the temporal variability and controls of POM concentrations and elemental ratios across different ocean regions (Collaboration University of California, Irvine, **Talarmin et al., 2016**) and across the three maritime façades of France (collaboration national SOMLIT network led by N. Savoye and C. Liénart). **Talarmin et al. (2016)** showed that the relationships between long-term changes in environmental conditions and particulate organic matter concentrations or ratios were ambiguous, but interactions between changes in temperature and nutrient availability were important at the scale of oceanic regions. This study demonstrated significant changes in elemental ratios at long-term and seasonal time scales across regions, but the underlying mechanisms are currently unclear. The study led by Liénart et al. (2017) was based on carbon and nitrogen elemental and isotopic ratios, which are used for running mixing models. This study showed that for the SOMLIT ecosytems, the POM of the estuary is dominated by terrestrial material (93% on average), whereas the POM of the other systems is dominated by phytoplankton (84% on average). Nevertheless, for the latter systems, the POM composition varies in space, with 1) systems where POM is highly composed of phytoplankton (≥ 93%), 2) systems characterized by a non-negligible contribution of benthic (8 to 19%) and/or riverine (7 to 19%) sources, and 3) the Mediterranean systems characterized by the contribution of diazotroph organisms (ca. 14%). A continent-to-ocean gradient of riverine and/or benthic POM contribution is observed. Finally, time series reveal 1) seasonal variations of POM composition, 2) differences in seasonality between systems, and 3) an inshore-offshore gradient of seasonality within each system that were sampled at several stations. Spatial and seasonal patterns of POM composition are mainly due to local to regional processes such as hydrodynamics and sedimentary hydrodynamic (e.g. resuspension processes, changes in river flows, wind patterns influencing along-shore currents) but also due to the geomorphology of the systems (depth of the water column, distance to the shore) (Liénart et al., 2017).

In a collaboration between our team and the DIPO team (UMR 7144, collaboration A.-C. Baudoux, N. Simon), we combined the physico-chemical data collected at the SOMLIT-Roscoff site with the biological data collected by the DIPO team to evaluate the interplay between the genetic clades of *Micromonas* and their viruses in the Western English Channel (Baudoux et al., 2015).

As mentioned above, on a regional and national level our team has been responsible for the SOMLIT sampling and analysis of all physico-chemical parameters of this national network for the past 15 years in close collaboration with the FR2424 (T. Cariou, F. Jalabert and the INSU crew). This collaboration led to several peer-reviewed papers with the colleagues of the UMR7144, FR2424 and national network SOMLIT as described above. On an international level the team is very involved in global observatories such as JERICO-Next (Joint European Research for Coastal Observatories – Novel European eXpertise for coastal observatories, EU H2020 2015-2018) and ICOS OTC (Integrated Carbon Observation System – Ocean Thematic Centre) to provide long-term oceanic observations, which are required to understand the present state and better predict future behaviors of the global carbon cycle and climate-relevant gas emissions. Thus, our team is part of a large European and national consortium and will continue to co-sign community papers on global carbon budgets as detailed above. These projects provide long-term measurements but also aim at developing new high-frequency observations and sensors as described in theme 3 below.

Theme 3 : Development and deployment of novel *in-situ* sensors

In parallel of the low-frequency SOMLIT network, the French community decided to implement a high-frequency observatory network (COAST HF) at the same coastal sites. Our team has been involved in developing observations at high-frequency in the past years and is a leader in COAST HF. In 2007 we equipped a buoy of opportunity off Roscoff with classical CTD and atmospheric sensors. In 2015 we added a SAMI-CO_2 sensor to our buoy. This award winning sensor (Wendy Schmidt Ocean Health 2015 xPrize) is developed by the Sunburst Company (Montana, USA). In close collaboration with Sunburst, we have been performing *in-situ* and laboratory tests and our engineers (T. Cariou, E. Macé) are now experts in the deployment of this sensor. We coordinate and serve as expert in the installation of similar sensors at the SOMLIT-Brest, SOMLIT-Banyuls, SOMLIT-Marseille sites. This work, performed in the framework of the COAST HF, the ICOS and JERICO-Next projects, will support the research of our new PhD student (Jean-Philippe Gac, funding acquired from Region Bretagne and UPMC (ED129), start date October 1st 2017).

In the JERCIO-Next project, we continue our work performed during the JERICO and MARINEXUS projects (EU FP7 2008-2014) by deploying and maintaining FerryBox systems onboard the *Armorique* (Roscoff-Plymouth) and *Pont-Aven* (Roscoff-Cork) ferries in collaboration with the Brittany Ferries. These Ferry Box systems provide continuous records of surface ocean data (e.g. SST, SSS, pCO_2, DO, fluorescence, turbidity). The team has been a leader in the national community by installing these two ferry boxes at the end of 2010 in collaboration with IFRMER-Brest. As mentioned above, the data collected on these platforms have supported the PhD thesis of P. Marrec (**Marrec et al., 2013, 2014, 2015**) and contributed to the global synthesis of CO_2 air-sea fluxes of the international community (**Bakker et al**., 2014, **2016**; Le Quéré et al., 2015). Our engineer E. Macé and former PhD student P. Marrec (2011-2014) have maintained those novel instruments and are now recognized as experts in the national and European communities for these sensors. E. Macé has been invited to participate to the commission of experts to evaluate how to equip the new national float as part of the partnership between GENAVIR and INSU. Dr

Marrec has continued to develop Ferry Box systems during a post-doc at the MIO (Mediterranean Institute of Oceanography), and adapted a new model of CytoSense automated flow cytometer (AFCM). This innovative adaptive strategy was applied during the OSCAHR cruise, with a combination of several multidisciplinary and complementary approaches involving high-resolution in-situ observations and sampling, remote-sensing and model simulations provided a deeper understanding of the marine biogeochemical dynamics through the first trophic levels (Marrec et al. 2017).

Finally, as part of the Blue Valley project (B. Kloareg, SBR) we initiated a public-private collaboration with one of our former PhD student (S. Raimund, SubCtech, Kiel, Germany) to develop their FerryBox systems and their novel MK2 pCO_2 sensor. During the Master of Jean-Philippe Gac, we performed an inter-comparison of 3 new pCO_2 sensors onboard Ferries and in laboratories. Data were refitted and validated with frequent discrete measurements performed at the SNAPOCO2 (LOCEAN, Paris). The first results from these tests will be published during the PhD thesis of Jean-Philippe Gac and will serve to the international community for the choice of the best current pCO_2 sensors.

CHIM SWOT analysis

Strengths

Expertise in high-frequency approaches to assess the processes controlling air-sea CO_2 fluxes at various scales.
Multiple and long lasting regional, national and European collaborations for the observations of coastal ecosystems and deployment of novel sensors.
Technical and staff capacities for the analysis of a large amount of biogeochemical parameters both at sea and in laboratories offers frequent collaborations from the UMR to the European scientific community level.
Data regularly submitted to international database such as SOCAT contribute to the global synthesis of CO_2 air-sea fluxes of the international community.

Weaknesses

Only one researcher in the previous Marine Chemistry team, which supported both research and observations activities with the technical staff.
Research focused on only one GHG (e.g. CO_2).
International collaborations outside of Europe need to be reinforced.

Opportunities

The new EDYCO team will have a more balance ratio of researchers and technical staff compared to the previous situation in the Marine Chemistry team.
Starting November 1st, a new researcher (C. Boulart) will join the team and work on the CH_4 marine cycle using novel *in-situ* spectrometer, thus reinforcing the themes 1 and 3 of the Marine Chemistry Unit and potential international collaborations.

Threats

The deployment of Ferry Box systems has been largely supported by the Marine Chemistry team essentially by E. Macé and former PhD student P. Marrec. Financial and staff support will be needed to maintain this activity at the SBR in the coming years.

Vague D
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UMR 7144 Adaptation et Diversité en Milieu Marin
Ecogéochimie & Fonctionnement
des Ecosystèmes Benthiques (EFEB)
Bilan 2012-2017

Composition durant le contrat actuel

Personnel Permanent	mouvement	Personnel Temporaire	période
DAVOULT Dominique (PR, HDR)		BORDEYNE François (DOC)	Oct 13 - Déc 16
MARTIN Sophie (CR)		De BETTIGNIES Florian (DOC)	Depuis Oct 16
MIGNE Aline (MC)		LECLERC Jean-Charles (DOC)	→ Déc 13
RIERA Pascal (MC, HDR)		LEGRAND Erwann (DOC)	Depuis Oct 14
BOHNER Olivier (T CNRS)	Depuis Déc 15	QUI MINET Zujaila (DOC)	Depuis Oct 14
COUDRET Jérôme (AI CNRS), 25%		NOISETTE Fanny (DOC)	→ Déc 13
LOISEL Stéphane (AI CNRS), 50%	Depuis Sep 16	STAGNOL Doriane (IE)	→ Sep 16
MICHEL Renaud (T CNRS)	Décès Fév 15		

Ecogeochemistry and Functioning of Benthic Ecosystems Team Presentation

The team is mainly working on coastal benthic communities at the community level, on diversity and functioning (primary and secondary production, food webs), both with *in situ* and laboratory approaches. Main studied communities are kelp forests, intertidal rocky shores and maerl beds. Main topics are functioning of communities in "natural" (low anthropogenic pressure) conditions (baseline knowledge), functioning under high anthropogenic local pressure (e.g. kelp and intertidal-macroalgae harvesting), and functioning under global climate change pressure (lab controlled experiments)

Theme 1 Communities under low anthropogenic pressure

The first topic was the study of coastal benthic communities under low anthropogenic pressure in the aim to understand their functioning in terms of primary and secondary production (how much, CO_2 sink or source, what are the main producers, when – during immersion or emersion), food web structure (main pathways, role of dominant macroalgal species, trophic redundancy, trophic connectivity.

These points were studied by monitoring simultaneously macroalgal and macrobenthic diversity, CO_2/DIC fluxes during emersion/immersion, and C and N isotopes of main sources and consumers.

Results obtained on the *Laminaria hyperborea*-dominated community revealed, for example, that *L. hyperborea* could play seasonally a major role, higher than previously supposed, in the food web through the pool of suspended organic matter (**Leclerc et al., 2013a** & b); studies on *L. hyperborea* were performed in collaboration with Ifremer (M. Laurans) and PNMI (Parc Naturel Marin d'Iroise). Comparison (coll. Station Marine de Wimereux) of 2 populations of *Laminaria digitata* highlighted the phenotypic plasticity of the species and its ability to acclimate both in clear-light (Brittany coast) and turbid-light (Dover Strait) environments (Delebecq et al., 2013). Our work on kelp forests led to a collaboration with several foreign institutes (mainly the Norwegian Institute for Water research and the University of Western Australia) for comparing canopy interactions and physical stress gradients in subtidal communities (Bennett et al., 2015). Research on kelp forests led to the publication of 9 articles during the period.

Another important point was the study on the functioning of fucoid-dominated intertidal communities, particularly those associated to *Fucus serratus* and *Fucus vesiculosus* canopies. Measured primary production was higher than previous estimations (**Bordeyne et al., 2015**) and the emersion period has been revealed to be the most favorable one (**Bordeyne et al., 2017a**), although most researchers, until recently, considered no production during emersion. The food web of these two communities appeared very similar and presented an important seasonal stability despite growth variability of most primary producers (**Bordeyne et al. 2017b**). These communities were compared to other canopy-dominated intertidal communities along a European latitudinal gradient: results highlighted the mechanisms of stability (Cusson et al., 2015) and the control of canopy-forming species on the understory species and the strength of compensatory dynamics (Bulleri et al., 2012). Research on the structure and functioning of canopy-forming intertidal communities led to 6 articles during the period and collaboration, issued from MarBEF European network, occurred with 6 European laboratories.

Theme 2 Communities under anthropogenic pressure

The other part of the team project was to deal with anthropogenic pressure, both local and global.

The first point was to understand the effect of local high anthropogenic pressure (e.g. kelp and intertidal-macroalgae harvesting) on coastal benthic communities. *L. hyperborea* harvesting appeared to have an effect both on the diversity and the isotopic signatures of numerous consumers (Leclerc et al., 2015). Studies performed on harvested intertidal communities showed a strong short-term impact for all communities but a rapid recovery for most of them, with the notable exception of the *Ascophyllum nodosum*-dominated community (**Stagnol et al**., 2013, **2016a** & b). Following our studies, legal rules changed in France and *A. nodosum* is now cut 30 cm above the ground instead of 20 cm. We also published some length-weight and dry-fresh weight relationships that should help to standardize harvest-free monitoring and legal harvesting declaration (Stagnol et al. 2016c). Community recovery was also studied at the Europen scale (**Crowe et al., 2013**) and at local scale in different European regions (Valdivia et al., 2012; Migné et al., 2015). This research led to 6 articles during the period.

The second point was to understand the impact of climate change on coastal benthic communities. We participated to a modeling approach of the ecological niche of *Laminaria digitata* at the European scale under climate-change pressure. Results suggested complete population loss on the French coast from around 2050 (Raybaut et al., 2013). We also performed laboratory experiments to understand the effects of temperature increase and acidification of oceans. The team focused on calcified red algae (e;g. Martin et al., 2013; **Noisette et al., 2013**) and the invasive gastropod *Crepidula fornicata*, both at larval and adult stages (**Noisette et al., 2014** & 2015). Several collaborations have been initiated on these species as well as on other Mollusks and on fish with Iceland (**Egilsdottir et al., 2013**), Oceanic Observatory of Villefranche (Dorey et al., 2013; Gazeau et al., 2013) and several other European marine laboratories (e.g., **Kamenos et al., 2013**; Brodie et al., 2014; Nash et al., 2016). Last developments on this topic consisted in understanding the effects of climate change on trophic interactions, e.g. between macroalgae and herbivores (Riera et al., 2016). This research led to 19 articles during the period.

EFEB SWOT analysis

Strengths

The main strength of the team is the ability to look at the same time at diversity and functioning (primary and secondary production, food webs), *in situ* measurements and monitoring and long-term (3 to 6 months) laboratory experiments. We obtained technical support during the last years both for lab experiments (Jérôme Coudret, AI 25%) and field experiments (Olivier Bohner, T 100% and Stéphane Loisel AI 50%), that allows us more ambitious long-term lab experiments and field measurements. The use of colonization panels in the field (Ph-D F. Bordeyne, 2016; coll. Ch. Lejeusne, see below) will allow us to increase experiments at the community scale.

Weaknesses

We need to increase our ability to test climate change at the community scale or, at least, on some crucial interactions within the studied communities, by mixing more strongly *in situ* approaches (e.g. *in situ* colonization panels, *in situ* experiments on climate change) and laboratory experiments.

Opportunities

We started from 2016 a collaboration with Christophe Lejeusne (team Div&Co) on harbour communities (diversity, including introduced species, and functioning – respiration) that could lead to develop community-scale experiments.

There is also an important project led by FR2424 to build instrumented mesocosms allowing performing experiments at larger scale with better controlled conditions.

Finally, the future composition of the team, including chemists working on greenhouse gases, should help to consolidate the understanding of near shore processes and climate change.

Threats

Threats are concerning our ability to mix different approaches, including population scale (dynamics of dominant, or harvested or endangered species, connectivity), community scale (including trophic interactions, diversity - both taxonomic and functional - and the role of increasing numbers of introduced species) and the link with the dynamics of greenhouse gases in intertidal and the close subtidal environment greatly forced by local tidal currents and the high productivity of coastal community (e.g. CO_2 fluxes due to canopy-dominated communities).

Another crucial point is the replacement of the isotope mass spectrometer of FR2424 that is used by our team for almost all our research (*in situ* measurements and lab experiments) and allows us to develop new methods in collaboration with Cédric Leroux, responsible of the spectrometry platform. This equipment is now almost 20 years old and absolutely needs to be replaced. Development of methods adapted to our research cannot be performed by using external equipment.

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Campagne d'évaluation 2017 – 2018
UMR 7144 Adaptation et Diversité en Milieu Marin
Equipe: "Diversity and connectivity in coastal marine landscapes" (Divco)
Bilan 2012-2017

Composition durant le contrat actuel

Personnel Permanent	mouvement	Personnel Temporaire	période
BROQUET, Thomas (CR1)		BOUCHEMOUSSE Sarah (CRC)	Dec 15 – Jun 16
COMTET, Thierry (CR1)		GUZINSKI, Jaromir (CRC)	Nov 14 – Mar 17
COUDRET, Jerome (AI, 25%)	Since Feb 2012	KENWORTHY Joseph (CRC)	Jun 16 – Feb 18
DAGUIN-THIEBAUT, Claire (IR2, 90%)		LE CAM Sabrina (CRC)	Dec 13 – July 15
GENTIL, Franck (MCF)	Retirement Jan 2013	LECLERC Jean-Charles	Sep 14 – Sep 15
LEJEUSNE Christophe (MCF)	Hired (UPMC) Sep 14	MURPHY, James (CRC)	Nov 13 – Oct 15
LOISEL Stephane (AI, 25%)	Hired (CNRS) Dec 16	NICOLLE, Amandine (CRS)	Aug 12 – Oct 15
NICOLLE Amandine (MCF ENSTA)	Since Mar 2015	BACOUILLARD, Lise (DOC)	Oct 16. On going
THIEBAUT, Eric (PR, HDR)		BOUCHEMOUSSE, Sarah (DOC)	Nov 12 – Dec 15
VIARD, Frédérique (DR1, HDR)		DIJOUX, Laury (DOC)	Oct 10 – Jun 14
		GAUDIN, François (DOC)	Oct 13 – Mar 17
		MALFANT, Marine (DOC)	Nov 14. On going
		RIGOLET, Carine (DOC)	Oct 09 – Mar 13
		RIBARDIERE Ambre (DOC)	Oct 14. On going
		RIQUET Florentine (DOC)	Nov 09 -Oct 12
		SEREBRYAKOVA Alexandra (DOC)	Oct 14. On going
		BOUCHEMOUSSE Sarah (AI)	Avr 12 – Oct 12
		SCHOENN Jennifer (AI)	Mar 14
		DUBOIS Guillaume (IE)	Oct 13 – Jul 14
		ROBY Charlotte (IE)	Jan 12 – Jul 15
		LE MOAN Alan (IE)	Oct 15 – Feb 16

1- Divco: eco-evolutionary studies of marine dispersal and diversity

Pursuing along the lines of the project set-up in 2008, the team Divco is developing researches at the crossroads between ecology and evolutionary biology, notably through the study of natural or human-mediated dispersal in marine ecosystems. Dispersal is a complex and key eco-evolutionary process: it is influencing the diversity, the structure and the functioning of populations, species and communities. The team is studying dispersal at different temporal and spatial scales (e.g. through phylogeography, gene flow analyses, contemporary larval dispersal estimates). The work conducted is integrative across diverse spatio-temporal scales and biodiversity levels thanks to the complementary expertise of the team members who use and combine a diverse set of methods including experimental field work, field surveys, molecular analyses, and modelling. During the last five years, the team put particular efforts in developing new research questions (e.g. among-species gene flow) as well as new technologies to address unresolved questions. For instance, the team has developed i) elemental tagging to better understand larval dispersal paths and ii) SNPs using Rad-Sequencing or transcriptome data to investigate invasion and hybridization processes. In addition, community studies were also strengthened with progress towards i) coupling community diversity and functional ecology and ii) the use of metabarcoding to assess biodiversity. These developments have led to original results, opening windows towards new research projects. They are briefly presented in sections 2 to 4 below. As detailed in Annex 4, this research work led to the publication of 76 scientific papers (5 upon invitation; 23 from PhD (co-)supervised by Divco) and has been communicated over more than 70 congresses. Part of this work involved PhD theses (5 defended, 3 on-going). The research conducted in Divco has been built on International partnerships, as exemplified by the 38 (50%) papers published with foreign scientists, the membership in two international networks (GRDIs DEBMA and MARCO), the participation in 5 European projects (3 Era-net - NETBIOME, SEAS-ERA, Biodiversa, 2 Interreg projects), as well as bilateral exchanges and hosting of researchers from Chile, UK, Spain and Poland. Besides academic research, the team has also been strongly involved in outreach, teaching and expertise activities that are detailed in section 5.

2. Research activities - Theme 1: Dispersal ecology

Projects: PNEC EC2CO Geoprint, Dexpo; ANR CoManche, ANR-Biodiversa PERCEBES
Collaborations: LEMAR, LCABIE (Pau), ENSTA Bretagne, IFREMER Brest and Port-en-Bessin, University of Aveiro
Students: Master: Claire Bessin, Justine Doré, Florence Lebioda, Morgane Guillam
Network: GDR MARCO

Population connectivity in marine landscapes (i.e. seascapes) is a key feature for understanding major processes like population and community dynamics or the evolution of local adaptation. It is also a key parameter to predict population and species response to climate change (e.g. ability to migrate and colonize new territories), and to help designing marine protected areas. In many marine animals, connectivity relies on the dispersal of free-swimming pelagic larval stages. Determining connectivity patterns and understanding its consequences, thus rely on accurately quantifying larval dispersal and more broadly studying the ecology of larval dispersal. To address these questions, Divco members have developed for several years a multi-disciplinary framework mainly based on larval dispersal modelling (Theme 1) and population genetics studies (Theme 2). In the last five years, research was focused on two axes: 1) a better integration of biological traits and larval behavior in modelling and 2) the development of new methods, elemental fingerprinting, to get more accurate predictions about larval dispersal.
For the first axis, efforts were focused on the scallop *Pecten maximus*, a mollusk of ecological and economic interests, studied in the framework of the ANR project CoManche. The work by **Nicolle et al. (2017)** is exemplifying these researches: by incorporating in a hydrodynamic model several parameters describing temperature-dependence of the Pelagic Larval Duration (PLD) and swimming behavior, these studies showed the key role played by these biological features on the distribution of the larvae following their production. If it demonstrated the need for better integrating individual life-history traits to make more predictions of larval spread, it also highlighted the need to take into account demographic parameters (e.g. reproductive output, phenology) to properly describe the long-term persistence of local populations. Because of the expertise of the team in larval dispersal studies, team members were invited to contribute to European networks about this theme (e.g. **Phillipart et al. 2012**).
The second axis is a new one developed during this 5-year contract. The core idea behind our willingness to develop new methods to investigate larval dispersal came from lessons of our past pluridisciplinary studies: *post hoc* comparisons between population genetic studies and larval transport modelling most often showed discrepancies, notably because they address different time scales and developmental stages. We developed and tested the usefulness of an alternative method, biogeochemical tagging, using the slipper limpet *Crepidula fornicata* for which the Divco team had obtained many results based on alternative approaches (genetics, modelling). Two master theses carried out in the framework of a national project leaded by Divco (PNEC EC2CO GEOPRINT) showed that the method is reliable and promising to assess connectivity at the scale of the Western English Channel. For instance, the combination of 5 elements (Ni, Pb, Sr, U, Zn) measured in the embryonic shell of *C. fornicata* allowed to accurately distinguish individuals originating from the bay of Brest.
Each of the above mentioned methods have been extensively used individually or in combination using *post-hoc* comparisons. But studies merging data generated simultaneously (i.e. same species and same area) by modelling, genetics and elemental fingerprinting are rare. We have now tools and data that can be used for going beyond *post hoc* comparisons, through the development of a Bayesian framework that incorporates genetic and microchemistry data through the likelihood function, and the connectivity predictions from the biophysical model through priors on migration rates. This project has been submitted to the ANR (coordinated by Divco) although not yet funded.

3. Research activities Theme 2: Dispersal, gene flow and micro-evolutionary processes

Projects: ANR HySea & ISOBAR, Era-net Seaprolif & Invasives, Interreg Marinexus, PIA IDEALG, PICS Biol-In-Crust

Collaborations: ISEM (Montpellier), IMBE (Marseille), (Poitiers), ENTROPIE (Noumea), CCMAR (Univ. Faro), Aberdeen (UK) MBA (UK), Southampton Univ (UK), UCSC (Concepcion,Chile), Dublin (Ireland), EBD-CSIC (Sevilla, Spain), U. of South Pacific (Fidji Isl.).
Students: PhD: Sarah Bouchemousse, Laury Dijoux, Marine Malfant Ambre Ribardière, Florentine Riquet, Alexandra Serebyokava (co-tutored with U. Faro); Master 2: Bonnie Bailet, Aurelien Courteille, Jamie Hudson (co-tutored U. Southampton), Javier Pinochet (co-tutored UCSC Chile), Mathilde Salamon.
Network: GDR then GDRi MARCO, GDRI DEBMA, networks built on VECTORS European project
Invitation: International Symposium MoolTools; 5 invited papers leaded or co-authored.

Migration and genetic drift are two key evolutionary forces that have direct implications on the way genetic diversity is structured over time and space. They act in tight interaction with ecological processes relying on reproduction (influencing the effective size and thus genetic drift) and dispersal (sustaining exchanges of individuals, thus gene flow). The Divco members have a long-standing experience in using population genetics (theory and tools) to investigate these ecological processes. During the past five years, efforts were made to develop genomic tools (e.g. Rad-sequencing) to balance some limitations of more traditional methods. As pointed out in a review paper, co-authored by Divco under the GDR Marco umbrella (**Gagnaire et al. 2015**), these tools may offer new opportunities for more accurate assessment of marine connectivity. During this contract, we continued to work on diverse taxa (tunicates, mollusks, isopods, shrimps, seabirds, and algae), with a focus on: 1) unexpected patterns of genetic differentiation (chaotic genetic patchiness) that are commonly observed in marine species, 2) processes sustaining the successful establishment of introduced marine species, thus focusing on human-mediated dispersal, and 3) hybridization and introgression patterns, to investigate among-species gene flow, and their relationship with reproductive isolation mechanisms (e.g. sexual selection, genetic incompatibilities). Below are summarized some of our research outcomes.

Unstable genetic differentiation is often described in marine species with a free larval stage; such a pattern is unexpected because it occurs at a scale below the dispersal range of larvae (invited review **Eldon et al. 2016**). By using theoretical and simulation studies (e.g. **Broquet et al. 2013**), we showed that such patterns can however arise from a combination of strong variance in reproductive success (sweepstakes reproductive success) and collective dispersal (i.e. correlated dispersal path of two or more larvae from the same cohort). We tested these predictions by carrying empirical studies using *Crepidula fornicata* as a case study. We showed relationships between size and reproductive success and that sperm storage might be a key parameter of sex-change in this protandrous and gregarious species (**Broquet et al. 2015**). These life history traits may play an important role in buffering genetic drift reducing the likelihood of sweepstakes reproductive success. On the other hand, unexpected evidences in support of collective dispersal were obtained by studying pre- (larvae) and post- (benthic recruits and adults) dispersal stages (Riquet et al. in revision). This result calls for further studies to document the extent of collective dispersal in marine environments.

Besides natural dispersal, human activities are responsible for long-distance and jump dispersal. Successful biological introductions are puzzling processes (i.e. the invasion paradox). Conversely to what has been hypothesized for a long time, introductions in marine environment do not rely on a few introduced individuals. Using diverse taxa (e.g. algae, molluscs, tunicates) characterized by diverse life history traits (with or without larval stages, selfing or outcrossing), we showed that most introductions rely on multiple introductions, enhancing the genetic diversity of introduced populations. These findings and their evolutionary implications were the focus of two invited reviews (e.g. **Viard et al. 2016**). Two scenarios can explain the relation between genetic diversity and introduction success. We examined (and rejected) the hypothesis of selection on standing genetic variation on *Crepidula fornicata* (**Riquet et al. 2013**); an unlikely hypothesis also for the seaweed *Undaria pinnatifida* (PIA IDEALG, Guzinski et al. in prep.). The other scenario, i.e. success due to evolutionary novelties arisen from admixture between introduced lineages was notably addressed by examining hybridization processes (see below).

Understanding among-species gene flow and ascertaining species delineation are required for accurate connectivity studies, as pointed out in an invited review paper co-authored with partners of the GDRI MARCO (**Pante et al. 2015**). This research received support from two ANR projects coordinated by Divco (ANR ISOBAR and ANR HySea). In HySea, we investigated the extent of hybridization between native and non-native tunicates of the genus *Ciona*. By developing a post-genomic SNPs panel, combined with extensive field surveys and experimental work (laboratory crosses), we showed that the two species are not hybridizing in the wild: apparent hybridization patterns are in fact the outcome of ancient introgression (differential across the genome) between the two taxa (**Bouchemousse et al. 2016**). This isolation most probably results from genetic incompatibilities rather than environmental selection (PhD thesis of Marine Malfant). This work is exemplifying the need to take into account the long-term history of species when analyzing patterns observed with contemporary secondary contacts. Along the same lines, i.e. understanding the limits of inter-specific gene flow, the PhD thesis of Ambre Ribardière is investigating barriers to gene flow in the species complex *Jaera albifrons*. Combining field surveys, breeding experiments, microsatellite and RAD-seq analyses for two species (*J. albifrons* and *J. praehirsuta*), we found that i) these two species experience introgressive hybridization in some mixed populations while they are reproductively isolated in others (**Ribardière et al., 2017**), ii) ecological isolation and sexual isolation are both stronger in non-hybridizing sympatric populations, iii) introgression is differential across the genome and asymmetric sexual isolation is still acting in hybridizing populations, iv) the genomic diversity of hybridizing and non-hybridizing populations most likely results from a history of divergence followed by secondary contact with more or less gene flow between species. We are currently completing linkage map and genome scan analyses to describe the genomic architecture of divergence between species. All these results will be used to better characterize the different reproductive barriers and how they have evolved towards reproductive isolation or hybridization following secondary contact.

4. Research activities - Theme 3: Dispersal and community dynamics

Projects: Interreg projects VECTORS, VALMER, MARINEXUS, Aquanis2.0 (Fondation TOTAL), PNEC EC2CO BenthoClim, Conseil Général du Finistère, Brittany Region SAD
Collaborations: MBA (UK), PML (UK), Ifremer Brest & Dinard, UBO,
Students : PhD : Lise Bacouillard, Sarah Bouchemousse, François Gaudin; Master : Lucie Camanez, Marjorie Couton, Sophie Delerue-Ricard, François Gaudin, Katja Geiger, Guillaume Rolland, Jennifer Schoenn.
Network: GDR then GDRi MARCO, networks built on VECTORS European project
Invitation: International Symposium MoolTools; 1 invited paper

Dispersal and migration have not only consequences at the species level but also strongly influence community diversity and its changes over time. For instance, because migration allows escaping from unfavorable environmental conditions and colonizing new territories, spatial community shifts are expected (and has been documented) under climate change. Also, with human-mediated long-distance dispersal, new (introduced) species will contribute to the native community. As compared to the previous contract, studies at the 'community' level have been strengthened, in particular thanks to the PhD thesis of François Gaudin and the arrival in 2014 of a new lecturer, Christophe Lejeusne. Three axes were particularly well-developed during the last five years: 1) the analysis of long-term changes in community structure and functioning, 2) the investigation of communities established in marine urban habitats, still poorly studied and 3) the examination of the community diversity at pelagic larval stages.

As part of the PhD thesis of F. Gaudin, an in-depth investigation of the effects of climate change on species range distribution was carried out, using the English Channel as a case study. This area is a well-known biogeographical transition zone where many species reach their distribution range limits. Comparison of data collected with similar protocols and tools during a cool (1960-1970) and a warm (early 2010s) period showed that the documented warming did not translate into broad range shifts but into sharp changes in occurrence of cold-temperate (decrease) and warm-temperate (increase) species (Gaudin et al. in revision). In addition, species distribution models showed the importance of edaphic factors besides climatic factors. Ongoing climate change could lead to a decrease in benthic diversity at range limits, especially where connection routes are lacking for new migrants.

Climate change is only one facet of global change that is interacting with migration and dispersal. Habitat destruction and biological invasions are also important components of species range and abundance changes. This is exemplified by marine urban habitats, which are not surrogates of neighboring natural habitats. The Divco members have been studying harbors for a long time but with a focus on particular species (for marine invasion genetics studies). The team expanded its research to community level notably thanks to the PhD thesis of S. Bouchemousse and the post-doctoral researches of J.-C. Leclerc and J. Kenworthy. As part of the Marinexus project, regional assessments (in both France and UK) showed that non-indigenous species may represent up to 30% of the species established in harbors (**Bishop et al. 2015**). The proportion of non-indigenous ascidians can even reach locally 60% depending on marina and season (PhD Sarah Bouchemousse). *In situ* experimental approaches then showed that community diversity and structure is strongly influenced by the development of habitat-forming species, among which are conspicuous tunicate invaders, with implications on both facilitation processes and biotic resistance to invasion (Leclerc & Viard, in revision). Thanks to new projects, supervised by C. Lejeusne, the abiotic component is also now fully integrated. Biofouling assemblages are examined to investigate the response of native *vs.* non-native species to environmental factors in marinas. Using environmental survey and experimental approaches, the aim is to

understand how abiotic factors are drivers of harbor community assemblages and may potentially favor non-native species. First results seem to indicate a strong effect of abiotic parameters (e.g. pollution) within harbors with microscale heterogeneity and suggest a strong environmental filtering shaping harbor communities.
For studying community as a whole, Divco also developed new tools based on e-DNA and metabarcoding studies, which are very promising as pointed out in an invited review paper leaded by Divco (**Comtet et al. 2015**). We made a focus on non-indigenous species and larval stages in the pelagic community. Preliminary data were obtained during the Marinexus project: the data analyzed by Marjorie Couton (Master student starting a PhD in Oct. 2017, under the supervision of T. Comtet & F. Viard) showed that these approaches are very efficient for identifying non-indigenous species in the pelagic community: for example the larvae of *Crepidula fornicata* or *Ruditapes philippinarum* are easily recovered following Illumina sequencing on e-DNA obtained from pelagic sampling, in agreement with results obtained from traditional methods (morphological identification or use of DNA barcoding on single larvae). These preliminary results led the path for investigating several issues related to non-indigenous species expansion and dynamics, for instance the extent of propagule pressure in artificial *vs.* natural habitats, a topic addressed in the Aquanis2.0 project, funded by the Fondation TOTAL.

Other activities towards an enlarged community

Training and teaching activities have always been an important component of Divco activities: in the past five years, the team supervised master (9 M1 and 18 M2) and PhD (8 among which 5 defended) students and had been involved, including CNRS researchers, in teaching at licence, master and doctoral levels. Team members supervise master courses at UPMC, for instance EMGE, Divmarpol (since 2014) and Ecopop (until 2014), BioMex Faune. They belong to the scientific council of the Doctoral School ED227 (Sciences de la Nature et de l'Homme: écologie et evolution) and of the Doctoral School ED129 (Sciences de l'Environnement d'Ile de France). They are also involved in international courses as co-supervisor (e.g. one week Magistere course on molecular ecology applied to marine species, set-up by C. Daguin and F. Viard in collaboration with A. Brante and F.Tellier from UCSC Concepcion, Chile) or participant (e.g. Marine Evolutionary and Ecological Genomics 2017).
The team members disseminated their work **towards general public and scholars**, notably during the former Marinexus project in which public conferences, practical with scholars and various media (interviews, leaflet, movies) were used to disseminate the outcome of the project regarding biological introductions and marine conservation issues. This is now pursued with the Aquanis2.0 project (coord. F. Viard, funded by Fondation Total). Altogether, **23 person.outreach actions** occurred during the five past years**,** for example the team members participated to 1 national radio show (France Inter), 1 2x52 min movie for France 5 (national TV channel), 3 chapter books for general public (two as chapter leader), 3 articles for general public and 7 public lecture and debates.
It is a pressing issue to communicate science to an enlarged community regarding the numerous challenges in conservation of marine coastal environments. Divco members support **knowledge transfer to public bodies and decision-makers**, notably in the field of **biological invasion management** and **marine biodiversity conservation**. The basic research work carried out has repeatedly been the basis for more applied work, leading to the publication of reports, position papers or applied research papers in the fields of ecosystem services, marine conservation and indicators of trends (e.g **Araujo et al. 2016**, **Gallon et al. 2017**), and biological invasion managements (e.g. **Dias et al. 2017**). Due to their research expertise in fields strongly connected to on-going socio-economic and policy issues (e.g. marine protected areas, invasion biology), the team members have been contributing as consultant and contributed to eight reports/advices (e.g. farming of the non-indigenous brown alga wakame, Typology of marine habitats etc.). They contributed to different working groups on the Marine Strategy Framework Directive (descriptors 1, 2 and 4). They were appointed as members of national scientific councils (e.g. Marine Protected Area Agency then French Agency for Biodiversity) as well as in international advisory boards and expert groups (e.g. ICES-WGITMO, ICG-COBAM (OSPAR commission), lead author for ECA assessment report to IPBES, WRIMS).
Divco team members have been also strongly involved in **research management** in particular as deputy director of the Station Biologique of Roscoff (E.Thiebaut, who is in addition director of the OSU SBR) and deputy director of the Research unit AD2M (F.Viard). They are also members of **advisory boards & scientific councils** (e.g. MNHN scientific council, CNRS INEE scientific council (F.Viard)).

SWOT analysis

Strengths

1) Scientific skills of the team members are highly complementary.
2) Researches encompass a large number of approaches from theoretical predictions to empirical studies.
3) Very good knowledge in innovating tools (elemental fingerprinting, genomic) applied to non-model organisms,
4) Good visibility of our research (acknowledged by invitations for papers and conferences).

Weaknesses

1) Small team (5 PIs) including two PIs with responsibilities at local (e.g. E. Thiébaut deputy director of Station Biologique of Roscoff) level and participations to several advisory boards and scientific councils, and thus frequently absent from Roscoff.
2) not all PIs in the same building reducing the opportunities for informal discussions.

Opportunities

1) Strong scientific identity of the team regarding “connectivity – dispersal” and “invasion biology” which promote invitations and thus increase participations in national and international networks/projects,
2) mastering innovative tools that may benefit to other research groups,
3) Strong link with socio-economic activities/sectors,
4) Support from SBR technical and scientific core services (Mer, Genomer & ABIMS).

Threats

1) ANR lottery that makes difficult to build-up a scientific strategy,
2) scientific environment (remote site, outside of a traditional campus) involve efforts to contribute to collaborative researches and decreases the likelihood to attract very good students.

Vague D

Campagne d'évaluation 2017 – 2018

UMR 7144 Adaptation et Diversité en Milieu Marin

Adaptation et Biologie des Invertébrés en Conditions Extrêmes (ABICE)

Bilan 2012-2017

Composition during the current contract

Permanent Personnel	movement	TemporaryPersonnel	Time periode
ANDERSEN Ann (MCHC)		BIOY Alexis (DOC)	Oct 14 →
HOURDEZ Stéphane (CR1, HDR)		CASCELLA Kevin (DOC)	Oct 11 →Oct 14
JOLLIVET Didier (CR1)		DETREE Camille (DOC)	Oct 12 →Oct 15
LALLIER François (PRCE, HDR)		FUENZALIDA Gonzalo(DOC)	Apr 12 →Dec 16
LE GUEN Dominique (T)	→Apr 15 (deceased)	GUEZI Hayat (DOC)	Oct 10 →Dec 13
MARY Jean (MCF)		MANDON Perrine (DOC)	Oct 14 →
RUAULT Stéphanie (T)	Aug 16 →	PAPOT Claire (DOC)	Oct 13 →
ROSE-LE PORT Anne-Sophie (T)	→ Jul 14 (dispo)	PIQUET Bérénice (DOC)	Oct 16 →
TANGUY Arnaud (MCF)		THOMAS-BULLE Camille (DOC)	Oct 16 →
TOULLEC Jean-Yves (MCF, HDR)			

Adaptation and Biology of Invertebrates in Extreme Conditions Team Presentation

The ABICE group currently comprises 5 teachers-researchers (TR) and 2 researchers (R), as well as one technician. The group includes all the TR/R who work on marine extreme environments at the Station Biologique de Roscoff. The studied models all come from deep-sea hydrothermal vents, cold seeps, and polar environments (Arctic and Antarctic). The expertise and varied approaches used in the group allow us to tackle questions regarding the response to environmental variations and the evolution of adaptations. The group has established and maintains collaborations with local, national, and international partners.

Over the past 5-year contract, the ABICE group has published a total of 61 articles, and 45 communications were made in scientific meetings. A total of five PhDs were defended and four are currently underway. Our research activities were organized along two main research axes.

Axis 1- Evolution of species genomes under strong environmental constraints.

Resp. D. Jollivet

Other researchers involved: S. Hourdez, J. Mary
Main models: Annelids (families Alvinellidae and Polynoidae)
Multi-species approach, phylogenetic context, history of adaptive changes
Main Objectives: Adaptation to temperature and Adaptation to hypoxia

Axis 1.1 - Evolution of proteomes

Over the past 5-year contract, the research group has continued its efforts of trasncriptome sequencing for the two taxonomic groups that have been its main targets. We currently have a total of 12 Terebellidae/Alvinellidae and 15 species of Polynoidae that have been sequenced, representing different environments. A series of scripts written by Eric Fontanillas (post-doc, 2012-2013) allowed us to determine groups of orthologous genes between species for each taxon/family and to analyze the codon usage bias, and of their products in terms of protein sequences. By phylogenetically-constrained approaches, we were able to test the hypothesis of the directed character of some types of replacements, to evaluate the substitution rates, and to evaluate the selective pressures that acted on these genes during their evolution (e.g. **Bruneaux et al.**

2013). In the family Alvinellidae, our analyses showed that the common ancestor to all existing species was thermophilic (**Jollivet et al. 2012**) and that a relaxation of selective pressures, and even positive selection could have been associated to the colonization of colder environments and an evolution of proteins towards more flexible molecules, better adapted to lower temperatures (**Fontanillas et al., 2017**). An analysis based on the comparison of 13 transcriptomes of Polynoidae from shallow water Antarctic, temperate areas, abyssal areas, and deep-sea hydrothermal vents was also performed (P.-G. Brun, Masters 2). In this family, the inclusion of cold species from shallower depths did not show an adaptation to temperature but rather to depth (and therefore pressure).

Axis 1.2 – 'Adaptive' polymorphism and selection mechanisms in extreme environments

This topics is central to Alexis Bioy's PhD work (defense in Fall 2017) and is a direction towards which the research group has moved and will further be developed in the near future. The approach initially followed was the use of RNAseq on 6-10 individuals per species, choosing a pair of species (Terebellidae/Polynoidae) for each environment (Antarctica, intertidal and hydrothermal). Because of experimental problems, we shifted our approach to ddRAD sequencing. The pilot RNAseq study on an Antarfctic species of Terebellidae allowed us to show a reduced genetic diversity compared to other marine invertebrates. A wider study in terms of individuals and populations has also been started on alvinellid polychaetes (*A. pompejana* and *A. caudata*) and the species complex *B. azoricus/B. puteoserpentis* to evaluate the relative role of positive selection in the processes of on-going speciation in these species (PhD thesis: C. Thomas-Bulle).

Axis 1.3 - Evolution of specific genes and history of adaptive changes

During the past 5-year contract, we took advantage of full-length cDNA sequences of the enzyme phosphoglucomutase in the polychaete *A. pompejana* to (1) sequence the corresponding gene in its entirety and (2) characterize the charge polymorphism responsible for the different isoforms of this enzyme. These allozymes exhibit different thermal sensitivities (Jollivet et al., 1995, Piccino et al. 2004). The results showed that the 3 main forms found in the natural populations are the result of only two QE mutations both located on exon 3. An analysis of the nucleotidic polymorphism showed that these allelic lineages are maintained by balanced selection (strong inter-allele divergence), with a polymorphism that pre-existed the North/South differentiation of the species, about 1-2 Mya. In addition, the production of the different isoforms by directed mutagenesis and overexpression of the proteins showed that the double QE mutation is indeed responsible for the different thermal stability of the three isoforms (EE, QE, and EQ) by modifying the stability of the molecule near these specific sites.

A study of polymorphism of heat shock proteins (Hsp70s) was also carried out in two species of Antarctic euphausids (*E. superba* and *E. crystallorophias*) at the base of the trophic chain of all austral seas. This study aimed at evaluating the adaptive potential of these species in the context of the announced global climate warming and to evaluate the specific role of these chaperones in case of thermal stress through experiments (CTmax, DL50, heat shocks). The study showed that these proteins evolved by successive duplications to form at least 5 forms, all only lightly inducible. Form C (described as inducible in Crustacea) exhibits a balanced polymorphism of two diverging lineages and that one of the duplicated B forms was lost in *E. crystallorophias*. An combined analysis with the different Hsp70s loci and mitochondrial genes showed that *E. crystallorophias* experienced a strong bottleneck of its population and lost part of its evolutionary potential for this family of proteins, and therefore exhibits a more pronounced sensitivity to temperature.

In Polynoidae, the presence of hemoglobin is characteristic of deep-sea hydrothermal vent species, the littoral species only possess small amounts of an intracellular globin in their nervous system (neuroglobin). Some species also possess a tetradomain hemoglobin that arose through tandem duplication of an intracellular single-domain form (Projecto-Garcia et al., 2010). We showed that this tandem duplication produced strong structural constraints that produced positive selection on some amino acids potentially located in interdomain contact zones (**Projecto-Garcia et al., 2015**). Intracellular hemoglobins from Alvinellidae also exhibit interesting characteristics in response to temperature variations: the hemoglobin from *Alvinella pompejana* exhibits a reduced sensitivity compared to that of *Paralvinella grasslei* that possesses a normal sensitivity. We are using a directed mutagenesis and overexpression approach to decipher the structural bases of this different behavior.

Axis 2- Response of organisms to environmental conditions.

Resp. A. Tanguy

Other researchers involved: A. Andersen, F. Lallier, J. Mary, J.-Y. Toullec
Main models: Bivalve mollusks (deep-sea and littoral) and krill (polar environments)
Approach on target species (*Bathymodiolus*, *Loripes*, *Euphausia*), integrative (transcriptomics, proteomics, *in situ* hybridizations)
Main objectives: Response to environmental variations (temperature, oxygen, metals, sulfide, etc...).

Axis 2.1 - Mechanics of adaptation

Our research group studies the host-gill microbiont relationship in deep-sea mussels of the genus Bathymodiolus, among which some species inhabit hydrothermal vents, and others cold seeps. In the species we are studying, the mussels host either a single type of symbiont (sulfide-oxidizing, SOX) or two types of symbionts (SOX, and methanotrophic, MOX), both acquired from the environment. To study the mechanisms involved in the establishment and maintenance of the host-symbiont relationship, we analyzed the transcriptome and the proteome of mussels that were moved out of the fluid that contains sulfide and methane, essential for their symbionts (**Guezi et al. 2014**). This approach was carried out for *B. thermophilus* during the cruise MESCAL in 2010, 2012, and on *B. azoricus* during the cruises BioBaz and Momarsat in 2013. Compared to the mussels that were left on their original site, the displaced mussels experienced loss of symbionts that increased with time of displacement. In *B. thermophilus*, comparative transcriptomics on these mussels allowed the identification of 7000 genes whose expression varied according to the symbiont density. Among these genes, those involved in the inhibition or activation of apoptosis were noteworthy. The phenotypic study of apoptosis by histology (TUNEL) confirmed the trancriptomics results. A comparison of mussels collected under isobaric and non-isobaric conditions (BICOSE cruise, 2014) allowed us to show that decompression did not cause apoptosis and that the observed differences were likely due to the presence of symbionts (PhD B. Piquet, Oct 2015 →). In *B. azoricus* and *B. puteoserpentis*, the proportion of cells undergoing apoptosis is high (about 30% on average) compared to non-symbiotic littoral mussels (about 1%), suggesting a link between apoptosis and symbiosis, although the bacteriocytes are not the only cells affected. Apoptosis is not the sole regulatory mechanism either in the gills of mussels. Other studies are under way to investigate these cellular regulation mechanisms such as autophagy.

In *B azoricus*, we focused our attention on the analysis of two protein families of the host that are involved in the immune response: lysozymes and bacterial peptidoglycan recognition proteins (PGRP), as well as their potential role in the regulation of the symbiont load (PhD C. Détrée, defended Oct 2015). We first identified the diversity of isoforms in the transcriptome of *B. azoricus* then quantified the expression level of the different isoforms in animals that lost almost all their symbionts and compared it to those from individuals from the original populations. This allowed us to suggest that one of the six lysozyme isoforms could be involved in the degradation of the symbionts in the gills in individuals that have spent a long time away from the fluid source (**Détrée *et al.* 2016**). This study also showed that one of the five PGRP isoforms could be involved in the recruitment of the symbiotic bacteria (**Détrée *et al.* 2017**). Additional analyses have been conducted on the apoptotic process. We identified a large set of genes belonging to the different apoptotic pathways present in mollusk species. We found a complex response pattern and the involvement of specific isoforms of apoptotic regulators in response to symbiont loss (Giolland et al, in prep).

We also conducted a study on the response of *B. azoricus* to metals by combining natural and experimental population studies (PhD G. Fuenzalida). We combined transcriptomic and biochemical analysis to identify molecular mechanisms involved in metal response. We first found a large diversity of isoforms in gene families known to respond to metals (e.g. MT, SOD, ferritins) and detected specific expression patterns between populations illustrating the possibility to use such transcriptomic pattern as a population signature of environmental heterogeneity. However, we found a strong tissue partitioning according to metals that can be used as a population signature when coupled with the transcriptomic pattern. We also found a possible role of symbiotic bacteria in the process of metal tolerance and detoxication in *B. azoricus*. The microarray analysis also revealed that new pathways may be involved in metal response such as DNA repair, DNA methylation, energetic metabolism and immunity. Additional genetic analysis (mainly detection of SNPs) are conducted to identify putative correlation between genotype and phenotype (here using transcriptomic pattern).

Axis 2.2 - Response to temperature in polar species

Euphausids, also called krill, are a good model to study the diversity of adaptations, in particular to temperature, because they have a high species diversity and species exhibit a differential latitude distribution. They also are the main prey of marine predators such as sea birds or marine mammals. They thus form a keystone of the local food chain and a direct trophic link between extreme levels of that chain. The posterchild of this family of crustaceans is the Antarctic krill stricto sensu, Euphausia superba. It is also the most abundant, representing 50% of the zooplankton biomass in the Austral ocean. Euphausids includes

several members (Jarman et al., 2000), and all have circumpolar distributions, with borders that are mostly governed by their tolerance to temperature. They therefore are very apt models for phylogenetically-constrained studies whose goal is to understand the mechanisms that underlie the resilience/sensitivity in the context of global warming. The comparison between krill species from different environments (temperature, variability of temperature, …) showed differences in response to a thermal stress. In particular, these differences highlight the existence of strategies adapted to different environments, not only the CTmax but also the response of Hsp70s (**Cascella et al., 2015**; Huenerlage et al., 2016; **Papot et al., 2016**).
It then seemed important to widen the comparative aspect of this study by increasing the number of studied species according to their origin by following, for example, a gradient of latitude, with Antarctica as the most extreme. In this context, a transcriptomics approach is currently under way, on Antarctic and Subantarctic species, as well as boreal krill species to search for molecular signatures potentially associated with their geographic origin. To date, 4 krill transcriptomes are available in our laboratory: those from two Antarctic *Euphausia* (*E. superba* et *E. crystallorophias*) (Clark et al., 2011; **Toullec et al., 2013**) and those of two *Thysanoessa* from the Arctic (*T. raskii* et *T. inermis*) (Huenerlage et al., 2016). The sampling of the 6 new krill species (*E. frigida*, *T. macrura*, *E. triacantha*, *E. vallentini*, *E. longirostris*, *E. similis*) necessary was performed during the REPCCOIA 2017 cruise on the subantarctic-antarctic gradient. The sequencing is planned for the upcoming months.

Outreach and wider impact

Actions towards schools and a wide audience

The ABICE research group regularly takes part in the Fête de la Science, both through the visits of groups (schools and adults) and through talks/presentations given in local schools. We also regularly take part in the Nuit des Chercheurs organized at Océanopolis (Brest) during which 4000 people usually visit the different groups yearly. Finally, we have been invited to different radio emissions (France Inter, France Info) to communicate on the biology in extreme environments, and our Antarctic research was part of a France2 documentary.

Taxonomy workshops

The ABICE research group (A. Andersen, S. Hourdez) takes part or organizes workshops in taxonomy on polychaete families (Spionidae, Capitellidae, Polynoidae) opened to the private sector, in particular to employees of ecology consultancy firms.
S. Hourdez is a corresponding scientist for the Museum National d'Histoire Naturelle (MNHN) for annelids and has organized two identification workshops for the annelid fauna from the Tropical Deep-Sea Benthos research cruises in this context.

ABICE SWOT analysis

Strengths

A major strength of the ABICE research group was in the complementary nature of the expertise of the researchers and teachers-researchers that form the group, allowing us to the topics of adaptation to extreme environments under different lights. The range of expertise also allowed us to bridge different time scales, from the structure-function of proteins, to the evolution of species and of their genomes, via their physiological response to environmental variations, and in particular temperature, oxygen, methane, and hydrogen sulfide. The group also benefits from the recent acquisition of sequences from numerous transcriptomes of polychaetes, bivalves, and krill. It also possesses three eukaryotic genomes for our study models. The recognition of the 'Roscoff group' in the national and international community working on the biology of organisms from extreme environments is also great added value to develop collaborations (CONNECCT, InterRidge, …).

Weaknesses

Beside these great strengths, the research group suffers from a lack of technical help (only 2 technicians for 7 researchers and teachers-researchers). During the past 5-year program, this lack was especially pronounced after the departure of our two technicians. One of the two technicians (UPMC) indeed moved to Tahiti for 3 years (July 2013-August 2017) to follow her husband who was deployed there. The UPMC did not grant us her temporary replacement, despite oral promises. The other technician (CNRS) passed away in April 2016, after being ill for 5 months. She was only replaced 18 months later, through a FSEP call.

Over the past 5 years, our group also suffered from a lack of recruitment of young researchers and Engineer/Technician personnel. We applied every year for a bioinformatics engineer position, absolutely necessary to the progress of our studies on genome evolution in extreme environments. Although the Station Biologique de Roscoff has a bioinformatics service, most of their work is directed towards outside needs and the needs of local groups like ours cannot be satisfied. We have been asking for a bioinformatics engineer position for over 8 years and our research cannot progress as fast as it could because of this lack.

Opportunities

The lack of technical help is common to a lot of groups in the UMR 7144. With the planned fusion of the research groups, we hope to optimize the work on the technical help but without the recruitment of a large number of people, the problems can only last. The ABICE group has established fruitful collaborations to obtain and study the genomes of some of our model organisms, in particular from *Bathymodiolus azoricus* (collab. N. Satoh, Japan, hosting of a japanese post-doctoral fellow T. Takeuchi for 1 year), and from *Alvinella pompejana* and *Paralvinella sulfincola* (A. Claridge-Chang, Singapore). We will maintain these collaborations that allow us to expand our work in the future.

Threats

Access to our model organisms (hydrothermal vents, Antarctic/Arctic) remains difficult and costly. This makes a lot of in vivo experiments or breeding experiments to validate the phenotype/genotype relationships difficult. We have however been successful at obtaining funded expeditions and will continue to coordinate expeditions at sea (BioBaz, Chubacarc) and to Antarctica or the Arctic (KREVET, POLARIS, REPCCOIA) to collect the organisms from extreme environments. The past acquisition of samples and the large number of genes obtained by massive sequencing already allows us to work for a long time on the adaptive mechanisms of species without the need for the acquisition of new samples. Our collaborations also allow us to obtain samples from different regions of the globe.

Vague D

Campagne d'évaluation 2017 – 2018

UMR 7144 Adaptation et Diversité en Milieu Marin

Diversité et Interactions au sein du plancton marin (DIPO)

Bilan 2012-2017

Composition durant le contrat actuel

Personnel Permanent	mouvement	Personnel Temporaire	période
BAUDOUX Anne-Claire (CR1)		Pei GE (CRC)	Apr 2014-Feb 2016
		Marie LATIMIER (AI)	Mar 2013-Oct 2014
		David DEMORY (DOC)	Aug 2014-Jan 2017
		Laure ARSENIEFF (DOC) -50%	Oct 2015--
		Pierre-Yves MOCAER (DOC)	Nov 2016--
VAULOT Daniel (DRCE, HDR)		LOPES dos SANTOS (CRC)	Sep 2012-Oct 2017
		Catherine RIBEIRO (CRC)	Sep 2016--
		Valeria JIMENEZ (CRC)	Oct 2016--
		Margot TRAGIN (DOC)	Sep 2014-Dec 2017
NOT Fabrice (CR1, HDR)		Charles BACHY (CRC)	Oct 2016- Sep 2018
		Valeria JIMENEZ (CRC)	Oct 2016- Mar 2019
		Emilie VILLAR (CRC)	Juin 2016-Mai 2018
		Loic PILLET (CRC)	Dec 2013-Mai 2015
		Andres GUTIERREZ (CRC)	Sep 2013-Avr 2015
		Wei-Ting CHEN. Visiting PhD student. (Univ. Taiwan)	Nov 2016-Oct 2017
		Tristan BIARD (DOC)	Oct 2012-Dec 2015
GUILLOU Laure (DR2, HDR)		Aliou DIA (DOC) 50%	Oct 2010-Dec 2013
		Frédéric LEPELLETIER (DOC) 50%	Oct 2010-Dec 2013
		Khadidja KLOUCH (DOC)	Oct 2013-Dec 2016
		Ruibo CAI (DOC)	Oct 2016 --
		Lourdes VELO-SUARES (CRC)	Jan 2015-Oct 2015
		Mathieu GURI (CRC)	Jul 2012-Sep 2013
		Estelle BIGEARD (AI)	Dec 2008-Oct 2014
		Valérian LE ROY (AI)	Dec 2014--
		Marie LATIMIER (AI)	Mar 2015-Sep 2015
		Delphine SERPIN (AI)	Oct 2015-Sep 2016
		Martina STRITTMATTER (IR)	Jan 2017--
SIMON Nathalie (MCU, HDR)		Laure ARSENIEFF (DOC) – 50%	Oct 2015 --
BIGEARD Estelle (AI)	Since 2014		
LE GALL Florence (IE2)	Promot. 2016		
MARIE Dominique (IR1)			

Diversity and Interactions in Oceanic Plankton
Team Presentation

These last five years, the DIPO team published 118 publications (6 in Science, 2 in Nature, 6 in ISME J., 1 in PNAS, 1 in Ecology Letter). This work has been conducted through a range of national and international collaborations, in particular with Germany, Canada, Japan, Vietnam, Norway, Chile and Brazil and the team participated to field work in Antarctica (Jan 2015) and in the Arctic (Baffin Bay, May 2016) and all together our team spent collectively > 300 man-days on board of oceanographic ships to collect samples. The attractiveness of the team can be estimated by the number of PhD students and postdoc/IR hosted by the team (8 PhD and 12 postdoc). This activity was supported by our active participation in ANR projects (8 in total, 4 as coordinators) and European projects (especially Macumba and Micro B3). Since 2014, Estelle Bigeard obtained a permanent position as AI, and Florence Le Gall was promoted from AI to IE. The number of HDR increased in number from 2 to 4.

From new isolates in culture to complex community analyses, our main efforts focused on discovering and describing new species and symbiotic interactions (parasitism or mutualistic endosymbiosis), describing the geographical distribution of major planktonic groups and how symbiotic associations take place and shape temporal dynamics. Our projects covered different scales, from species and infraspecies diversities, from blooms to seasonal patterns, from local to large geographical scales.

1- Diversity of phototrophic marine protists

Marine microbes are a reservoir of hidden diversity and innovative evolutionary strategies. They have promising biotechnological and genomic potentials, but exploiting this potential is limited by a poor isolation success and low growth rates in culture. In the frame of the EU MaCuMBA project, we made a substantial effort to “cultivate the uncultivable”. The most important improvement is the development of a novel high throughput culturing approach based on flow cytometry sorting (**Marie et al. 2017**). Using this approach and others more classical techniques such as serial dilution, we isolated more than 600 strains of microalgae from a range of oceanic environments (Arctic, Atlantic and Pacific Ocean, coastal waters) that have been all deposited to the Roscoff Culture Collection. New isolates helped us improving the alpha-taxonomy of some important plankton taxa for which we revisited the taxonomy. Within green algae, we defined two new classes of Prasinophytes and 8 new species (**Lopes dos Santos, submitted**). We also proposed a complete revision of the genus *Micromonas,* one of the most abundant and cosmopolitan coastal picoplanktonic taxon **(Simon et al. in press)**. In collaboration with Japanese collaborators, we also revised the taxonomy of the flagellated Bolidophyceae by merging them with silica covered Parmales (**Ichinomiya et al. 2016**).
The majority of species living in symbioses are however refractory to isolation. This is the case for obligatory mutualistic symbioses. We used alternate strategy and made a long lasting effort to establish a high quality, morpho-molecular, reference database for Radiolaria and their microalgal symbionts using a single cell approach (**Biard et al. 2015, Decelle et al. 2012 & 2013**). All primary information (*i.e.* picture, sequence, collect location) related to this effort is stored in a dedicated database, Renkan (http://abims.sb-roscoff.fr/renkan/). This basic work led to significant re-assessment of the classification for two major groups of Radiolaria, the Acantharia and the Collodaria but also allowed building evolutionary history of the symbiotic relationships. We demonstrated the wide diversity of microalgal taxa involved: for example the widespread haptophyte genus *Phaeocystis* sp. forming symbiotic associations with the Acantharia (Radiolaria). We established the existence of a novel type of symbiosis between a unicellular alga (Haptophyta) and a nitrogen-fixing cyanobacterium (U-CYN). While the cyanobacterium provides fixed nitrogen to its host, the alga provides carbon to the cyanobacterium, which lacks carbon-fixation genes (**Thompson et al. 2012**). Recent works have shown that this symbiosis could be the major source of nitrogen fixation in the ocean, far exceeding that of *Trichodesmium*.

2- Spatial distribution

Metabarcoding approaches have opened new avenues for large scale global analyses. A very important step has been to establish reference databases (PR2: **Guillou et al. 2013**, Phytoref: **Decelle et al 2015**) critical for the analysis of the metabarcoding data, with the help of an international consortium of taxonomic experts. We then apply metabarcoding approaches to a wide range of systems and scales. As members of the coordinating body of several large international scale projects aiming at characterizing protist diversity through metabarcoding approaches, we actively participated to the global description of community diversity and structure. These projects focused on coastal European waters (BioMarKs project, **Massana et al. 2015,** Ocean Sampling Day**)** and oceanic ecosystems (Tara Ocean expedition, **de Vargas et al 2015**). We also led more focused investigations such as the role of oceanographic structure called the Agulhas rings on the transport of plankton communities from the Indian to the South Atlantic oceans (**Villar et al, 2015**).

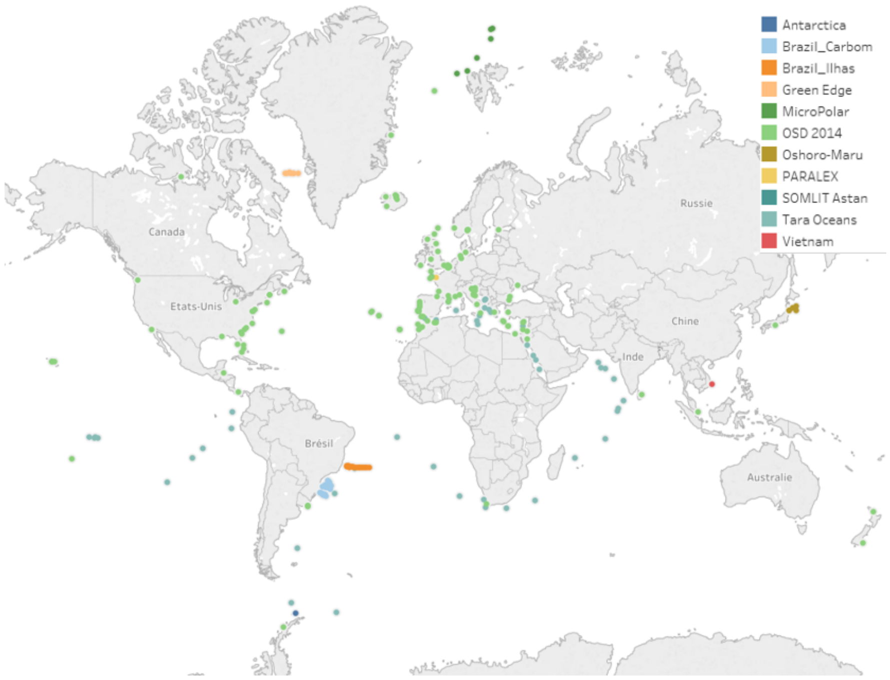


Fig. 1. Global map of the samples analyzed during the reference period, either global datasets to which we had access (OSD, Tara-Oceans) or from cruises to which we participated or for which we obtained samples (e.g. Green Edge, Oshoro-Maru).

We examined critically some taxonomic groups of algae such as Chlorophyta (**Tragin et al. 2016**) and Haptophyta (**Edvardsen et al. 2016**) and radiolarian. We analysed the spatial repartition of specific important taxonomic groups including Prasinophytes clade VII in oceanic waters (**Lopes dos Santos et al. 2016, 2017**), two genotypes of *Bathycoccus* differentially distributed in the open ocean (**Vannier et al. 2016**), different species and environmental clades of Bolidophyceae, demonstrating in particular that one species *T. pacifica* dominates this class in many ecosystems while another species *T. mediterranea*, initially isolated from the Mediterranean Sea, is indeed restricted to this oceanic area (**Ichinomiya et al. 2016**). We also focused on Radiolaria which are protists with a relatively large cell size. Some of them, the Collodaria, can form colonies that can reach several centimeters in size. Taking advantage of the large size of these radiolarian protists we used in situ imaging tools, deployed a several oceanographic research campaigns, to demonstrate their high abundance and contribution to oceanic biomass (**Biard et al. 2016**).

3- Temporal dynamics

Seasonal successions of plankton species and associated variations in biomass are keys to understand plankton ecology. The mechanisms producing the succession of planktonic species that takes place during a seasonal cycle are not totally elucidated. The SOMLIT-Astan time series has been established in the permanently mixed waters of the Western English Channel. The DIPO team has the scientific responsibility for microscopic phytoplankton species counts recorded since 2000 (RESOMAR-Pelagos database). In order to uncover the seasonal behaviour of all functional groups we produced 18S V4 metabarcodes from samples corresponding to the 2009-2011 period. Using this dataset, we recovered the classical cyclic successions of plankton taxa with a much higher precision than with classical methods and showed that the whole community (i.e. all functional groups as well as both abundant and rare taxa) were involved in the cyclic succession process (**Simon et al. in press**). Tight biotic interactions (involving highly specific symbiotic/parasitic associations, such as those observed for *Micromonas*, **Baudoux et al. 2015**) are among the key factors involved in the resilience of seasonal cyclic successions at the SOMLIT time-series site. To test this hypothesis, we monitored the seasonal fluctuations of the different *Micromonas* species together with their coexisting viruses. In most cases, a diverse viral community, specific of a given host species, controls the cyclic successions of *Micromonas* species (**Baudoux et al. 2015**). Co-speciation (tested using co-phylogeny approaches) predominates in this alga-virus system (**Bellec et al. 2014**). Our data suggest that prasinoviruses evolve more slowly than their microalgal hosts.

We also started to work at the population level. For that, we isolated a large number of strains from the toxic microalga *Alexandrium minutum* during blooms in the Penzé and the Rance estuaries (Brittany). We recorded the spatio-temporal genetic diversity using microsatellite markers (**Dia et al. 2014**), through a local collaboration with researchers from UMI3614. Results revealed a surprisingly high genotypic and genetic diversity, as well as the importance of sexual reproduction. We observed a significant spatial and temporal genetic differentiation during and between blooms. Concomitantly, we isolated about 300 strains of eukaryotic parasites infecting dinoflagellates (Perkinsozoa, Syndiniales, Fungi). We cross-infected *Alexandrium minutum* with co-occurring microeukaryotic parasites (**Lepelletier et al. 2014**) using strains isolated at different bloom periods and locations (**Blanquart et al. 2016**). We demonstrated that coevolution was possible even over the short time span of a bloom, although this pattern was geographically variable. Finally, through the co-supervision of a PhD student with IFREMER (Brest), we analyzed by a paleoecological approach based on ancient DNA (aDNA) the multidecadal dynamics of the toxic dinoflagellate *Alexandrium minutum* in the Bay of Brest (France) using historical records from dated sediment cores (over about 150 years). Although the first toxic bloom was observed in July 2012, presence of this species in the area can be dated back to 1873 ± 6 (**Klouch et al. 2016**).

4- Symbiotic interactions; establishment and stability

Using our models, we addressed the question of the stability of holobionts over time and in response to various environmental parameters. Radiolarians that are important contributor to oceanic biomass, form symbioses with dinoflagellate species in a similar way corals do. The aim of the IMPEKAB project, funded by the ANR (2015-2019), is to test whether plankton bleaching could occur. We perform experiments to test the effects of temperature rise on a radiolarian symbiosis (using Collodaria as models). We also performed sampling and experiments to understand the role of DMSP in planktonic symbiosis (**Gutierrez-Rodriguez et al. 2017**). DSMP and derived dimethylated sulfur compounds, are molecules playing important roles in biology (e.g. as antixoydants) but also at the ecosystems level (cloud formation, sulfuric rains). We demonstrated that planktonic symbiosis is a potentially significant but still unconsidered source of marine DMSP. Other abiotic factors such as natural nutrient amendment (through aerosol deposition and river flow) were also shown to have a significant impact on trophic interactions and more specifically on infection dynamics. Using mesocosms, we observed that Saharan dust deposition, which delivers N and P, induced notable changes in the abundance and composition of bacterial community, which coincided with an increase in virus abundance while heterotrophic nanoflagellate concentration remained unchanged (**Pulido-Villena et al. 2014)**. Numerical simulations of both dinoflagellates and their protozoan parasites indicated that they are both directly affected by nutrient availability (after heavy rains for example), but that the efficacy of the parasitic control of dinoflagellate blooms under temporary eutrophication depends strongly on the structure of the plankton community as a whole (**Alves-de-Souza et al. 2015**).

Laboratory studies revealed that temperature is a key factor in parasitic interactions (**Demory et al. 2017**). In *Micromonas*-virus host systems, temperatures below the host optimal temperature (T_{opt}) lengthen lytic cycle kinetics and reduce viral yield while infection at temperatures above T_{opt} prevent cell lysis in most case. Two mechanisms operated: hosts either prevented the production of viral progeny or maintained their ability to produce virions with no apparent cell lysis, pointing to a possible switch in viral life strategy.

We used a combination of physiology, transcriptomic and metabolomic approaches to characterize key molecular processes involved in symbiotic associations. Since our organisms are not well studied biology models and genomic data are lacking most of time, we started by acquiring reference transcriptomic data on holobionts (host + symbiont assemblage), and on host and/or symbiont alone **(Balzano et al 2015, Lu et al. 2014**, **Lu et al. 2016).** For example, two complete genomes of the parasite *Amoebophrya* (Syndiniales, about 150 MB) infecting dinoflagellates and having contrasting host specificity were sequenced and assembled in the frame of the ANRs HAPAR (in preparation).

Comparative structural analyses (proteomics, cryo-tomography) were also conducted to identify viral proteins involved in *Micromonas* host recognition, binding and specificity (ANR REVIREC). *Micromonas* virions package a complex suite of proteins not only involved in the structure of the virions but also in different functions that are required during the infection process (DNA replication, recombination and repair, nucleotide metabolism and transport, transcription, protein and lipid synthesis, signaling). This analysis led us to predict specific gene cassettes that contain proteins with strong similarities to bacteriophage tail spikes typically involved into host recognition.

5- Transversal activities (Teaching, Mediation/formation, Expertise)

A lot of long-term symbiotic associations, like parasitism or mutualistic symbioses, have been described a long time ago (sometime more than one century ago). Accessibility to publications is often limited because either the pdf are not available or the articles have been written in other languages than English (Russian, French, or German). We combined old and new literature in a web site (Aquasymbio:

http://www.aquasymbio.fr), focusing first on models we are currently focusing on (Syndiniales, Radiolarians).
The team plays a key role in the development of the Roscoff Culture Collection (RCC, which has become one of largest, if not the largest, collection of marine algal cultures in the world with over 4,000 strains that are distributed to both academic and private institutions in the five continents. The team has an important role providing novel cultures to the RCC through the isolation it carries during field cruises and projects but also by providing an invaluable taxonomic expertise to determine the identity of RCC strains. The RCC is also a critical resource for the team to conduct physiological and genomic studies of important protist species.

DIPO SWOT analysis

Strengths

Good cohesion of the team, with one annual 2-days retreat and mensual meetings.
High complementary of problematics, models and techniques between PI.
High dynamism of PI, with at least one ANR granted project per scientist of the team
High rate of international collaborations.
Expertise in taxonomy recognize at the international level
High attractiveness for students and postdocs
A taste for communication from a wide general audience to more specialists

Weaknesses

Long term curation of databases, which is a priority in most of our projects but very time consuming and difficult to finance via classical funding calls.
Big data are difficult to face in absence of qualified agent (bioinformatic).
Our leadership at the international level should be improved
Low collaboration with US

Opportunities

The three teams of the plankton group used to share resources and laboratory space. We propose to merge these three teams to form the unique ECOMAP team. All together, we expect to gain in visibility, competence and attractiveness at the national and international levels. This will help us also to smooth some thematic redundancy, and increase rates for scientific and technical exchanges between members. All together, we expect to share also fundamental resources such as database and tools (we are thinking about a unique structures for molecular databases, with tools and interfaces developed in common).

Risks

Big data: they are more and more easy to produce, but their analysis remains the main bottleneck. We miss competence in bioanalysis, databases, web-tools. This is a big risk for long-term common resources, in particular for reference databases.

Vague D
Campagne d'évaluation 2017 – 2018
UMR 7144 Adaptation et Diversité en Milieu Marin
Equipe Procaryotes Phototrophes Marins (MaPP)
Bilan 2012-2017

Composition during the current contract

Permanent staff	Temporary staff	Period
Laurence GARCZAREK (DR2, HDR)	Ngoc AN NGUYEN (CRC)	Oct 14 – Sep 16
Christian JEANTHON (DR2, HDR)	Dominique BOEUF (DOC)	Sep 09 – May 13
Dominique MARIE (IR 25%)	Dominique BOEUF (CRC)	Jun 13 - Dec 14
Frédéric PARTENSKY (DR1, HDR)	Delphine DUFFIEUX (AI)	Sep 13 – Dec 14
Morgane RATIN (IE)	Florian HUMILY (DOC)	Sep 09 – Jun 13
Christophe SIX (MCF, HDR)	Frédéric LE PELLETIER (DOC 50%)	Sep 10 – Dec 13
	Gregory FARRANT (DOC)	Sep 11– Mar 15
	Justine PITTERA (DOC)	Sep 13 – Dec 15
	Klervi CRENN (DOC)	Nov 13 – May 16
	Hugo DORÉ (DOC)	Sep 14 – on
	Théophile GREBERT (DOC)	Sep 14 – on
	Solène BRETON (DOC)	Nov 15 – on
	Ulysse GUYET (DOC)	Oct 16 – on
	Charles HALOUZE (IE)	Mar 13 – Aug 15
	Delphine SERPIN (AI)	Oct 15 – Apr16

Marine Phototrophic Prokaryotes Team Presentation

Members of the MaPP team are studying the most abundant bacteria living in the upper lit layer of oceans, which play a key role in biogeochemical cycles of major elements as well as in the functioning of the microbial loop. These include cyanobacteria, aerobic anoxygenic phototrophic (AAP) bacteria and proteorhodopsin (PR)-containing bacteria. Our main goals are to better understand the ecological success of these microorganisms as well as their *in situ* community structure by studying them at different taxonomic and organizational scales: gene, cell, community, ecosystem and the global ocean. By linking the biology and ecology of these microorganisms, this multi-scale approach allows us to decipher the genetic determinants and adaptations responsible for their respective distribution patterns.

In the 'perspectives' section of the previous 5-year report, our project was split into three main unifying topics that exploited at best the very complementary skills of the 4 researchers of the team:

1. Role of the genetic and/or pigment diversity on the distribution of phototrophic prokaryotes in culture and *in situ*.
2. Effects of environmental factors (biotic/abiotic) on the physiology of marine phototrophic prokaryotes
3. Adaptive mechanisms and genome evolution of marine picocyanobacteria

The past 5-year period gave rise to 2 book chapters and 43 publications ranked A including 1 Science, 5 PNAS and 3 ISME Journal with a mean impact factor of 5,9/article. In terms of training, our team has supervised 16 Master students, 10 PhD students, including 5 who defended their thesis during the past 5 years, with an average number of 4.25 publications per thesis.

Topic 1 Diversity and distribution of phototrophic prokaryotes

1- Diversity of cultured strains

In the framework of the EU-FP7-MaCuMBA (2012-2016) program, an important effort was brought toward the isolation and characterization of novel strains, notably for photoheterotrophic bacteria, since a large fraction of this genetically diverse component of marine prokaryotic communities remained uncultivated. About 1,300 strains were isolated from oligotrophic environments using a high-throughput dilution cultivation technique in low nutrient heterotrophic media that mimicked environmental conditions. The complete screening of the isolates revealed the presence of new genera and novel species, including members of uncultivated clades, whose complete characterization and genome sequencing are under way (Crenn et al., 2016; Jeanthon et al., in prep). Furthermore, more than 200 *Synechococcus* strains isolated and/or maintained by the Roscoff Culture Collection (RCC) were systematically characterized both genetically (*petB* sequencing) and in terms of pigment content (fluorescence excitation spectrum). Coupled with physico-chemical data measured at strain isolation sites, this information has notably been used to better understand the factors responsible for the ecological distribution of the main *Synechococcus* clades and pigment types (**Pittera et al., 2014**; **Farrant et al., 2016**; Grébert et al., subm. to PNAS).

2- Distribution and diversity of natural populations

The genetic and pigment diversity of phototrophic bacteria was also examined *in situ* in various trophic regimes and/or spectral niches in order to determine the niche partitioning of the different taxa at the global scale, a work notably supported by the EU-FP7-MicroB3 program (2011-15). The influence of environmental factors on the genetic diversity and distribution of the marine phototrophic bacteria was determined either by cloning-sequencing or next generation sequencing using the high resolution markers *petB* (encoding cytochrome b_6; Paulsen et al. 2016), *rpoC1* (RNA polymerase; Xia et al., 2017), *pufM* (encoding a subunit of the photochemical reaction center of AAP bacteria; **Boeuf et al., 2013**) and proteorhodopsin (PR) genes (**Boeuf et al., 2016**) or by recruitment from the 111 bacterial metagenomes of the *Tara* Oceans expedition (*petB* gene; **Farrant et al., 2016**) and from 139 metagenomes of the Ocean Sampling Day (*pufM*, PR and *petB* genes; Kopf et al. 2015; Fernandez-Guerra et al., in prep; Doré et al., in prep).

2.1- Cyanobacteria

These approaches have allowed us: i) to confirm the remarkable ubiquity of the *Synechococcus* genus, whose distribution extends up to 82.5 °N, ii) to unveil at the global ocean scale the specific ecological niches occupied by the different genetic groups of picocyanobacteria, iii) to reveal the global ecological importance of a few groups that were previously largely underestimated (CRD1, EnvB, sub-cluster 5.3) and iv) to show the occurrence of a wide microdiversity within populations previously considered as belonging to the same ecotype. Correlation analyses also showed that temperature, as well as iron and phosphorus limitation are the main factors affecting the distribution of marine *Synechococcus*. These studies open the path to predicting models of the distribution of phytoplankton in a context of global change.

The application of similar approaches to markers specific of the different *Synechococcus* pigment types also allowed us to i) determine the relative abundance and realized environmental niches of each pigment type at the global scale (Grébert et al., subm.) and ii) reveal the unexpected global abundance of chromatic acclimaters, *i.e.* cells able to change their pigment content according to the predominant light color (blue or green), which can account for up to 100% of the *Synechococcus* population at high latitude (Xia et al., 2017; Grébert et al., subm.). These data suggest that the ability to switch pigmentation according to the ambient light color likely confers a strong adaptive advantage with regard to strains displaying a fixed pigment content.

2.2- AAP and PR bacteria

The diversity and biogeography of AAP and/or PR bacteria was evaluated at different spatiotemporal scales from samples collected in the Arctic Ocean (Malina and Arctic cruises), in the Western English Channel (two-year cycle at Roscoff observatory site) and the global sequencing campaign OSD. Our analyses showed that: i) PR and AAP bacteria exhibit clearly opposite distribution patterns. While AAP bacteria can dominate transiently in temperate to cold freshwater influenced environments, PR bacteria prevail in oceanic waters (Boeuf et al., 2014), ii) AAP and PR communities can be structured differently according to geographical location and environment (**Lehours et al., 2015; Boeuf et al., 2016**). A clear distinction was observed between temperate and subtropical marine regions.

Using sets of *pufM* sequences from different oceanic biomes (**Boeuf et al., 2013; Lehours et al, 2015**), we prioritized the processes underlying AAP biogeographical patterns. Our results unambiguously indicate a dominant role of deterministic processes in influencing the continental-scale structuring of AAP bacteria at different taxonomic levels and reveal that AAP bacteria show strong habitat associations that have likely emerged through evolutionary adaptation. The identification of ecological cohesive clades for AAP bacteria suggests that prediction of AAP bacterial assemblages is possible from marine habitat properties (Lehours et al., Sci. Rep. in rev.).

We examined PR seasonal dynamics and temporal patterns of PR gene expression at the Roscoff observatory site. PR diversity exhibited a marked seasonal pattern. Nitrates and phosphates transported into the coastal zone from intense inland agriculture were major drivers in winter and fall, while the distribution of summer and spring communities were best explained by temperature, chlorophyll a and day length. Absolute abundances of major PR types demonstrated that SAR11 PR-type over-dominated stocks. PR types affiliated to SAR86 group and to Rhodobacterales were occasionally abundant in spring. The temporal separation of PR expression by the various PR types suggests distinct in situ physiological responses to environmental fluctuations (Boeuf et al., subm.). In the frame of above studies, we developed MicRhoDE, a comprehensive, high-quality and freely accessible database that should be highly valuable for upcoming studies of the biogeography, diversity, distribution and evolution of microbial (type 1) rhodopsins (Boeuf et al. 2015).

Topic 2 Ecophysiology of marine phototrophic prokaryotes

A second research topic of the team has consisted in understanding the responses of marine phototrophic prokaryotes to various environmental factors (biotic and abiotic) by studying the physiology of representative isolates.

1- Biotic factors

We studied interactions occurring between the diatoms *Thalassiosira* and *Chaetoceros* and their epibiotic bacteria in culture (long-term associations) and in natural communities (short-term associations). Culture and molecular approaches demonstrated that both diatoms carry distinct epibiotic bacterial communities in short- and long-term associations. Our results suggest that in controlled laboratory culture conditions bacterial-diatom and bacterial-bacterial interactions select for a simplified, but specific, epibiotic microbiota shaped and adapted for long-term associations (Crenn et al., subm.). Numerous commensal interactions have been identified, corresponding to the bacterial remineralization of organic matter. This study also highlighted that the surface of microalgae is a peculiar ecosystem where nearly half isolates represented new taxa (Crenn et al., 2016). In the light of our results, adaptation and specificity between bacteria and phytoplankton hosts may have an implication on the ecological structuring of phytoplankton communities in the ocean. Our results reflect the complexity of biotic interactions and provide methods and model organisms to further investigate the functional role of interacting partners using omics approaches.

2- Abiotic factors

2.1- Cyanobacteria

While most of the current knowledge about the physiology of marine *Synechococcus* derived from only 3 *Synechococcus* model strains, we have investigated during the 2012-2018 period a much larger panel of *Synechococcus* strains, representative of the major clades occurring in the field.

The effect of temperature was studied by measuring the optima and boundary limits for growth as well as short-term physiological responses to temperature of six strains isolated from different latitudes. These responses revealed the existence of *Synechococcus* lineages adapted to distinct thermal niches (**Pittera et al., 2014**). A further investigation of the physiological and molecular bases of this “thermotypic” differentiation showed that i) the thermostability of their light-harvesting complexes, and in particular of the phycobiliprotein located at the base of the phycobilisome rods (phycocyanin), varied according to the average sea temperature at strain isolation site (Pittera et al., 2016) and ii) the regulation of membrane fluidity occurs through specific mechanisms that adjust the composition of the membrane lipidome and that involve distinct sets of ecotype-specific lipid-desaturase enzymes (**Pittera et al., 2017**). Altogether, it seems that the thermoadaptability of marine *Synechococcus* has largely contributed to the remarkable ubiquity of these picocyanobacteria in the ocean. Besides temperature, we have also compared the photoacclimation strategies of *Prochlorococcus* and *Synechococcus* strains with regard to the light/dark cycle, supplemented or not with UV radiations (**Mella-Flores et al., 2012**). This study tends to support the view that *Prochlorococcus* is a specialist, restricted to a narrow environmental niche and surviving stressful hours of the day by launching a minimal set of protection mechanisms, while *Synechococcus* is more of a generalist able to cope with more variable environmental conditions, a difference consistent with their distinct niche partitioning and dynamics in the field.

2.2- Anoxygenic phototrophic bacterial mats

Mass blooms of purple sulfur bacteria develop during summer on sediments in the intertidal zone, especially on macroalgal deposits. The microbial composition of different types of mats differentially affected by the development of purple sulfur bacteria (*Chromatiaceae*) was examined, at low tide, using a set of biochemical markers (fatty acids, pigments) and composition was assessed against their influence on ecosystem functions (sediment cohesiveness, CO_2 fixation). We demonstrated that proliferation of purple sulfur bacteria has a major impact on intertidal mats diversity and functions (Hubas et al., 2013). Indeed, assemblages dominated by these bacteria were efficient exopolymer producers and their biostabilisation potential was significant. In addition, the massive growth of purple sulfur bacteria resulted in a net CO_2 degassing, whereas diatom dominated biofilms represented a net CO_2 sink. We combined stable isotope probing and NanoSIMS analysis to quantify carbon and nitrogen fluxes at the single-cell scale. Anoxygenic phototrophic mats incorporated a substantial amount of dissolved bicarbonate although they probably favoured organoheterotrophic pathways for their growth. Due the wide dispersion of purple sulfur bacteria in intertidal sediments, our study supports their unsuspected importance in the coastal carbon cycle (Hubas et al., subm.).

Topic 3 Adaptive mechanisms and genome evolution

1- Genome evolution and functional diversity of marine picocyanobacteria

During the last 5-years, we performed the assembly, functional annotation and comparison of 97 marine picocyanobacteria, including 32 unpublished *Synechococcus* strains, covering most of the genetic and pigment diversity known so far within this group. To do this, we have notably developed a custom-designed semi-automatic scaffolder, WiseScaffolder (Farrant et al., 2015) and a sophisticated information system Cyanorak v2 (www.sb-roscoff.fr/cyanorak/), which allows the manual curation of cluster of orthologous sequences. These genomic data were used i) to assess the relative weights of gene gain/loss *vs.* genetic divergence in the adaptation of marine picocyanobacterial clades to environmental niches (Doré et al., in prep.), and ii) as references to analyze the *Tara* Oceans meta-omic datasets in order to study the functional diversity of natural populations and its relationship with ecological niches. This approach has notably be used to better understand the functional bases of the strong shifts in the community composition occurring at small geographical scale along the *Tara Oceans* transect. A first study focused on 'Agulhas rings' (large water bodies generated in the Indian Ocean that drift across the South Atlantic Ocean) revealed a drastic shift in *Prochlorococcus* and *Synechococcus* communities, which, besides temperature, could partially be due to a nitrite anomaly within a young ring since the ecotype taking over the *Prochlorococcus* population had specific N assimilation uptake systems (**Villar et al. 2015**). A second study focused on the Marquesas Islands area, where the proximity of the island induced an Fe enrichment with regard to surrounding High Nutrient Low Chlorophyll (HNLC) waters, showed that while the *Prochlorococcus* community remains constant and transcriptionally unresponsive, the *Synechococcus* community shifted from a typical HNLC population to one more adapted to Fe-replete conditions in the vicinity of the island and displaying a strong transcriptomic response to Fe enrichment (Caputi et al., in rev). Thus, besides diversity studies, the availability of these genomes also allows us to target subpopulation displaying specific functions in the field.

2- Genomic bases and evolution of pigment diversity

Besides being genetically diverse, members of the *Synechococcus* genus also exhibit a wide pigment diversity, with three main pigment types defined based on the phycobiliprotein composition of phycobilisomes, pigment type 3 being itself subdivided into 'blue light specialists', 'green light specialists' and 'chromatic acclimaters' (CA4; see §1). Our knowledge on the genetic bases and ecological importance of CA4 has considerably advanced during the past 5-years, through a nice series of studies. Indeed, we have: i) discovered a small genomic island specific of CA4 strains and that has two possible configurations depending on clades: CA4-A and CA4-B (Humily et al., 2013), ii) biochemically characterized the function of several key genes of the CA4-A island including the phycobilin lyase-isomerase MpeZ (Shukla et al., 2012) and the dual regulation system FciA/B (**Sanfilippo et al. 2016**), and iii) characterized the role of four other lyases: MpeY and MpeU that are critical for blue and green light adaptation, respectively (Mahmoud et al. 2017; Sanfilippo et al. subm.), and the MpeW/MpeQ lyase couple that is specific of CA4-B strains (Grébert et al. in prep.). Most of this work was held in close collaboration with David Kehoe (Indiana University) and Wendy Schluchter (University of New Orleans). In parallel, we have compiled and maintain a public database, Cyanolyase, gathering information about phycobilin lyases from all sequenced cyanobacteria and proposing a prediction of their pigment content based on their specific lyase content (Bretaudeau et al. 2012).

Other activities and results

Besides studies on prokaryotic models, a number of collaborative works have been done on eukaryotes, including diatoms (Passarelli et al., 2015; Amiraux et al., 2016, Lavaud et al. 2016), dinoflagellates (Nézan et al. 2014; Blanquart et al., 2016), green picoalgae (Botebol et al. 2015, 2017, Cuvelier et al. 2017, Demory et al. 2017, Simon et al. 2017), perkinsozoans (Lepelletier et al., 2014), chytrids (Lepelletier et al. 2014), gastropod larvae (Leroy et al., 2012) and red macroalgae (Noisette et al. 2013). Advances made by the team on the biology, ecology and genome evolution of marine phototrophs as well as their involvement in photosymbioses were summarized in the context of the extant literature in three review articles (Coehlo et al., 2013; Hess et al., 2016; Not et al., 2016).

In the framework of transversal activities, members of the MaPP team are also involved in communication toward the general public and scholars through participation to conferences, open doors and general press articles, and in various scientific committees (EC2CO, Biogenouest, OSU Rennes). Lastly, the MaPP team is also heavily involved into academic teaching through the activity of C. Six, associate professor at UPMC, who is responsible for 3 teaching units (Licence and Master Degrees) and participated to the setup of the online teaching platform *e-MARIN'LAB*. The CNRS scientists also participated to some specialized courses to French or international students (e.g., summer course on "Marine Evolutionary & Ecological Genomics").

SWOT Analysis of the team

Strengths

1. Very complementary skills (topics and techniques) of the team members, allowing the production of multifaceted studies
2. Funding and/or staff already secured for a part of the objectives (until 2020)
3. Ease to recruit students interested by our topics, thanks to the presence of an associate professor in the team
4. Numerous omics data accumulated (genomes, transcriptomes, Tags from long-term monitoring stations)

Weakness

1. Lack of permanent ITA staff, in particular in bioanalysis and database development, which has been the subject of a staff request to the CNRS every year since 2009

Opportunities

1. Local: insertion of the team into the Plankton group allows: i) increased visibility facilitating the access to European projects; ii) sharing of skills, staff and equipment.
2. FR2424: access to common infrastructures: CRBM (RCC), long-term monitoring station (ASTAN) through the SOMLIT program and technical platforms (sequencing, bioinformatics, structural biology)
3. Regional: access to Biogenouest platforms (genomics, bioinformatics and transcriptomics)

4. National: involvement into EMBRC France and collaborative programs (Genoscope)
5. International: access to extended meta-omics datasets through several collaborative projects (Malaspina, *Tara* expeditions, OSD, etc.); insertion into European program (ASSEMBLE +).

Risks

1. Funding still to be acquired for some of the objectives
2. Recruitment of PhD students, indispensable to the realization of work projects, will be more difficult with the end of the OBEX targeted grants currently proposed by the Région Bretagne.
3. Management and analyses of massive NGS data requiring much manpower, storage and calculation power.
4. Loss of knowledge and bioinformatic skills due to poor transmission efficiency between CDD or PhD students, due to the lack of permanent engineer in bioinformatics.

Vague D

Campagne d'évaluation 2017 – 2018

UMR 7144 Adaptation et Diversité en Milieu Marin

Evolution des Protistes et des Ecosystèmes Pélagiques EPEP

Bilan 2012-2017

EPEP team membership during the period 2012-2017 (3 permanent, 9 postdoc, 7 PhD, 6 'ITA' ; total of 25)

Personnel Permanent	mouvement	Personnel Temporaire	période
DE VARGAS Colomban (DR2 - HDR)		MAHE Frédéric (CRC)	Jan 10 - Juillet 12
		MORARD Raphael (CRC)	Jan 11 - Juin 12 (2)
AUDIC Stéphane (IR1)	démission CNRS → Juin 2017	GOBET Angélique (CRC)	Fev 11 - Juillet 12 (4)
		COLIN Sebastien (CRC / IR)	Nov 12 – Aout 17 (4)
ROMAC Sarah (AI)	arrivée Sept 2015 →	RICHTER Daniel (CRC)	Nov 13 - Jan 17
		BERNEY Cédric (CRC)	Avril 14 - 19 (4)
		MULOT Matthieu (CRC)	Oct 16 - Oct 18
		BENDIF El-Mahdi (DOC/CRC)	Juin 08 - Nov 12 (2)
		DECELLE Johan (DOC/CRC)	Oct 09 - Avril 15 (3)
		LE BESCOT Noan (DOC)	Dec 10 - Sept 15 (4)
		HENRY Nicolas (DOC/IR)	Oct 12 - Avril 18 (4)
		RAMOND Pierre (DOC)	Oct 15 → 18
		RUBINAT Laura (DOC)	Oct 16 → 19
		CORRE Ewen (DOC)	Juillet 17 → 20
		GARRET Marie-Jose (AI/IE)	Mars 13 - Fev 15 (2)
		ROMAC Sarah (AI)	Jan 12 – Aug 15
		DIMIER Céline (IR)	Fev 10 - Aout 12 (3)
		MORDRET Solenn (AI)	Juillet 14 - Aout 14
		BERGER Calixte (IE)	Jan 15 - Aout 16 (2)
		GUIFFANT Damien (IR)	Juillet 13 - Dec 16 (3)
		POLLINA Thibaut (IE)	Oct 15 - Avril 16

Evolution of Protists and Pelagic Ecosystems
Team Presentation

The EPEP - *Evolution of Pelagic Ecosystems and Protists* - team, created in 2006 by a CNRS ATIP fellowship, is captivated by the co-evolution between eukaryotic Life and the Earth system. We are studying: (*i*) the biodiversity and ecological biodiversification of protists ; (*ii*) the physiogenomics and cell biology features of key marine protists, particularly from the plankton; (*iii*) the combination of (*i*) and (*ii*) into a systems ecology understanding of the plankton world, integrating across global organismal and spatio-temporal scales, including paleo-oceans. For this, we are applying novel tools in molecular and organismal aquatic ecology, allowing to bridge ecosystemic scales from genes to cells, to communities and biomes. We are notably developing innovative automated high-content microscopy and single-cell –*omics* technologies matching the extreme structural and genomic complexity of marine protists and allowing interpretation of their ecosystemic function by comparison to global meta-*omics* datasets. We believe that protists and plankton are exceptional models to understand self-organisation of complex adaptive systems at both the cellular and ecosystemic levels.

Keywords: marine plankton eco-systems biology and evolution; biodiversity of eukaryotes; protists, rhizarians and haptophytes; symbioses, mixotrophy, sex, and biomineralization in marine protists; co-evolution between protistan life and the Earth system.

Activities & Results (2012 - 2017)

Introduction. In the period 2012-2017, the EPEP team has **created and coordinated 4 major international research efforts toward a global, eco-systemic understanding of protist and plankton ecology and evolution**. In ***BioMarKs*** (EU EraNet, 1.6 million €; http://www.biomarks.eu), we developed standardized sampling protocols to collect meaningful morpho-genetic information from total eukaryotic plankton communities, from the smallest cells to animals, as well as several molecular ecology and eco-bioinformatics protocols to assess total biodiversity of marine protists through DNA metabarcoding (e.g. **Guillou et al. 2013**; **Logares et al. 2014**; Massana et al. 2015). In *POSEIDON* (ANR, 556 K€) and ***OCEANOMICS*** (PIA, 7 million €; http://www.oceanomics.eu/), we applied and extended the *BioMarKs* protocols (e.g. Alberti et al. 2017) toward an eco-systemic sampling of the world ocean plankton (Pesant et al. 2015) across global biogeographical and organismal scales (from viruses to animals) during the *Tara Oceans* expeditions (**Bork et al. 2015**), which we initiated with colleagues from EMBL (E. Karsenti et al.), Villefranche/Mer (G. Gorsky et al.), Genoscope (P. Wincker et al.), and ENS (C. Bowler et al.). Most of the last 5 years were dedicated to creating, coordinating, and playing a central role in *OCEANOMICS*, **the core research effort to organize, process, exploit, and share the samples and data collected during the *Tara Oceans* circum-global expeditions**. In ***UniEuk*** (1.14 million €, http://unieuk.org/), we are building a community-based and expert-driven, online adaptive taxonomic framework for eukaryotes, allowing not only to create a common language in protistology, but also to centralize and organize current community eco-mopho-genetic knowledge on protists, and link it to the deluge of protist meta-omics data emerging from environmental surveys (**Berney et al. 2017**). In P2 - ***Plankton Planet*** (http://planktonplanet.org/), we have streamlined sampling-protocols from *BioMarKs*/*Tara* Oceans into eco/user-friendly citizen plankton kits, and launched the first program of citizen oceanography aiming at linking the sailing and scientific communities in an effort to sample, understand and model marine plankton at unprecedented levels of resolution.

Our activities and results are summarized below in 3 points.

1. Assembling a conceptual, methodological, and database framework toward global protist and plankton systems ecology.

Tara Oceans (*T*O)' long-term goal is to understand the ecological and evolutionary principles underlying the functioning of a complex adaptive ecological system at the planetary scale. During two circum-global navigations, we systematically collected eco-morpho-genetic data at 210 sites and 3 depths, covering most biogeographical provinces of the world's ocean. We came back with a treasure-trove of ~40,000 standardized plankton samples embedded into a rich context of physico-chemical parameters. Thanks to *OCEANOMICS*, the consortium could generate, organize, and start analyzing data generated from these samples: >250 billion paired DNA reads (or >50 Terabases of raw DNA data) and >6 million images of single plankton (>30 Terabytes of raw data), obtained across 11 organismal size-fractions (>8 500 plankton sub-communities) with a combination of innovative multi-omics and automated imaging protocols. This represents today by far **the most comprehensive, publicly available, description of a planetary biome, and a critical base line to assess Earth-system changes.**

One of the strength of the program is the strict standardization of sampling and data-generation procedures, and the archiving of samples and data collections in **long-term open access European infrastructures** for DNA sequences (**ENA**, http://www.ebi.ac.uk/ena), images (**EuBI**, http://www.eurobioimaging.eu/), and environmental data (**PANGAEA**, http://www.pangaea.de), ensuring that this plankton knowledge base remains FAIR (Findable, Accessible, Interoperable and Reusable) to all. The first *Tara* Oceanomics results had significant scientific and societal impact, with notably the publication of 9 papers in *Nature* and *Science* in 2015/16 (**de Vargas et al., Sunagawa et al, Brum et al., Lima-Mendez et al., Villar et al. 2015**; **Guidi et al.**, Roux et al., Biard et al., **2016**), and 3 more under revision in *Nature* in 2017 (Carradec et al., Richter et al., Caputi et al, 2017). A synthetic view of *Tara* Oceanomics results is available in our '*2017 Tara Oceans/Oceanomics State of the Art*' report *(13 Mo)*.

We - *EPEP* team - are responsible for protist samples and data in *T*O. >45% of *T*O morpho-genetic sampling effort was focused on protists. We applied the full power of our multi-omics (metabarcoding, metatranscriptomics, metagenomics, single-cell genomics) and automated imaging (eHCFM, FlowCam, Zooscan, UVP) workflow to generate ~170 billion DNA paired-reads and >1.5 million images from ~1,000 plankton communities in 4 organismal size-fractions from pico- to micro-plankton. This is **by far the largest consistent morpho-genetic dataset of protist biocomplexity from a single biome** (see Annex 4 I.5, Databases 1, 2), which we leveraged by creating a series of new protist DNA barcodes (e.g. **Guillou et al., 2013**; **Decelle et al., 2015**; Morard et al. 2015) transcriptomes (Annex 4 I.5, Databases 3c), and single-cell genomes (Annex 4 I.5, Databases 4) **reference databases** for taxonomic and functional annotation of the deluge of new environmental omics data. We are also building a universal taxonomic framework for eukaryotes implemented at EBI (*UniEuk*: http://unieuk.org; **Berney et al., 2017**), in order to unite the complex past and future phen-omics protist data under a single ontology. One of the 3 *UniEuk* modules, the *EukBank*, combines a home-made ultra-fast algorithm generating stable clusters of amplicons (*Swarm*, **Mahé et al. 2015**) and state-of-the-art methods of phylogenetic placement, to centralize, standardize, and reduce/integrate the complexity of eukaryotic high-throughput DNA metabarcoding datasets into a unique and community-explorable reference repository. This should dramatically boost collective knowledge toward a global, trans-biome (e.g. **Mahé et al. 2017**) perspective on eukaryotic diversity.

Arguably our main technological development is a new imaging method, denoted **e-HCFM** (for **environmental High-Content Fluorescence Microscopy**), which can interface advanced cell biology with ecology and evolution of the bewildering environmental diversity of microbial eukaryotes. The e-HCFM workflow (in press in eLIFE; **Colin et al. 2017**) enables quantitative 3D-fluorescent imaging of cell structures (and potentially expressed genes) across the full diversity of microbial eukaryotes, while recognizing and classifying the imaged taxa. It can further be used to explore the multipartite (transkingdom) symbioses that all eukaryotic cells are made of, including mitochondria, chloroplasts, and extant organisms. Finally, in the frame of our *Plankton Planet* - P2 initiative, we have developed a streamlined plankton sampling protocol, requiring neither chemicals nor electricity, to collect plankton from citizen sailing boats for total diversity analyses by DNA metabarcoding. Following the same philosophy, we are working on a new modular and low-cost miscroscope, the *planktoscope*, for quantitative live imaging by citizen sailors (*planktonauts*!), in collaboration with Dr. Prakash, Standford University. The long-term goal is to deploy these P2 protocols every other year, along 5 major navigation loops cornering the world oceans, in order to get a much denser and wider spatio-temporal sampling of plankton from the world surface oceans.

2. Main findings in marine planktonic protists biodiversity, ecology, and evolution.

Our primary large-scale DNA metabarcoding analysis (**de Vargas et al., 2015**) revealed ~150,000 eukaryotic genera in the euphotic zone of the world ocean, >85% of which are protists, essentially heterotrophic taxa (e.g. **Flegontova et al., 2016**), including many uncharacterized parasites and symbionts (Cabello et al., 2016; Cornejo-Castillo et al., 2016; **Mordret et al., 2016**), in addition to the better known components of plankton ecosystems such as diatoms (Malviya et al., 2016), dinoflagellates (**Le Bescot et al. 2015**), or ciliates (Gimmler et al., 2016). Reconstruction of the first global plankton interactome (**Lima-Mendez et al., 2015**) and plankton sub-networks (**Guidi et al., 2016**) confirmed the central role of parasitic and photosymbiotic protists as keystone taxa increasing the connectivity of plankton food-webs and the flux of carbon to deeper layers of the ocean. Underwater video-profiling reinforced the abundance of giant photosymbiotic rhizarian protists whose biomass exceeds that of all zooplankton in (sub)tropical oceans (Biard et al., 2016). In a collaborative effort led by the Genoscope team, we then sequenced ~450 community transcriptomes together with ~300 genomes from single cells of mostly heterotrophic protists. While our single-cell genomics survey unveiled hidden functional complexity and niche differentiation partly explaining the wide diversity of heterotrophic protists (Seeleuthner et al., in revision; Vannier et al. 2016), the metatranscriptomics data revealed an extreme richness of >116 million, mostly unknown eukaryotic genes, without reaching saturation (Carradec et al., in revision; Annex 4.5 Databases 4) – note that lower sequencing efforts of prokaryotic and viral plankton size-fractions have saturated gene richness at respectively 40 million (**Sunagawa et al. 2015**) and 1 million (**Brum et al., 2015**). Thanks to this *Tara* Oceans effort, protists emerge today as the richest biotic compartment in the world plankton, their fundamentally symbiotic nature increasing the complexity and connectivity of ecosystems.

Beside this eco-systemic view of marine planktonic protists, we pursued our more focused research on haptophytes (e.g. **Read et al. 2013**; Bittner et al. 2013; **Von Dassow et al. 2015**; Durak et al. 2016), photosymbioses (e.g. **Decelle et al. 2012**; **Mordret et al. 2016**; Cornejo-Castillo et al. 2016), and biomineralization (**Marron et al. 2016**).

3. Oceans systems ecology and evolution.

We contributed significantly to the *T*O consortium effort to assess marine plankton systems ecology across global spatial, temporal, and taxonomic scales. Drafting the first global plankton interactome spanning all domains of life (Annex 4 I.5 Databases 4f), we discovered that biotic interactions predominate over environmental influences in shaping community structure (**Lima-Mendez et al., *Science*, 2015**). A further potentially paradigm-shifting finding was the prevalence of symbiosis *sensu lato*, challenging the classical view of food webs of producers and consumers. In **Guidi et al (*Nature*, 2016)** we went further and applied systems biology inspired network-partitioning methods to identify euphotic plankton sub-communities and gene modules associated with carbon export from the upper photic zone to the ocean interior, demonstrating our capacity to shift focus from genes to ecosystems and extract insightful hypotheses about key ocean biogeochemical processes. The **Villar et al. (*Science*, 2015)** study of the impact of the Agulhas choke point on plankton ecosystems (Annex 4 I.5 Databases 4f) demonstrated how the *T*O eco-morpho-genetic dataset can address basin scale oceanographic questions. The resulting hypothesis about the impact of Agulhas Rings on transported communities from the Indian to the Atlantic Ocean, successfully simulated in the MIT-GCM model, was only possible via the integration of *in situ* metagenomics data with fine grained physico-chemical contextual measurements. This achievement in deciphering plankton dispersal has been continued with a global analysis of the influence of ocean circulation on plankton biogeography that shows the dominating role of lagrangian currents in shaping plankton communities on a characteristic timescale of 1.5 years (Richter et al, *Nature*, *in revision*). Finally, in Caputi et al (*Nature*, *in revision*) we described the dynamic plankton response, from genes to communities, to the key micronutrient iron. Specifically, we identified sub-communities that displayed global distribution patterns associated with iron concentrations, responding locally to iron with different evolutionary strategies. Collectively, these initial studies represent unprecedented scale systems biology analyses of a global ecosystem and are today an international reference.

EPEP SWOT Analysis

Strengths

- a long-term scientific vision that marine eukaryotic cells and planktonic ecosystems are great models for (eco)systems biology, to be explored at various levels of spatio-temporal resolution, from molecules to biomes, from past to modern oceans. It is likely that the ‘systems’ properties of eukaryotic cells, driven by their exceptional capacity for symbioses, a largely determining the properties of today’s ecosystems.

- a capacity to unite strong international teams around this scientific vision. We played a central role in convincing key members of the *Tara* Oceans consortium to jump on board for the long route, and attract critical collaborators. In particular we convinced the Genoscope team (J. Weissenbach and P. Wincker) to embark and have initiated the Genoscope to oceans ecology; we recruited also M. Sieracki (USA; currently head of NSF oceanography), S. Acinas (ICM Barcelona), and H. Ogata (Kyoto Uni, Japan) and P. Hingamp (MIO), who respectively coordinate the fields of ‘single-cell *omics*’, ‘prokaryotes’, and ‘eukaryotic viruses’ in *T*O. We organized a series of international symposia around our research themes (see Annex 4 II.4), including the first EMBO EMBL symposium on aquatic micro-eukaryotes in 2016.

- the recruitment and tutoring of brilliant PhD and postdoc collaborators, who have all pursued their scientific career (see Annex 4.II.5), including 3 with permanent jobs in Israel (Jerusalem Uni), Germany (MARUM), and France (CIRAD).

- a capacity to get and manage significant research grants and share discoveries and knowledge through high-level publications. All together, we raised and managed over the last 5 years a budget of 10.8 million € contributing to the global ‘plankton eco-systems’ research, half of which was channeled directly through the UMR7144 (see Annex 4 II.7). In the same period, the EPEP team has co-authored 105 publications, including 47 with impact factors >5 (Annex 4 I.1; Bibliometric Table + EPEP papers). The productivity of the team has significantly increased over the last 3 years, with 61 papers including 6 *Science*, 6 *Nature*, 3 *Nature Communications*, 1 *PNAS*, 1 *eLIFE*, 2 *Current Biology*, 8 *ISME J.*, etc.

Weaknesses

- some difficulty to establish collaborations within the ‘Station Biologique de Roscoff’, as compared to our strong international network.

- a clear taste to uncover new frontiers and start exploring new ideas, sometimes at the expense of getting deeper into promising discoveries.
- a difficulty to deal with the ever-increasing administrative and emails load, which seems to be proportional to the success rate of a team.

Opportunities

The new proposed structure in 3 larger groups will hopefully increase collaborations and knowledge sharing at the level of the UMR7144, although the organization in smaller teams associated in a medium-size group sharing material, space, ideas and skills as in the previous ‘groupe plancton’ proved to be highly manageable and successful. However, the new ECOMAP team will build upon pre-existing organized subgroups, and by proposing new federative research axes should favor integration between the researchers that cover complementary expertises in plankton ecology (viruses, prokaryotes, eukaryotes, ecosystems).

Beyond Roscoff, the *Tara* Oceans international consortium is today a highly structured and vibrant group, with synergizing skills in plankton ecology, oceanography, cell and systems biology, genomics, imaging, and long-term databasing. The EPEP team plays a pivotal role in this network involving top-notch individuals from CNRS (Roscoff, Villefranche/Mer, Banyuls, Nantes, Marseille), EMBL and EBI (Heidelberg, Cambridge), ENS-Paris, CEA (Evry, Grenoble), the TARA Foundation (Paris), and several foreign institutes in Italy, Spain, Belgium, Japan, and the USA. The *T*O consortium has not only assembled the most comprehensive collection of homogenous samples and data for any planetary biome (still largely untapped), but is today pioneering a pan-ecosystemic modeling of the world Ocean based on actual biological data embedded into a rich context of physico-chemical parameters. This represents a great opportunity for the ECOMAP team, in terms of samples and data flow, as well as analytical expertise (notably in ecoinformatics and systems modeling), and the EPEP sub-group will make sure that the *T*O savoir-faire permeates the ECOMAP team.

Risks

At the level of the team:

- the impossibility to continue great work with highly-skilled research associates, who do not have good-enough CV to get permanent job at CNRS or UPMC, but are perfectly fine with CDD contracts easily renewed by the quality of the work generated. This has been the case notably for 2 key functions in the team: research management and automated fluorescent microscopy. Given the scarcity of permanent position at CNRS (and even more so at UPMC), and the increased mobility/adaptability of researchers, this becomes a very serious barrier to develop ambitious innovative research.
- the resigning from CNRS in 2017 of S. Audic, bioinformatician research engineer in the team playing a critical role in all EPEP projects (all dealing with heterogenous eco-morpho-genetic big data). The replacement/conservation of this position is critical for the continuity of the long-term, well-funded research effort, including *Tara* Oceans.

At the level of the UMR:

- the inverted pyramids between to many researchers/research directors and to few engineers and technicians, combined to the idea to share the IT time between all CR/DR. This may strongly and negatively impact the overall *savoir-faire* and the motivation of the ITs.

4. AD2M SWOT Analysis

Research	**Strengths**	**Weaknesses**
	Consolidation of technical staff for experimentation and lab analysis A broad palette of scientific skills among researchers and engineers allowing a wide coverage of models and approaches Globally good funding leverage (ANR, Regional, Foundations,...) Still at the leading edge for -omics applied to marine ecology, and for high frequency in situ data acquisition Top publications and high national (CNRS silver medal, Acad Sc prix mer) and international recognition with a broad range of international collaboration. Also true at local, regional scale: good complementarity with Brest for example	Still a low permanent technical support (1 for 2 researchers), and particularly no UPMC investment in research units on this aspect Some difiiculty to attract excellent PhD students (less so for post-docs) or new researchers* in the "small and remote Roscoff campus"; *top level needed to enter CNRS Training temporary staff and having to get rid of them too soon Decrease of new European funded projects
	Opportunities	**Threats**
	A few Starting or Advanced ERC candidates may show up A new university context (Sorbonne U & Institut des Sciences de la Mer) may offer new opportunities Reorganized, larger teams to promote even more complementarity and increase internal exchanges of technics and ideas	End of PIA projects (Oceanomics, IDEALG, EMBRC-Fr) Big Data: we need permanent engineers to better exploit the amount of excellent data we collect (bioinformatics / databases) New developments hard to maintain in lab on the long run (HF acquisition, cytometry, databases,,...) ANR is too much of a lottery and some teams are not lucky (e.g. proposal rated very good but rebutted 4y in a row). Makes it difficult to build a scientific strategy
Training through research	**Strengths**	**Weaknesses**
	Maintenance of previous strengths Good balance between researchers and teachers in the lab Strong contribution from (and towards) Master (10/y) and PhD (6/y) students, thanks to regional support. Strong involvement of teachers and researchers in Master classes	Heavy cost of master training impact research funding Weak involvement of UPMC in the main doctoral school for our lab (ED227)
	Opportunities	**Threats**
	Renewed Masters at SU: Marine Sciences, Biodiv-Ecol-Evol Blue Train program in some aspects (help for local training of master and PhD students)	Support for PhD from regional sources may decrease after end of PIA programs Politique attribution CD par UPMC à ED227 Blue Train program in some aspects (teachers' involvement outside academic scope)
Socio-economic impact	**Strengths**	**Weaknesses**
	More programs including socio-economic partners (e.g. IDEALG, OCEANOMICS, PERLE,...). Good recognition of Roscoff scientific merit by regional, national or international institutions (e.g. AMP, FRB, IPBES,...) or foundations/companies	Hard to preserve our excellence in fundamental research if applied projects take precedence

	Opportunities	**Threats**
Management, structure, governance, scientific environment	**Strengths**	**Weaknesses**
	Usefulness of technical platforms and access to marine resources at SBR Lab life appears amenable and efficient to the majority of lab staff. Slight improvement for lab and office space... to be continued.	Some difficulties linked to current human problems in some SBR general services Complexity of administrative networks and a continued trend to increase the burden for lab staff (do-it-yourself softwares) Lack of topical meetings to promote internal collaboration (scarcity of funds and volunteers) Difficultés liées aux pb RH de la FR dont nous dépendons pour plusieurs services
	Opportunities	**Threats**
	Brand new context: new lab and SBR heads, new university, re-organization of SU "Stations marines" may convey a dynamic setting	Re-organization of Science faculty and "Stations Marines" within SU: concerns about lab support, observation, teaching, ...

5. Scientific Project for AD2M

Introduction

The laboratory "Adaptation et Diversité en Milieu Marin, AD2M = UMR7144) has been created in 2005 and we are now asking to renew it for the 4th time. This continuity emphasizes its stability and the relevance of the research activities performed during the last 13 years. No major changes are anticipated with respect to the scientific topics that will be addressed within the frame of the new contract. All expertise available in the research teams of the laboratory will come together into ***one coherent scientific project, focusing on the study of marine biodiversity and its dynamics, at several levels of integration from genes to community, in the context of on going environmental changes***. Functional and evolutionary processes driving marine biodiversity will be investigated from abiotic constraints (*e.g.* water chemistry, currents) to biological communities.

Yet scientific knowledge and the context in which scientific research in ecology and evolution is performed are, by essence, constantly evolving. For instance, the advent of high throughput molecular technologies, the developing awareness of the holobiont concept, the consideration of functional diversity in complex assemblages as crucial to assess ecological processes, requires greater integrative approaches. In this context, we propose an evolution of the structure of our laboratory towards a less fragmented team composition. The project proposed for the next 5 years is organized around ***three newly formed research teams focusing on 1- the eco-geochemistry and dynamics of coastal ecosystems (EDYCO), 2- the dynamics of marine diversity (DYDIV), and 3- the ecology of marine plankton (ECOMAP).*** These teams exhibit clear specificities and their members are well recognized internationally in their respective field of research. In the next contract we intend to boost synergy between researchers by working on common objectives through support of scientific interactions and increasing communication. Ultimately, along with participating in advancing knowledge at the forefront, based on our dynamism and high-level scientific status we aim at becoming even more attractive to brilliant students and young researchers.

Scientific objectives of the laboratory

Results and outcomes of the laboratory during the last contract are highly respectable and we ambition to maintain, and possibly intensify, a similarly good and efficient scientific production and international influence. The detailed projects, along with skills and tools available for each of the three teams of the laboratory, are provided later in this document. In particular, regional, national, and international research programs onto which they will rely at short and mid-term are presented. Therefore, we will only expose here the main framework and overall objectives of the laboratory that are based on the SWOT analysis of the past activities, a number of prospective documents produced (e.g. "sea" and "ecology" prospective from the CNRS-INEE) and the scientific policy of our supervising institutions, *i.e.* the CNRS-INEE and Sorbonne University.

Community ecology aims at understanding what factors determine the assembly and dynamics of species assemblages at different spatiotemporal scales. As in the previous contract, we intend to work at different levels of integration with some noticeable evolutions such as a stronger emphasis on species assemblages, both on experimental and *in situ* approaches, and a further integration of the holobiont concept. Focusing on community structure, ecosystem functioning and responses to environmental disturbances, ***we ambition to build on synergies and skills available in the laboratory to strengthen our leadership on "marine ecology" by promoting involvement in coordination of European or other international projects.*** At the national level, we intend to be an active member of the French community on marine ecology and evolution, for instance by pursuing our regular participation at the CNRS prospective (*e.g.* INEE, INSU) and our involvement in the ocean-related structures at the Sorbonne University (*e.g.* the European Marine Biological Resource Center -EMBRC, the federation of marine observatories "OSU mer"). Following internal prospective discussions, three specific strategic axes and common objectives have been identified for the laboratory.

1/ Investigate further the functioning of coastal ecosystems facing environmental disturbances

Coastal ecosystems are at the land-sea interface and constant human population growth and development are critical drivers of changes in coastal zones. They generate a high pressure on coastal ecosystems and natural resources through increased utilization, species transfer and habitat destruction. Investigations of coastal ecosystems are critical in the context of environmental disturbances and global change. In that respect, in 2013, it has been identified as one of the three priority research axes in the "seas" prospective by CNRS-INEE.
Our laboratory concentrates a unique task force on coastal ecology with expertise going from water chemistry (e.g. CO2 fluxes) through genes to physiological response of organisms and communities. For instance, the overall objective of the EDYCO team follows precisely that research line as it will investigate the responses of marine species assemblages, integrating the complexity associated with such experimental and *in situ* approaches, to different levels of anthropization, such as climate change (ocean acidification and temperature increase), coastal eutrophication, artificial systems and exploitation of coastal areas. These investigations will be performed by taking into account the functional diversity, production and trophic network properties of coastal communities. It will be complemented and combined with activities performed by the other two teams of the laboratory. For instance, the DYDIV team investigates spatiotemporal dynamics of diversity in urbanized, exploited, or naturally dynamic environments (axis 3). Identifying the drivers of species responses to changing environment at different scales of organisation (from genes to communities) is also an identified strategic axis for the ECOMAP team (axis 1). Within the course of the next contract we will work on better integrating the expertise from members of the 3 teams of the laboratory to achieve this scientific objective.

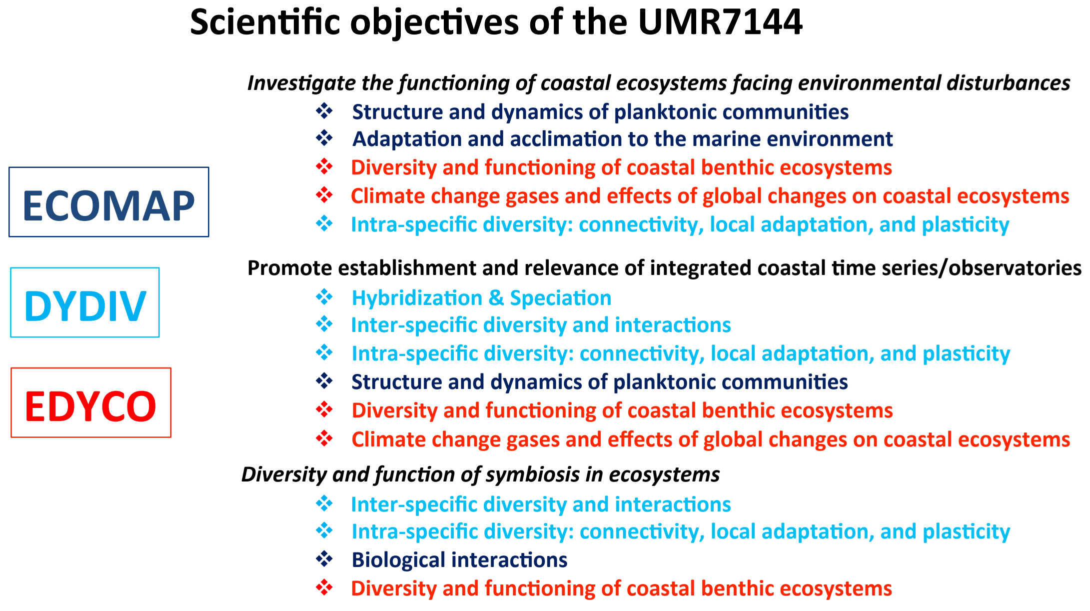
2/ Promote establishment and relevance of integrated coastal time series/observatories

Monitoring coastal ecosystems diversity and health is one of the main missions of the Station Biologique de Roscoff. The Roscoff Observatory infrastructure is managed by the FR2424 and currently directed by E. Thiébaut member of AD2M. Strong connections exist between our laboratory and the observatory. Indeed while the infrastructure supports various research activities performed in our laboratory, several medium- and long-term time series rely on the involvement and expertise of researchers from the AD2M laboratory (*e.g.* stable isotopes, physico-chemical parameters, biodiversity). Such coupling between research and observation is critical to evolve and ultimately transfer methodological and conceptual knowledge to environmental monitoring. With the advent of high throughput sequencing technologies, the use of genomic tools (*sensu lato*) for ecological research is becoming unavoidable. Since the early 2000's, researchers of the AD2M laboratory have played a pioneering role in these developments and molecular approaches to study marine ecology has proved valuable (*e.g.* population genetics on benthic species, plankton diversity and ecology). Molecular tools are particularly relevant not only for diversity monitoring studies but also for functional ecology approaches (*e.g.* acclimation, adaptation, trophic interactions). Along with this molecular expertise, another strength of our laboratory is the taxonomic and ecological expertise existing for nearly all compartments of marine life, ranging from viruses to macrobenthos. A number of macrobenthic organisms have a planktonic life stage (*i.e.* the meroplankton), therefore at coastal observatories, integrated studies over the whole plankton compartment must be considered as it provides a rather holistic perspective of ecosystems functioning.
Building on this rare combination of expertise in a single laboratory, a priority research axis has been identified to develop an augmented genomic planktonic observatory integrating multi-omics approaches (metabarcoding, metagenomics and metatranscriptomics) and the strong existing expertise in taxonomy, imaging and functional diversity, to investigate both fundamental ecology questions such as the driver of plankton community succession or species connectivity in fragmented landscapes, but also societal questions related to urban marine habitats or invasive species. Overall, during the course of the next contract we aim at finding synergy and positioning

our laboratory at the forefront of coastal ecosystems monitoring. As a laboratory, involving members from the different teams, we intend to participate actively to the coordination of joint international projects on this topic.

3/ Integrate the marine holobiont concept in ecology and evolutionary perspectives

Characterizing and understanding the role of symbiotic interactions (*i.e.* any type of close and long-term interactions between two different biological organisms, be it mutualistic, commensalistic, or parasitic) in marine environments was already one of the objectives in the previous contract of the UMR 7144. Since then, the awareness of the significance of symbiosis has even amplified and more people in the scientific community are considering the holobiont (*i.e.* the consortium of organisms living in symbiosis) as the biological unit at which acclimation and adaptation work. Focusing on photosymbioses (symbioses involving at least one photosynthetic organism) and chemosymbioses in benthic extreme environments (axis 2 and 3 of ECOMAP and DYDYV teams, respectively), we will investigate the diversity, functioning and role of symbioses in marine ecosystems. These investigations ranging from molecular mechanisms involved in the regulation of symbiosis to the resilience of symbiosis to environmental disturbances implicate common tools and approaches. For instance, ecophysiology combined with gene expression (*i.e.* transcriptomics) or metabolomics that is also becoming largely used to study chemical interactions at both the biological and ecological levels. Based on our publication record on these topics and our multidisciplinary expertise, our objective is to reinforce our leadership position in the international context to understand the role of symbioses in marine environments. Together with other laboratories at the SBR (*e.g.* UMR 8227) which have also identified symbiosis as a strategic research axis and FR2424 core facilities, we will work in coordination toward integration of these activities into a future European project on marine holobiont research. Ultimately, because of the originality of biological models from marine environments (*i.e.* some lineages are exclusively marine), our ambition is to contribute to fundamental findings of general interest for evolution and ecology.



Scientific objectives of the UMR7144

ECOMAP

DYDIV

EDYCO

Investigate the functioning of coastal ecosystems facing environmental disturbances
- **Structure and dynamics of planktonic communities**
- **Adaptation and acclimation to the marine environment**
- **Diversity and functioning of coastal benthic ecosystems**
- **Climate change gases and effects of global changes on coastal ecosystems**
- **Intra-specific diversity: connectivity, local adaptation, and plasticity**

Promote establishment and relevance of integrated coastal time series/observatories
- **Hybridization & Speciation**
- **Inter-specific diversity and interactions**
- **Intra-specific diversity: connectivity, local adaptation, and plasticity**
- **Structure and dynamics of planktonic communities**
- **Diversity and functioning of coastal benthic ecosystems**
- **Climate change gases and effects of global changes on coastal ecosystems**

Diversity and function of symbiosis in ecosystems
- **Inter-specific diversity and interactions**
- **Intra-specific diversity: connectivity, local adaptation, and plasticity**
- **Biological interactions**
- **Diversity and functioning of coastal benthic ecosystems**

Figure 1: Integrating the specific objectives of the 3 research teams (different colors) in the laboratory overarching goals.

Strategy of the laboratory to achieve the objectives

1/ Laboratory management team

In the upcoming contract, all components of the SBR will evolve simultaneously, providing a unique opportunity for fostering discussions and interactions between the research units (*i.e.* UMR *AD2M*, UMR *LIB2M* and UMI *EBEA*) and the FR2424. Indeed, besides running core technical facilities and infrastructures (*e.g.* Roscoff Culture Collection, coastal observatory, microscopy and genomic facilities, etc…), fundamental administrative tasks such as budget and human resource management are carried out by the FR2424 with which a smooth and concerted interaction is critical for our laboratory. In cooperation with the direction of the other components of the SBR, we will work towards this objective. Regarding the UMR itself, the direction staff will be composed of a director (Dr. F. Not, CNRS) and a deputy director (Pr. D. Davoult, UPMC) assisted by M^{me} C. Manceau (CNRS). The management of the laboratory will be done through *1*- regular meetings of the Scientific Council (CS) composed of the direction, the leaders of each research teams, the members in charge of scientific animation and communication coordination upon invitation and *2*- biannual meetings of the Laboratory Council (CL) composed of the direction, the Health and Security agent (AP), the Corresponding person for personnel's training (COFO), and members elected for the different staff categories. At the start of the new contract we anticipate 81 lab members composed of 45% female and 55% male.

As detailed in the previous section, in order to develop our scientific project and reach our objectives, we propose to reduce the number of research teams from 7 to 3. This evolution of the organization chart intends to promote and support scientific exchange between lab members, share experience and expertise while providing more flexibility in interactions. Fully considering the specificities of each lab member and the team it belongs to, globally we aim at reaching a higher degree of rationality in organization, for instance by increasing communication and accessibility to shared tools. As a tangible example, because our research activities involve an important amount of fieldwork we will organize storage and use procedures for the main equipment at the laboratory. All this organization will be structured through the setup of a LIMS (Laboratory Information Management System) that will be used by each team for its specific needs with the objective to reach progressively a common management tool at the laboratory level. All this organization will rely on a time-share of all laboratory agents to common tasks for UMR, giving the opportunities to anyone to take responsibilities and get involved in the life of the laboratory. Based on a recent inventory of skills and expertise we performed in the laboratory, staff members of the UMR7144 display a rich variety of competencies they currently apply on their research questions and models. Now we need to find a synergy and promote knowledge exchange to achieve our common scientific objectives. Because we are convinced that creativity is best at interfaces, along with the restructuration of the research team we intend to hold this organization on two pillars that are 1- an active scientific animation and 2- a remodelled communication inside and outside of the laboratory.

2/ Scientific animation

The scientific animation of the laboratory will be a major action during the course of the next contract. In coordination with the scientific council, it will be coordinated by a group of three persons (2 Researchers and 1 IT) with a dedicated budget. Three main actions have been identified to foster scientific exchanges between lab members. First, we propose annual incentive funding of 2 research projects and of 2 Master students when they are supported by at least two teams of the laboratory. Second, one day for non-topical exchanges will be organized based on posters presented at conferences during the previous year and reports from funded research projects. Finally, each year will be the opportunity to develop topical activities which will be organized as brainstorming, workshops along the year and end up by a one-day meeting in order to synthesize the work performed. Among the first topics that have been identified, we already select “measures of the biodiversity” and “microbiomes and holobionts” to start with. Every year we intend to produce a short prospective document that will feed scientific policies of our institutions and will also eventually lead to write joint review and opinion papers, or even specific joint research project proposals.

3/ Communication and outreach

Accompanying the reorganization of the laboratory, together with the scientific animation, we propose to develop a strategy for communication and use dedicated tools. Nowadays, there is an increasing and rapidly evolving amount of information circulating. So effective communication is becoming critical to maintain up-to-date and accurate information in a constantly evolving context. In coordination with the scientific council, the overall communication will be managed by a group of 3 persons representing all categories of colleagues (1 IT, 1 Researcher, 1 student or post-doc). They will be clearly identified as corresponding communication persons and, through interaction with lab members, they will collect and disseminate all information relevant to the scientific activity of the laboratory. This is particularly important for internal communication within the UMR in order to homogenise and facilitate procedures. The communication will rely on a redesigned, stable and reliable, intranet interface with constantly updated information. Along with the creation of a newsletter to circulate scientific and social information, another example of action is the formalization of a number of procedures as small guides of the laboratory to facilitate communication on laboratory daily life issues (e.g. arrival, place an order, etc). These documents will be produced in English as foreigners, including students, are regularly integrating the laboratory. Also, a database centralizing all the skills and competence of each lab member will be created and made available.

The 3 persons in charge of the coordination of the communication will also interact directly with the COMEDIS service at the SBR level to coordinate communication actions towards institutions and broad public. For instance, we intend to amplify the use of social network to communicate on the life and scientific outcome of the laboratory research activities. We believe this is important as the research proposed in the AD2M laboratory has strong connections with socioeconomic issues and important questions relevant for societies (*e.g.* ocean acidification, climate change, invasive species, toxic microalgae, biodiversity, coastal management). If some projects have already been well covered by media we want to expand the scope of the research topics on which we will communicate and have a better coordination of the outreach actions. We are convinced it is important to improve the visibility of our laboratory activities as we think it contributes to increase attractiveness towards researchers and students.

With respect to scientific production, we will promote publication of pre-prints on website such as BioRxiv and keep the effort on providing material on the open archive website HAL.

4/ Teaching and training through research

As in the previous contract, our laboratory will have a significant teaching activity with an anticipated staff of 10 assistant professors (incoming mobility of Dr. E. Bonnivard included) and 3 professors from Sorbonne University, in addition to the assistant professor at an engineer school A. Nicolle (ENSTA Bretagne). Teachers are involved in more than 20 teaching units, both in Paris and Roscoff, encompassing topics ranging from ecology to evolution, Master SM – Sciences de la Mer, Master BEE – Biodiversité, Ecologie & Evolution, Master BIP – Biologie Intégrative & Physiologie, Licence Biologie-Mathématiques, Licence Professionnelle Sécurité Alimentaire. Also with on average 7 PhD defended every year, our laboratory is strongly involved in student training through research. Among the 3 research teams of the laboratory, two (DYDIV and ECOMAP) will be affiliated to the doctoral school "Sciences de la nature et de l'homme : écologie et evolution" (*i.e.* ED227) and one team (EDYCO) to the doctoral school "Sciences de l'environnement d'Ile de France" (*i.e.* ED129). Funding sources for PhD come essentially from the doctoral schools, included interdisciplinary doctoral school (e.g. Interface pour le Vivant, Frontière du vivant), Brittany region, National Contracts (ANR), and European projects.

Together with other planned actions (*e.g.* scientific animation, communication), our two main objectives are 1- to maintain a high level of involvement in teaching and 2- to attract the best national and international students for training in our laboratory. For instance we are currently partner in two ongoing European International Training Network (ITN-EU) projects (*i.e.* SINGEK and MixITiN) and in the Erasmus+ International Master of Science in Marine Biological Resources (IMBRSea). In the proposed organization, along with the deputy director, a reference person will be in charge of the coordination of the relationships with the university, reporting to the CS all information related to the teaching and doctoral schools.

5/ Specific support required to reach our objectives

Finally, to be able to maintain and develop further the variety of activities (*e.g.* teaching, outreach, fundamental research, socio-economical involvement, and environmental monitoring, consulting and research management) performed at the AD2M laboratory we definitely need the strong and close support of our institutions. In particular, within the course of the next contract we intend to reinforce our research capacities, notably by recruiting a researcher working on the ecology of coastal areas, a particularly strategic topic in the context of increasing human pressures on these ecosystems. Also, as exemplified and stressed in the research projects of the AD2M teams (see below), and in line with the global evolution of the field of biological and environmental sciences having to deal with extremely large amount of data, a significant human resource support is urgently required in bioinformatics, both on bioanalyses/biostatistics and database development. These recruitments are indispensable for teams of the A2DM laboratory to maintain their level of excellence in a very competitive international context and tighten the synergy with the ABiMS platform of the FR2424.

UMR 7144 Adaptation et Diversité en Milieu Marin

Team : Eco-geochemistry and dynamics of coastal ecosystems (EDYCO)

Projet 2019-2023

Overview of the team

Over the course of the next contract, the EDYCO team intends to develop its research activities on coastal ecosystem functioning by taking into account the functional diversity, production and network properties of coastal communities in the context of global changes. Pascal Riera and Yann Bozec will lead the team from 1st January 2019.Our objectives will mostly focus on the responses of marine biodiversity to different levels of anthropization, namely, climate change (acidification and temperature increase), coastal eutrophication, artificial systems and exploitation of coastal ecosystems. Thanks to the cross disciplinary skills and expertise, the originality of our project is to consider ecosystem functioning from the abiotic level to benthic communities in order to link ecological and chemical processes, related for example to climatically active gases. To ultimately understand the intricate flows of energy and nutrients through food webs and to assess both the effects of anthropogenic pressures and to quantify the impacts of global climate change, our research activities mainly involve *in situ* and laboratory experimental ecology. This overarching objective will be developed through 2 main research axes presented hereafter and involving the following permanent staff.

Permanent Staff	Corps/Grade	Institution	HDR	Axis 1	Axis 2
BOHNER olivier	T	CNRS	N	80	20
BOULART Cédric	CR2	CNRS	N	20	80
BOZEC Yann	CR1	CNRS	N	20	80
COUDRET Jérôme	AI	CNRS	N	20	80
DAVOULT Dominique	PR	UPMC	Y	80	20
LOISEL Stéphane	AI	CNRS	N	50	50
MACE Eric	AI	CNRS	N	30	70
MARTIN Sophie	CR1	CNRS	N	20	80
MIGNE Aline	MC	UPMC	N	80	20
MORIN Pascal	DR1	CNRS	Y	0	100
NICOLLE Amandine	MC	ENSTA	N	100	0
RIERA Pascal	MC	UPMC	Y	60	40
SEVIN Laure	IE	CNRS	N	50	50
THIEBAUT Eric	PR2	UPMC	Y	80	20
VERNET Marc	T	CNRS	N	20	80

Scientific project

1/ Axis 1: Diversity and functioning of coastal benthic ecosystems

The analysis of the functioning of coastal benthic ecosystems will be addressed through the development of three complementary and inter-related approaches.

First, **functional diversity** is an important **metric** for exploring species coexistence in biological communities and effects of biodiversity on ecosystem functioning. Its measure is based on the uses of specific-species traits as indicators of multiple aspects of ecosystem functioning (*e.g.* productivity, nutrient cycling, resilience). While the **biological trait analysis** (BTA) has been extensively studied over the last two decades in terrestrial ecosystems, in particular on plant communities, it is still in its infancy in marine ecology, and the measure of functional diversity in benthic systems raises numerous methodological and conceptual questions that will structure this section of our project:

- ✓ What are the variations in the measures of functional diversity both within habitat (α-diversity) and between habitats (β-diversity) according to the number and nature of traits considered and the nature of biological data?
- ✓ What are the links and the complementarity between the different measures of specific, taxonomic/phylogenetic, and functional diversity? How do functional and phylogenetic distances contribute to understanding patterns of community assembly and can be used as a surrogate of ecosystem functioning?
- ✓ What are the processes governing the distribution of functional diversity?
- ✓ What are the responses of functional diversity to different anthropogenic pressures? How do the measures of functional diversity reflect anthropogenic disturbances and may provide indicators of ecosystem health?

These questions will be addressed on different systems included mainly subtidal soft-sediment systems (Lise Bacouillard PhD thesis; on-going REBENT project), rocky shores and artificial environments.

Second, the investigation of diversity-function relationships in temperate coastal ecosystems will continue and developed within **rocky shore communities** through quantitative observations of processes and patterns for understanding the response of these communities to ecosystem changes. We will investigate the structure and functioning of intertidal communities dominated by canopy-forming brown seaweeds. The role of the canopy will be investigated through the complementarity between the different canopy layers, which is hypothesized to explain the maintenance of high rates of community primary production throughout emersion periods (Bordeyne et al. *in press*). This implies *in situ* measurement of metabolism at the community scale using benthic chambers (CO_2/O_2 fluxes) with which it is planned to combine measurements at the specimen scale, using pulse amplitude modulated (PAM) fluorescence *in situ* (e.g. Gévaert et al. 2003). In addition to measures of functional diversity, the **production of subtidal kelp forests** at the community level will also be investigated through (1) the development of adapted benthic chambers (Program IDEALG), (2) the consideration of the macroalgae holobionts and epiphytes and the associated diversity on the bedrock (EC2CO project to be submitted in 2018). Anthropogenic pressure is also investigated through experimental monitoring of commercial-species harvesting, e.g. macroalgae (IDEALG) and goose barnacle (Biodiversa PERCEBES, 2017-2020).

Coastal trophic networks will be assessed through their functional responses and evolution to several **anthropogenic constraints**, such as seaweed harvesting or artificial systems (*e.g.* port areas, dykes). In fact, it is well recognized that due to their location at the continental-ocean interfaces and the diversity of sources, these networks are of major interest as descriptor of environmental changes. A better assessment of the consequences of anthropogenic impacts on food webs implies the actual combination of different tools, namely, experimental, instrumental and modelling for future researches (Trophic Ecology Research Group, INEE). Dynamics and evolution of network structures and major trophic pathways (*e.g.* trophic plasticity and connectivity, stability and resilience) must be considered through an integrative methodological approach, using different ecological tracers, in the context of comparative studies of coastal food webs. In order to improve our estimation of qualitative and quantitative trophic fluxes, natural and enriched **stable isotopes will be coupled** with complementary measurements including stoichiometric and essential fatty acids' (EFA) analyses, and more innovative, with heavy metals or *in situ* net secondary production of relevant benthic species. We aim to develop ^{13}C and ^{15}N labeling to assess specific trophic interactions within rocky shore habitats through *in situ* experimental ecology. In addition to rocky shore habitats macroalgae-dominated, our food web studies will also be focused on the **Bay of St Brieuc** including other habitat types (salt marshes, intertidal and subtidal sandy communities) through collaboration (project being drafted 2018).

It must be emphasized that these objectives are largely based on the acquisition of **long-term series of the Roscoff observatory** that we consider essential to understand the evolution of ecosystems structure and functioning under the effect of natural and / or anthropic constraints. Since 2010, we have initiated two long-term monitoring which make it possible (1) to link taxonomic, functional and trophic structures (2) to assess theoretical issues related to coastal habitats and communities in the long term:

- In subtidal communities of fine sands of the bay of Morlaix (Pierre Noire) for which recently developed isotopic indices will be applied to describe changes in the trophic structure and how variations in the community structure of benthic habitats should alter the energy transfer.
- In intertidal habitats dominated by *Fucus vesiculosus* and *Fucus serratus*. This unique monitoring within rocky shores proposes an integrative approach combining multiple community-based *in situ* metabolism approach and comparative isotopic analyzes of selected species among the most representative of these ecosystems subjected to seaweed harvesting.

Moreover, these researches will benefit from the long time-series of classical physico-chemical oceanographic parameters (nutrients, SSS, SST, etc…) performed at the FR2424 of the SBR within the national observation **network SOMLIT** and largely supported and carried out by members of the EDYCO team. The physico-chemical data collected over decades at these coastal sites will notably allow an assessment of the response of benthic communities to eutrophication. Our team is expert in deployment of high-frequency sensors on multi-platforms such as VOS and autonomous buoy for the study of GHGs in coastal environment. In the past 5 years we have equipped 2 Ferrys and 2 buoys on the western European Coastal Seas. We will continue to work closely with developers such as sunburst Inc. to test and deploy high-frequency sensors in coastal environments particularly at risk under Climate Change (e.g. Polar, coral reefs). Our team is also responsible for the long time-series of 13 physico-chemical parameters for the SOMLIT. We have all the expertise capabilities in our laboratories for analysis of these classic parameters.

The long-term changes in community composition, and then in ecosystem functioning, depend largely on the renewal of local populations. In collaboration with DYDIV team, we will continue our research on the study of larval dispersal, by focusing on our expertise in the development of high-resolution biophysical models to track larval trajectories and connectivity among populations. A peculiar attention will be given to key-species of rocky shores (e.g. mussels, stalked barnacles) in the context of global change (ANR-Biodiversa project 2017-2020).

Privileged partnership for axis 1: F. Gévaert (UMR 8187 LOG Wimereux), J. Grall, G. Schaal, O. Gauthier (IUEM, UMS 3113, Brest), N. Desroy, P. le Mao (IFREMER LER Dinard), A. Sturbois, A. Ponséro (Réserve Naturelle Nationale de la Baie de St- Brieuc), F. Charles (LECOB, UMR 8222, Banyuls), P.G. Sauriau (UMR 7266 La Rochelle), V. Kitidis, P. Somerfield (PML, Plymouth UK), H. Queiroga & J. Dubert (Aveiro University, Portugal) and team SIGLE, T. Wernberg, (UWA, Australia), T. Bekkby (NIVA, Norway)

2/ Axis 2: climate-change gases and effects of global changes on coastal ecosystems

Global warming and **ocean acidification** will have major consequences for the structure and functioning of ecosystems and there is now a growing interest to understand and predict how marine ecosystems will respond to these environmental changes. Ocean warming and acidification originate from Greenhouse gases (GHG) and are known to directly impact marine life (*e.g.* decrease in survival, calcification, growth and development). Thanks to its multidisciplinary expertise, the overarching objective of the axis 2 of the EDYCO team will be to investigate the effect of global changes from the mineral to the community levels and better understand its effects on coastal ecosystems. This implies characterizing the fluxes of GHG and understanding their impacts on coastal benthic communities.

One major task will be to constrain air–sea exchanges of GHG (e.g. CO_2 and CH_4) and their variability at various time and spatial levels in coastal ecosystems. Over the past decade, the coastal oceans have been the focus of several studies highlighting the key role of these ecosystems in the global budget of air-sea CO_2 fluxes. In these extremely heterogeneous and dynamic coastal ecosystems the direction and the magnitude of these fluxes present much larger gradients than in the

open ocean, which make coastal ecosystems relevant for global estimates of air-sea CO_2 fluxes despite their relatively small surface area. The spatial variability in air-sea CO_2 fluxes is large from one ecosystem to the other. In this respect, improvement of **the global estimate of the dynamics of air-sea CO_2 fluxes in costal ecosystems requires better constraining of variations due to processes occurring at daily to inter-annual scales.** Furthermore, measurements of the carbonate system parameters will be essential tools to **monitor the long-term modification of coastal ecosystems under ocean acidification (OA)**. Coastal ecosystems currently have the least-coordinated monitoring effort for ocean acidification (Nature article "Global network will track acidifying oceans"). International programs SOLAS (Surface Ocean Lower Atmosphere Study), IMBeR (Integrated Marine Biosphere Research) and LOICZ (Land-Ocean Interaction in the Coastal zone) strongly support process studies of air-sea GHG fluxes in the coastal zone and of their response to global change. In the context of climate change methane is the second most important greenhouse gas emitted by human activities, it has a far higher global warming potential than carbon dioxide on a per unit basis. It has large natural as well as anthropogenic sources. Still, methane cycles are even less understood than the carbonate system cycle, especially in view of changing physical and biological processes. A firm understanding and quantification of methane sources and sinks in coastal environments is key to adequately predicting future climatic and environmental changes during the ongoing Anthropocene.
Three main goals will be pursued in this task:

- Quantify by multi-scale approaches the processes controlling the carbonate system in key coastal ecosystems using new platforms (VOS, autonomous buoys) for High-Frequency (HF) measurements of the CO_2 systems parameters combine with new satellite approach, which are very efficient tools to investigate the present carbon cycle from daily to inter-annual scale. We will continue this effort in temperate ecosystems (H2020 project Jerico-Next) and extends our approach to understudied ecosystems (e.g. Arctic and Coral reefs) extremely sensitive to climate change (projects submitted to LEFE/CYBER and EC2CO calls).
- Assess the potential effect of anthropogenic alterations (OA, eutrophication) and climate change of the carbonate chemistry in coastal ecosystems. The HF datasets acquired within the first objective will be combined to long-term time series of the carbonate system already initiated in the temperate coastal ecosystems by our team for the past 10 years and will allow within the next 5 years to assess the effect of OA on the carbonate chemistry. It will also provide key data for the laboratory experiments that we will perform (see below) to assess the response of the benthic community to the combined effect of OA, eutrophication and global warming (current project MAERLchange, EC2CO 2017-2019, P.I. S. Martin).
- Reinforce and expand our research on GHG by including a CH_4 perspective***:*** A new Researcher (Cédric Boulart, CR2, CNRS) specialist of methane cycle in coastal and deep sea ecosystems will start in our team on November 1st 2017. The field and process studies of methane cycle will mainly carried out on similar study sites as for CO_2 and at deeper sites in collaboration with the DYDIV team of the laboratory. The main goal is to evaluate the source/sinks of methane at key sites and the response of methane cycle to climate change.

Impact of combined effects of ocean acidification and warming and local changes on biotic interactions: field and laboratory investigation. Although there was a growing research interest to understand how marine ecosystems will respond to global warming and ocean acidification, the combined effects of these factors with local environmental changes (such as eutrophication) remain poorly known. In addition, most research into the effects of ocean warming and acidification has involved experiments on single species making it difficult to predict effects at the community and ecosystem levels. However, it is clear that the impact of climate change and ocean acidification on marine ecosystems will depend on the combined influence of direct environmental impacts on individual species and indirect effects mediated by changes in **interspecific interactions**. Hence, it is now necessary to provide additional insights into the **community-level effects of warming and ocean acidification.** For this, we will develop long-term **multispecies laboratory (mesocosms) experiments** to investigates which organisms can tolerate or decline as a consequence of ocean acidification and warming in order to reveal how marine communities respond. Finally, we aim to identify the (additive, synergistic and/or antagonistic) effects of the interactions between global warming and ocean acidification, and more local environmental changes (eutrophication) on benthic communities in the temperate coastal zones in term of structure (biodiversity) and functioning (biogeochemistry).

These experiments should be repeated for populations inhabiting different environment to assess local adaptation. Ecosystems dominated by macroalgae in the subtidal zone **(maerl beds,** EC2CO MaerlChange) and intertidal rocky shore (**rock pools**) will be considered as privileged models. Particular attention will be paid to macroalgal community dominated by red calcareous coralline algae, which are among the most sensitive benthic calcifying organisms to ocean acidification due to the high solubility of their skeleton. Interactions (1) between primary producers (soft and calcareous macroalgae), (2) between macroalgae and herbivores, and (3) between herbivores and predators, will be considered. In order to reproduce natural variability of environmental parameters in the mesocosm experiments, *in situ* surveys of physicochemical parameters (collaboration with chemists) will be planned to characterize physico-chemical parameters associated with studied algal communities.

Biotic interactions will be tested experimentally (trophic relationships, ecophysiology and behaviour). In particular, stable isotopes have recently been oriented towards the study of the functional evolution of communities in the context of climate change and ocean acidification. Stable isotope labelling to estimate trophic fluxes has been already performed on microalgae or, in a lesser extent, on marine plants. In regards to macroalgae, recently, we initiated **enriched ^{13}C and ^{15}N labelling** for **macroalgae - grazers experiments** (PhD E. Legrand, IDEALG). Such promising research has been initiated at the Roscoff *via* the experimental route (mesocosms) and the isotopic enrichment (dual labelling techniques). Consequently, we propose to further develop macroalgae-herbivore trophic interactions at the community level through laboratory experiments including selected grazers exposed to different two $p\mathrm{CO}_2$/T° treatments. Trophic interactions among herbivores and macroalgae can be identified, quantified and classify using dual enriched stable isotopes. In particular, we hypothesize that high $p\mathrm{CO}_2$ and/or high T° conditions (1) may affect the qualitative and/or quantitative characteristics of macroalgae-herbivore trophic link (2) coexisting grazers may respond differently in term of feeding activity and/or assimilated food source when submitted to higher $p\mathrm{CO}_2$. This work will bring insights on the future of algal communities in a context of global and local changes.

The importance taken by the **experimental ecology** in our team implies the maintenance of the experimental design in an appropriate laboratory in order to test efficiently the effects of pCO2 / T° conditions on benthic assemblages functioning and behavior. The team will benefit of the new experimental infrastructures available at the Roscoff Biological Station.
From an analytical point of view, numerous analyses of necessary to our objectives are based on the equipment's available in the Mass Spectrometry Core Facility **METABOMER** (FR2424) including EA-IRMS (Elementary Analysis-Isotopic Mass Spectrometer) and GC MS (Gas Chromatography-Mass spectrometer). The platform METABOMER planned to request the **renewal of the EA-IRMS** which is necessary to increase the stable isotopes analytical capacities from tissues level to molecular level (fatty acids, amino acids), gaseous compounds (CO_2) and additional elements (^{18}O and ^{2}H).

Privileged partnership for axis 2: J-P Gattuso, F. Gazeau, (LOV, UMR 7093 Villefranche-sur-Mer), J. Grall, (IUEM, UMS 3113,Brest,), S. Roussel, (IUEM, LEMAR, UMR 6539, Brest), S. Bordenave, (MNHN BOREA, UMR 7208, Concarneau), V. Kitidis (PML, Plymouth UK), H. Thomas (Univsersity of Dalhousie, Canada), S. Painter (NOC, Soutampton, UK), S. L'Helguen, P. Rimmelin (IUEM) and team "Algal Chemical Defense and Signaling" (UMR8227).

UMR 7144 Adaptation et Diversité en Milieu Marin

Team : Dynamics of the marine diversity (DYDIV)

Projet 2019-2023

Overview of the team

The team *Dynamics of the marine diversity* will focus its work on the ecological and evolutionary processes that influence how marine species settle, spread and evolve in a given marine environment. This team will work on different levels of diversity, including **(1) intra-specific diversity (neutral and adaptive drivers of polymorphisms)**, **(2) hybridization and speciation (secondary contacts, isolating barriers and their evolution)**, and **(3) inter-specific diversity in communities (spatiotemporal dynamics of assemblages of species in urbanized, exploited, or naturally dynamic environments)**. Our research will be largely based on empirical approaches using a variety of marine species, selected according to the questions addressed. Some of these species have a key role in the trophic web (*e.g.* krill), represent habitat-forming and/or engineer species (*e.g.* alvinellid polychaetes, massive solitary tunicates, macro-algae), are non-native species (*e.g.* the mollusc *Crepidula fornicata*, the ascidian *Ciona robusta*, the macro-alga *Undaria pinnatifida*), or are involved in long-term interactions (*e.g.* the molluscs *Bathymodiolus* spp. and *Loripes* spp.).

The team will comprise 11 researchers (7 MCF/PR and 4 CR/DR) and 6 technicians or engineers (2 Tech, 2 AI, 1 IE, 1 IR, two of them shared with other teams; total ETP 4.4). Within this team, a group of 4 people (2T, 1IE, 1IR) will become a task force in molecular biology/biochemistry under the direct supervision of C. Daguin (IR) to address technological challenges in NGS/gene overexpression. The group results from the fusion of the teams *Diversity and connectivity in marine landscapes* (Divco) and *Adaptation and invertebrate biology in extreme conditions* (Abice) of the last 5-yr contract, with the addition of one new researcher (Eric Bonnivard, MCF; previously in UMR 7138 in Paris) and the departure of Eric Thiébaut to team EDYCO of our laboratory and Stéphane Hourdez to UMR 8222 (Banyuls/mer). Didier Jollivet and Thomas Broquet will lead the team from 1st January 2019.

Permanent Staff	Corps/Grade	Institution	HDR	Axis 1	Axis 2	Axis 3
ANDERSEN Ann	MC	UPMC	N	50	0	50
BONNIVARD Eric	MC	UPMC	Y	60	20	20
BROQUET Thomas	CR1	CNRS	N	30	70	0
COMTET Thierry	CR1	CNRS	N	50	0	50
COUDRET Jérome	AI	CNRS	---	30	30	40
DAGUIN Claire	IR	CNRS	N	35	30	35
JOLLIVET Didier	CR1	CNRS	Nov2017	40	30	30
LALLIER François	Pr	UPMC	Y	40	0	60
LEJEUSNE Christophe	MC	UMPC	N	40	0	60
LE PORT Anne Sophie	T	UMPC	---	35	20	45
LOISEL Stéphane	AI	CNRS	---	40	30	30
MARY Jean	MC	UPMC	N	20	0	80
RUAULT Stéphanie	T	CNRS	---	35	35	30
TANGUY Arnaud	MC	UPMC	N	30	10	60
TOULLEC Jean-Yves	MC	UPMC	Y	80	0	20
VIARD Frédérique	DR1	CNRS	Y	40	30	30
To be recruited in 2018	IE	CNRS	---	35	30	35

Scientific project

1/ Axis 1 – Intra-specific diversity: connectivity, local adaptation, and plasticity

1-1/ *Dispersal and neutral processes of differentiation*

The genetic diversity of a species is strongly affected by the spatial structure of its habitat (continuous or fragmented) and its capacities to disperse between populations and to colonize vacant habitats (population connectivity). In the marine realm, the idea that populations are "open" is a paradigm that has been increasingly challenged by results from population genetics, larval transport models, behavioural analyses, and dispersal studies based on natural geochemical tags. Marine populations appear to be constrained by *i)* local hydrodynamic conditions and the natural structure of some environments (*e.g.* estuaries, lagoons, hydrothermal vents) and *ii)* species life-history traits. In addition, human-mediated dispersal may add complexity by promoting long-distance dispersal between disjoint populations. Inferring dispersal is particularly important for non-native species (expansion over the new range) as well as for species that may have to respond to environmental perturbations. One key activity of the team will be to study dispersal and connectivity of marine species showing a range of life styles (from direct development, such as in *Jaera* isopods and *Hemimysis* mysids, to broadcasters with a massive production of planktotrophic or lecitotrophic larvae such as in *Ciona* ascidians and *Bathymodiolus* bivalves).

To this aim, we will combine several approaches, including studies of larval biological features, like behaviour (*e.g.* vertical migrations) and pelagic larval duration, and the factors controlling them, inferences based on population genetics using genomic data, and inferences based on geochemical tags in larval shells, previously developed during the last contract. In addition, in collaboration with the EDYCO team, we will continue to develop comparisons of observed patterns with predictions from larval dispersal modelling. For this project, we aim to resolve several issues such as the connectivity between hydrothermal vent sites (focusing on west Pacific back-arc basins; Cruise ChuBacArc 2019 which unites a large part of the team (ANR Cerberus 2018-2020), connectivity between Antarctic and sub-Antarctic island populations in the context of global warming, and persistence or expansion of introduced species (notably tunicates such as *Ciona robusta* and algae such as *Sargassum muticum;* for which genomics tools have been developed). More generally, dispersal is a key driver of diversity at all biological levels and dispersal studies will bear upon all or nearly all the scientific objectives developed below.

1-2/ *Local adaptation and the adaptive diversity of species*

The evolution and persistence of species in the face of global changes will depend in part on their adaptive potential. We need to investigate all aspects of a species' polymorphism that may evolve through selection (including allelic diversity and variation in gene copy numbers). This adaptive diversity has most often been shaped through a long history in more or less changing environments and we are interested in disentangling demographic effects from selection by the environment (initiated with A. Bioy, PhD thesis).

With this research axis, we aim to quantify synonymous *vs* non-synonymous polymorphisms in the transcriptome of marine invertebrates that live in contrasted thermal environments. This will be done in collaboration with S. Hourdez (UMR 8222, Banyuls sur Mer). We will also look at the diversity of transposable elements (ETs) in these species. As an important source of genetic variation, these mobile DNA sequences contribute to population differentiation, including variation in their insertion in response to environmental changes. Comparing the diversity in ETs between closely related species that live in contrasted environments (hydrothermal vents, coastal intertidal zone, polar regions) will help identify the role of ETs in the plasticity of genomes and their role in local adaptation. Adaptation to new environments may also develop on a contemporary time scale for instance thanks to evolutionary novelties arising from secondary contacts and admixture between genetically differentiated lineages, as illustrated by non-native species. Admixture, in addition to putative selection on standing genetic variation (which received little support so far), needs to be further investigated in marine systems and will be examined by means of population genomics, pursuing researches done in non-native tunicates (*Botrylloides* spp.).

1-3/ *Plasticity and ecophysiological response of marine invertebrates*

The DYDIV team will also look at the phenotypic plasticity of species and acclimation processes. We will focus on acclimation of marine species to rapid changes in seawater temperature, using polar and sub-polar Euphausiaceae crustaceans (*i.e.* krill) as model species. Our approach is based on analyses of species distribution on a latitudinal gradient and metabolic pathways involved in thermal preferences (using transcriptomics associated with thermal stress and CTmax experiments).

Understanding the physiological mechanisms underlying the resistance of organisms to thermal stress will help to explain the current distribution of species and their potential short-term response to global warning. This type of analyses will be used to study acclimation mechanisms in temperate coastal (e.g. the oyster *Ostrea edulis*) and freshwater environments (the bivalve *Dreissena polymorpha*), and will encompass different developmental stages (from larvae to adults). We will also explore the physiological mechanisms explaining the resistance of species to other stressful conditions (e.g. pollution, oxygen limitation, hypoxic and sulfidic environments). Performance of respiratory pigments within and between closely-related species (mainly haemoglobins: e.g. vesicomyid clams) to hypoxic and sulfidic environments will be also examined in the face of local conditions. We will also compare the resistance of native *vs* introduced species (*Artemia* species within hypersaline lagoons, tunicates within harbour environments) using RNAseq approaches.

2/ Axis 2 – Hybridization & Speciation

The tectonic and climatic past of our planet has driven species along complex evolutionary trajectories involving repeated periods of geographic isolation and secondary contacts. This expansion-retraction dynamics has produced a number of areas where previously isolated species now overlap and hybridize. Our team is interested in studying such secondary contact hybrid zones to understand isolating mechanisms between species and speciation processes. Focusing on ascidians of the genus *Ciona*, and expanding the researches made on *C. intestinalis and C. robusta* (ANR HySea grant 2012-2016), we will study the relationships between the levels of species divergence, reproductive isolation, and hybridization. We have shown that both the long-term evolutionary history and contemporary process (new introduction of species) interact to model the genomic architecture and possibly the fate of these species.

This research axis will combine crossing experiments, phylogenomics, and analysis of the genomic landscape of differentiation in order to better understand the trajectory of native and introduced species in secondary contact zones and contribute to provide knowledge for better species delineation by taxonomists. Related questions pertaining to the maintenance of hybridization and the evolution of reproductive barriers (ecological isolation, sexual isolation, and genetic incompatibilities) will be addressed using another small species complex (*Jaera albifrons*, littoral isopod crustaceans, follow-up on ANR grant 2014-2018). Beyond specific objectives that are linked with empirical case studies, we aim to better understand the genomic architecture of differentiation by analysing the genomic landscape of recombination (*Ciona*, *Jaera*), the distribution of loci involved in reproductive barriers (*Ciona*, *Jaera*), and the distribution of positive selection signals linked with local adaptation (*Ciona*, *Alvinella*, *Bathymodiolus*, and *Rimicaris*). Finally, the role of transposable elements in hybridization and speciation will also be investigated, notably using genomic data from species associated with hydrothermal vents.

3/ Axis 3 – Inter-specific diversity and interactions

3-1/ *Diversity of communities in a changing environment*

Studying the diversity of species within communities and its dynamics in space and time is challenging. Yet such analyses are key to understanding the main changes of marine ecosystems in the face of global change. These studies rely on exhaustive inventories of biodiversity at the species level or other useful phylogenetic levels. Our team has gained a strong expertise in molecular taxonomy (with the recent discovery of many cryptic species) and morphological features difficult to use in field assays (e.g. ascidians, bryozoans). We will benefit from our expertise developed during the last contract and on scientific interactions with the ECOMAP team on this topic, to complement traditional methods (individual-based, either through morphological or molecular identification) with the use of high-throughput sequencing technologies (metabarcoding / environmental DNA) to assess biodiversity. As part of the Aquanis2.0 project (2017-2021), focused on the benthic component of the marine communities we aim at using e-DNA for detecting and examining the distribution in time and space of various targeted non-native species. As part of another submitted project, we will expand these studies to the whole community to address important unresolved questions in marine invasion science, for instance the reasons behind the extent of the lag phase and of the rarity of non-native species in natural habitats surrounding introduction hotspots. An innovative aspect of this latter project will be to develop at the same time similar studies on the pelagic larvae. This will be used not only to assess the contribution of early developmental stages to the pelagic diversity (still rarely addressed), but also to specifically test the hypothesis of propagule pressure as a driver of the “invasive” success.

Another key aspect developed in this axis is to make a focus on urban marine habitats. Studying these habitats is not only of concern regarding our researches on non-native species (as introduction hotspots) but also because they are not surrogates of natural habitats and display particular species assemblages in coastal areas. They thus offer interesting case studies for examining assemblage rules, in particular the interplay between biotic and abiotic factors. To this extent, we will study the biodiversity of various artificial environments like harbours, focusing on the local scale heterogeneity in community composition and explore the environmental factors triggering such pattern through long term surveys and experimental approaches. One objective will be to study the community resistance to environmental stress (e.g. pollution). The functioning of these ecosystems will be explored in collaboration with members of the EDYCO team.

3-2/ *Species interactions*

At the crossroads between local adaptation and community dynamics, long-term interactions (symbioses) between metazoans and chemoautotrophic bacteria have long been an important research topic of our team. We propose to push further our analyses of molecular mechanisms involved in symbiont recognition and control by the bivalves *Bathymodiolus* and *Loripes* and the polychaete *A. pompejana*. We will focus particularly on genes involved in immunity, as it was shown recently that anti-microbial peptides contribute to control the *A. pompejana* epibiosis. Symbiosis will be studied using transcriptomics and fluorescent *in situ* hybridization (FISH) in order to identify cellular and molecular mechanisms that allow the coastal bivalve *Loripes* to acquire and regulate symbionts, with a particular focus on the role of immunity mechanisms (ANR grant application 2017). Empirical results from *Loripes* will be compared with other symbiotic species from the *Bathymodiolus* genus.

Because thermal stress can impede symbiosis through an action of transposable elements (translocation), we will investigate these effects by looking at the differential expression of transposable elements under different temperature conditions in shallow-water anemones and corals but also in vent species under controlled conditions. The molecular bases of immunity will be further explored in non-symbiotic coastal molluscs (genera *Mercenaria* and *Ostrea*) that display interesting host-pathogen interactions. Genome scan analyses will be used to identify genes associated with resistance to pathogens and parasites (endonuclear parasite QPX/*Mercenaria*, USDA grant; *Bonamia/Ostrea*, FEAMP grant).

3-3/ *Deep evolution of species living in extreme environments*

‘Extreme’ environments may have played a crucial role in the evolution of species in terms of adaptive strategies and thus have greatly contributed to the functional diversity of genes. More specifically, the long-term evolution of proteins to depth and temperature is of fundamental importance to our understanding of the environmental conditions that have prevailed with the ancestor of some of our biological models. During the last 4 years, our team developed a Galaxy suite of scripts (bioinformatic project Elixir IIB) to explore the gene/protein-product composition of closely-related species and to identify genes under positive selection by comparing large series of orthologous genes between RNAseq datasets. We therefore plan to test hypotheses about the thermophilic or shallow-water origin of ancestors by resurrecting ancestral proteins following directional mutagenesis and protein overexpression. Using a series of candidate genes, we will therefore reconstruct the ancestral sequence of some enzyme proteins and respiratory pigments at key ancestral nodes and, analyse their enzymatic kinetics and thermal denaturation for alvinellid and polynoid worms and krill species, for which we have a large set of transcriptomes.

Campagne d'évaluation 2017 – 2018 – Vague D

UMR 7144 Adaptation et Diversité en Milieu Marin

Team Ecology of Marine Plankton (ECOMAP)

Projet 2019-2023

Overview of the team

The team "Ecology of Marine Plankton" (ECOMAP) will combine the members of the Plankton group formerly composed by the DIPO, MAPP and EPEP teams. The projected composition of the permanent staff (see below) will gather all previous members, except Stéphane Audic (IR EPEP) who resigned from CNRS in June 2017. Christian Jeanthon and Laure Guillou will lead the team from 1st January 2019.

Permanent Staff	Corps/Grade	Institution	HDR	AXIS 1	AXIS 2	AXIS 3
BAUDOUX Anne-Claire	CR1	CNRS	N	30	40	30
BIGEARD Estelle	AI	CNRS	N	25	50	25
DE VARGAS Colomban	DR2	CNRS	Y	40	30	30
GARCZAREK Laurence	DR2	CNRS	Y	30	10	60
GUILLOU Laure	DR2	CNRS	Y	20	60	20
JEANTHON Christian	DR2	CNRS	Y	50	50	0
LE GALL Florence	IE	CNRS	N	50	50	0
MARIE Dominique	IR	CNRS	N	33	33	33
NOT Fabrice	CR1	CNRS	Y	30	50	20
PARTENSKY Frédéric	DR1	CNRS	Y	20	5	75
RATIN Morgane	IE	CNRS	N	30	10	60
ROMAC Sarah	AI	CNRS	N	33	33	33
SIMON Nathalie	MC	UMPC	Y	60	40	0
SIX Christophe	MC	UMPC	Y	20	0	80
VAULOT Daniel	DRCE	CNRS	Y	70	20	10

Scientific objectives

The main activity of the ECOMAP team members (10 researchers and 5 engineers) focuses on studying the diversity, ecology, and evolution of marine plankton organisms, including viruses, prokaryotes and microeukaryotes across various taxonomic and ecosystemic scales. Despite their impact on a planetary scale, we still know relatively little about the composition of many of these microbial communities and even less about how they interact, function at the ecosystem level and adapt to ecological niches. Relevant open questions addressed by the ECOMAP team during this project will focus on the identification of drivers explaining the distribution and interactions of these communities and how they will adapt and evolve in a rapidly changing world. We structured our project into 3 research federative axes that integrate our complementary scientific interests, skills and expertise. The team is historically tightly linked to the activities, the management and the development of the Roscoff Culture Collection (RCCDossier autoevaluation UMR7144.docx), one of the largest resources in the world for living microalgae that actually hosts, maintains, identifies and distributes more than 4000 strains of marine microalgae, protists, cyanobacteria, photoheterotrophic bacteria and viruses.

1/ Axis 1: Structure and dynamics of planktonic communities

Marine plankton communities are shaped by physical, chemical, and biological factors that influence organismal interactions with the environment in time and space. Differential adaptation or sensitivity to variability in these factors is likely to determine the dynamics of the functional and taxonomic/phylogenetic diversity of the marine plankton. In marine waters, the development of microbial blooms may generate strong positive or negative feedbacks on the trophic food webs. Deciphering the mechanisms by which few species are persistently selected is still an important unanswered issue in ecology. **Our common objective will be** to join our efforts in two main projects that cover extensive spatial and temporal scales.

Temporal scales. To test whether the abundance and dynamics of marine plankton taxa exhibit strong temporal patterns over time and whether these patterns are associated with abiotic or biotic factors, we will rely on samples collected at the SOMLIT-Astan observatory site (2.8 miles off Roscoff) that is characterized by permanently mixed waters and a marked seasonality. Since 2000, biological material, including size fractionated DNA, together with 13 abiotic and biotic contextual parameters have been sampled bimonthly in the frame of the SOMLIT program. Phytoplanktonic biodiversity based on morphological identification is recorded into the Pelagos database (http://abims.sb-roscoff.fr/pelagos) within the RESOMAR network (Réseau National des Stations et Observatoires Marins). Until now, this resource has been only occasionally and individually used to study a very limited number of viral, prokaryotic and eukaryotic groups. **Our common ambition is to develop this sampling site as a genomic planktonic observatory** combining high-throughput acquisition of advanced microscopic and multi-omics approaches (metabarcoding, metagenomics and metatranscriptomics) and fully capitalize on the strong expertise in taxonomy, imaging and functional diversity existing in the team and to larger extent at the Station Biologique (e.g. ABIMS facility). A continuous and joint cultivation effort will be pursued in close association with the RCC using high-throughput approaches developed in the previous period (dilution to extinction, flow cytometry sorting, cryopreservation) in order to **build a unique collection of local bacterial and microalgal species, and their viral and eukaryotic parasites**. Culture-dependent strategies and meta-omics datasets will be combined with single-cell genomic data (i.e. single amplified genomes) to access the transcriptomes/genomes of uncultivated organisms and to obtain a more complete view of microbial community functions and dynamics. Our shared vision is to promote the SOMLIT-Astan genomic observatory as an international reference. To achieve this goal, we are willing to coordinate national and European grants (ANR, H2020) and to develop courses/workshops based on our expertise in plankton sampling, taxonomy and computational analysis within the H2020 project Assemble Plus (2017-2021).

Spatial scales. The advent of meta-omics approaches opened new avenues regarding the structuration of marine microbial communities over large geographical scales. Recent studies emphasized the enormous reservoir of unexplored genetic diversity in marine communities of viruses, prokaryotes and single-cell eukaryotes (Brum *et al*., 2015, Sunagawa *et al*., 2015, de Vargas *et al*., 2015). Totally unknown lineages and undescribed biotic interactions within and across kingdoms (Lima-Mendez *et al*., 2015) remain to be explored at both phylogenetic and functional levels. Although time-consuming, formal taxonomic description of reference taxa is fundamental to assess the functional role of new lineages in marine waters. We will participate to the international effort to describe the infra species and alpha diversities for the lineages known only by their environmental genetic sequences. We will use large datasets obtained during the expeditions *Tara*-Oceans (2009-12), *Malaspina* (2010), *Tara*-Polar Circle (2013-14), *Tara*-Pacific (focusing on lagoons and nutrient gradients, 2016-18), *Tara*-Arctic II (exploration of polar waters, 2019-20) and *Tara*-Black Sea (2022) as well as datasets obtained from specific ecosystems, some highly relevant in the context of global change, and from cruises focusing on well-defined questions targeted in the frame of ongoing collaborations with Brazil, Chile, Norway, Canada, Japan and US. We hypothesize that unknown taxa, generally refractory to cultivation, are mainly driven by tight biotic associations. A main objective will be to correlate genetic to imaging information to assess the morphogenetic complexity of unknown key players (PIA ANR OCEANOMICS, 2012-20).

Common questions across the ECOMAP team expertise will emerge from this data-driven exploration of biological models and marine systems and hopefully foster our collective interest to organize a topical expedition, for instance using flexible platform such as *Tara,* specifically designed to address our main scientific questions.

All the above projects require the existence and maintenance of expert-curated reference databases for a reliable taxonomic assignment of metabarcoding sequences. Members of the ECOMAP team are developing databases dedicated to protists [UniEuk, universal taxonomic framework for eukaryotes (Moore Foundation, 2016-19); PR2, 18S rRNA region; Aquasymbio, symbiotic associations], microalgae (PhytoREF, plastidial 16S rRNA), proteorhodopsin (PR)-containing photoheterotrophic bacteria (MicRhoDE, PR gene) and cyanobacteria (CyanoDB, *petB* gene). These databases currently suffer from a lack of homogeneity between genetic analyses and dispersal of taxonomic expertise on specific groups. These resources require maintenance and development but institutional research support is difficult to obtain to fund them. **In the forthcoming years, we plan to i) gather such databases under a common interface, ii) develop bioinformatic tools to semi-automatically update them and iii) develop user-friendly analytical workflows in order to quickly and accurately determine the relative abundance of each microbial taxa or function from extensive environmental datasets** (RoskoBaz project, Région Bretagne).

2/ Axis 2: Symbiotic associations

Symbiotic associations in marine planktonic waters cover a wide range of effects, nature and strategies. Since a few years, the international scientific community, in particular microbial ecologists, are realizing that no species live in perfect isolation but that organisms are all holobionts (i.e. that live with all associated microorganisms as an entity). Photosymbiosis is a symbiotic relationship between two or more organisms, at least one of which is capable of photosynthesis. Like other forms of symbiosis, photosymbioses can involve the full spectrum of trophic interactions from mutualism through commensalism to parasitism. Photosymbiotic associations are frequently encountered in the marine pelagic environment and can involve various combinations of microalgae with viruses, prokaryotes, protists or metazoans. Within this definition (where the alga can also be the host), we are collectively interested by mutualistic (e. g. between rhizarians and microalgae, microalgae and bacteria such as haptophytes with nitrogen-fixing cyanobacteria, microalgae and bacteria), parasitic (viruses, bacterial and micro-eukaryotic parasites of microalgae), saprophytic (fungi and bacteria living in the phycosphere, endo/ecto-commensals of microalgae) and kleptoplastidy-based photosymbioses (Not *et al.* 2016). Despite the recognized key roles of oceanic plankton on the one hand and symbiosis on the other hand, the exact nature, diversity, and significance of pelagic photosymbioses as well as their regulation by environmental conditions are still poorly understood.

In a rapid changing world, our overarching goal will be to increase our knowledge on the diversity of symbioses and their roles in biogeochemical cycling. We will assess the range of marine hosts and symbionts at a global scale and explore how specific drivers influence these associations. **Our objective will be to estimate the relevance of symbiotic associations in the productivity, resilience/connectivity, and recycling capacity of marine planktonic communities.** Potential interactions between key members of the microbial communities (viruses, picocyanobacteria, bacteria, , picoeukaryotes, microalgae, mixotrophic protists, metazoans) will be studied by *i)* direct observations using a platform for aquatic ecology (e^2-phenOmics), linking state-of-the-art automated high-resolution cell imaging (PIA ANR OCEANOMICS) to single cell omics (EU project SINGEK, 2016-19), *ii)* isolation and experimental tests using laboratory cultures and co-cultures, and *iii)* graph-based co-occurrence analyses using the metabarcoding or functional gene data obtained from plankton samples during past and future oceanographic cruises. To understand the nature of specific associations and the capacity of partners to interact (and thus co-evolve) in the oceans, we will assess metabolic changes related to the interactions between two partners. The genomes, transcriptomes, proteomes and/or metabolomes of the holobionts will be analyzed and, when possible, compared to that of individual partners to monitor the differential expression of genes and the exchange of molecules/signals mediated by the interactions and/or identify molecules underlying specificities of partners (ANR HAPAR, 2015-19; ANR CALYPSO, 2015-19; ANR IMPEKAB, 2016-20, PIA ANR OCEANOMICS, ANR CORALGENE 2018-21). Using these approaches, we will explore how the extended phenotype of holobionts plays a role in processes such as resistance towards pathogens and grazers, facilitation for mutualistic symbioses, adaptation to a novel habitat and sexual reproduction. In addition to gene and protein functions, the relevance of cell-to-cell communication via waterborne molecules (e. g. allelopathic signals, pheromones) for the formation, maintenance or avoidance of these symbiotic associations will also be explored.

Together with other SBR laboratories (UMR 8227 and UMI 3614) and FR2424 core facilities, we will work toward integration of these activities into a future EU project on marine biological and chemical interactions. This task is also targeted as one of the thematic priorities at the SBR level.

3/ Axis 3: Adaptation and acclimation to the marine environment

Phytoplankton is responsible for nearly half of the photosynthesis on the planet. One major challenge for understanding the impact of global climate change on the productivity of the whole ocean is to study the capacity of phytoplankton to acclimate (physiology) and adapt (acquisition, loss or alteration of genes) to these changes. Vast expanses of the world ocean are depleted in one or several nutrients, and N-, P- or Fe-poor regions delineate specific niches to which local phytoplankton is adapted. Temperature is another key parameter that also entices strong adaptation processes. In particular, in polar waters, which are among the most productive areas of the planet, phytoplankton needs to survive the apparent adverse conditions of the complete winter darkness. Elucidating adaptation and acclimation mechanisms would notably provide hints about how a warmer ocean will affect the structure and dynamics of phytoplankton communities. **Our objective will be to develop a cross-scale systems biology approach to characterize and model the differential responses of species/ecotypes towards major environmental parameters.**

First, we will elucidate adaptability and physiological responses of cultivated and non-cultivated models to key parameters such as light, temperature and nutrients. Growth rate and photo-physiological properties will be used as proxies to evaluate the fitness of individuals under various conditions. As a case study, we will analyse how the regulation of membrane fluidity in *Synechococcus* clades/ecotypes influences acclimation capacity to temperature variations by analyzing their membrane lipidomes. We will also determine how environmental parameters can modify other traits or functions in several key eukaryotic organisms. For example, it has been shown that light and nutrient limitations could modify the trophic characteristics of some algae and enhance mixotrophy. We will evaluate the possibility that polar phytoplankton such as *Micromonas polaris*, the dominant picoeukaryote in Arctic waters, may be phagotrophic to cope with the extreme environmental challenges of the long polar night (ANR PHYTOPOL, 2016-20). Radiolarians may lost their photosymbionts (i.e. what we called the plankton bleaching to echo the term ‘coral bleaching’ where photosymbionts are lost during stresses), with significant effect on pelagic biomes (ANR IMPEKAB). We will evaluate the sensitivity of these planktonic photosymbioses to thermal stress conditions. Additionally, through the lysis of their hosts, viruses profoundly influence the diversity and biogeochemistry of the oceans. We will explore how environmental parameters such as temperature, pH, salinity and light, influence the activity of key molecules (depolymerases) to infect their bacterial host (ANR CALYPSO).

Then, we will export this basic knowledge into a more global approach, by applying a system-biology inspired bioinformatics approach based on the inter-comparison between *i*) genomic and transcriptomic data on reference strains and/or single environmental cells, *ii*) gene expression over various experimental conditions, and *iii*) meta-omics datasets collected over large oceanic scales. Marine picocyanobacteria represent a highly pertinent biological model for this approach. Indeed, their numerous assets (ubiquity, high abundance, ~400 strains representative of most of the genetic diversity occurring in the field, ~100 sequenced genomes, ~300 transcriptomes) make it possible to study them at all levels of organization from the genes to the global ocean and to decipher the molecular processes underlying adaptability to the various ecological niches, notably the huge but little studied, warm, Fe-limited areas of the Pacific Ocean (ANR CINNAMON, 2018-21). All available data will be integrated into co-expression and metabolic networks in order to build predictive models of growth and response to various stresses. At last, meta-omics data from *Tara* and *Malaspina* global expeditions will be used to validate at the population level observations made on cultured strains and to identify additional genes and biosynthetic pathways potentially responsible for their adaptation/acclimation capacities to colonize various environmental niches. This strategy will be also applied on eukaryotic and viral models, for which more and more reference genomes and transcriptomes are available today. In particular, we will target a set of marker genes to monitor and model key functions involved in mixotrophy/heterotrophy, breakdown of photosymbioses and viral infection (PIA ANR OCEANOMICS, EU project SINGEK, ANR IMPEKAB, ANR CALYPSO).

Finally, specific genes will constitute privileged targets for further functional analyses, including gene inactivation followed by physiological characterization of mutants that will be made available to the scientific community. Such approaches have been initiated in the laboratory for *Synechococcus* (PIA ANR EMBRC, 2011-19). This step will notably help to continue deciphering the molecular bases of the vast pigment diversity in marine *Synechococcus* spp. by characterizing the function of a number of genes involved in pigment synthesis/regulation, including chromatic acclimation processes. A possible biotechnological application of this study is to produce heterologous systems to control gene expression through changes in light color.

4/ Education and public outreach

4-1/ Teaching

The ECOMAP team includes two associate professors who are involved in several degrees at Sorbonnes University. A large part of their teaching activities will be included in the new Master 'Marine Sciences', which will be affiliated to the International educational program IMBRSea (http:www.imbrsea.eu), a joint Master organized by nine leading European universities in the field of marine sciences. In this degree, both associate professors are in charge of courses, practicals and excursions on marine ecology and biology, with an emphasis on marine microbes, macro-algae and halophyte plants. They will also co-supervise the teaching unit "Marine Microbes and Molecular Tools" (2nd year). For the Master courses that they organize, their objectives will be to maintain and develop a strong connection between research and teaching by *i*) organizing research workshops and *ii*) involving other ECOMAP team members in those workshops as well as in other teaching activities.

Besides the above programs, ECOMAP members will be involved in international courses organized in Roscoff (Advanced Phytoplankton Course, Marine Environmental and Ecological Genomics) and in Chile (ECODIM, Ecology and Diversity of Marine Microbes).

4-2/ Citizen science

We actively participated to the creation of Phenomer (http://www.phenomer.org/), a monitoring program of marine water discolorations caused by phytoplankton blooms launched in 2013. Beyond communication and outreach objectives, this project based on citizen alerts extended the area of monitored coastal waters in Brittany (France) and yielded scientifically valuable data on harmful algal blooms. The ECOMAP team will strongly support this project, in close association with IFREMER.

In order to sample plankton from the world surface ocean across large spatio-temporal scales, we will develop Plankton Planet (P2), the first citizen oceanographic program based on mass sequencing of DNA barcodes from extracts of plankton communities collected by citizen sailors (http://planktonplanet.org). In 2015, we launched the pilot phase of P2 and proved the concept by generating >200 million high-quality plankton DNA barcodes from 184 sampling sites visited by 25 crews. We propose to pursue the effort and organize, over the next 5-10 years, P2 sampling along major navigation loops cornering the world oceans.

4-3/ Scientific mediation

As part of the P2 project, we will pursue the development of user-friendly imaging systems for citizen sailors and kids on one hand, and 3D-microscopy inspired pieces of plankton arts (3D models, augmented to virtual reality) on the other hand (P2 project Plankton Arts, Fondation Total). During the last contract, members of the team have also initiated and coordinated an original outreach project, Planktomania (http://www.planktomania.org), towards children and large public. This project pioneered the use of new technologies such as augmented and virtual reality to bring plankton contribution to global ecology and more generally ocean related issues towards kids and broad public. This very successful initiative will be pursued and amended in the next contract.

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ANNEXES

NO Annexe 1 : Lettre de mission contractuelle

We never got such a letter for the present contract.

NO Annexe 2 : Équipements, plateformes

As stated in the text major equipments are mostly gathered on the technological platforms of the SBR FR2424

Annexe 3 : Organigramme fonctionnel

Provided

Annexe 4 : Sélection des produits et des activités de recherche

Provided

Includes

- a Lab part listing references for outstanding achievements and a selection of 84 publications among the 419 the lab produced during the period
- one part for each of the seven teams, with a selection of publications and communications and a detailed list of research products and activities

Other annexes may be downloaded for convenience

- full lists of publications for the lab, each present team, and each future team,
- summary tables for PhD students, socio-economic activities and attractivity