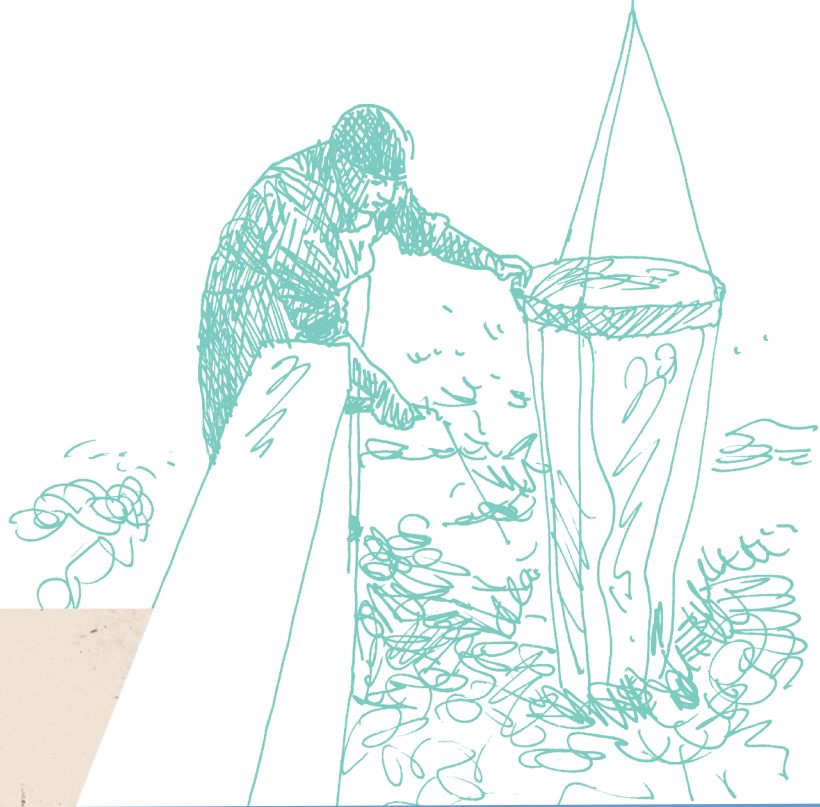




Station Biologique
de Roscoff

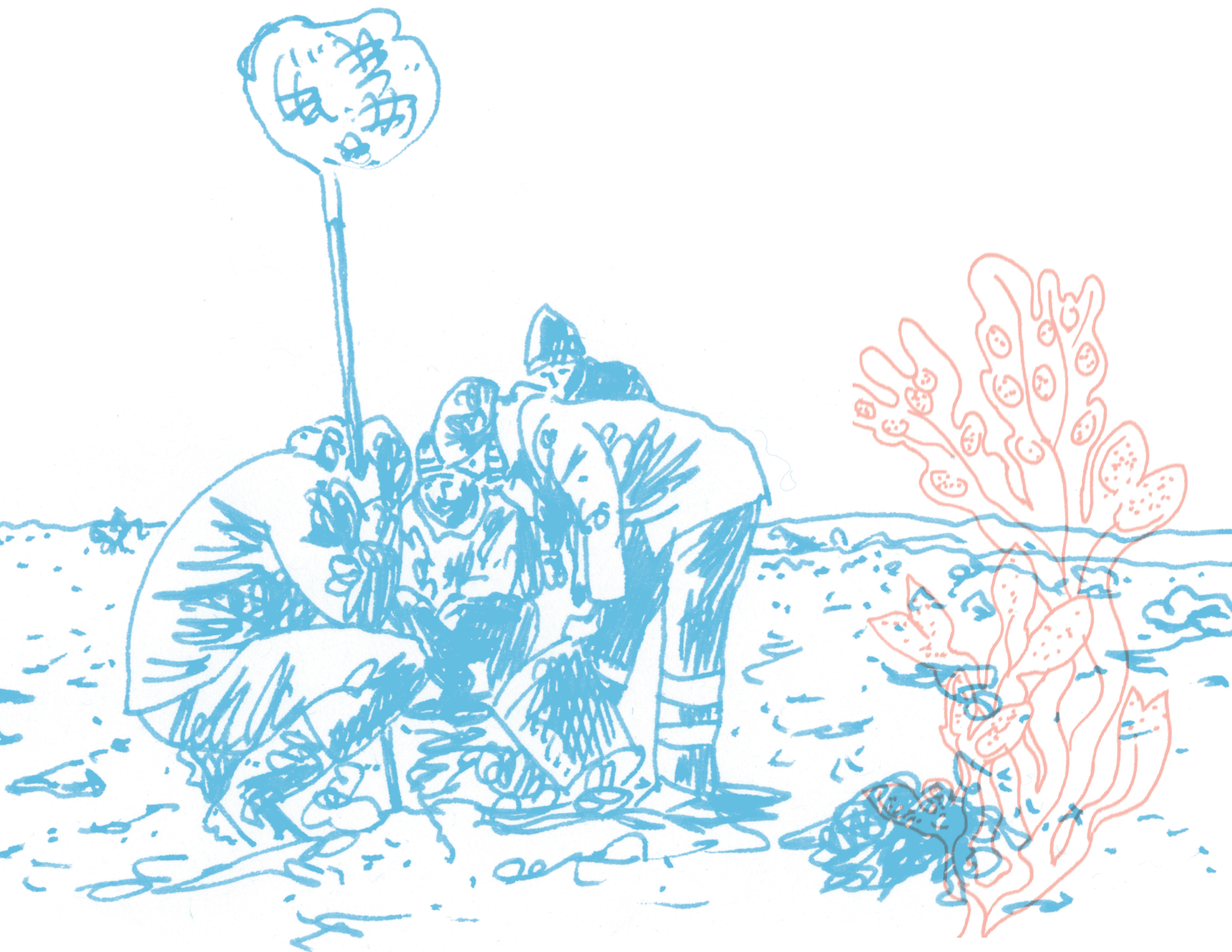


150 YEARS OF THE STATION BIOLOGIQUE DE ROSCOFF

6th and 7th october 2022



SYMPOSIUM PROGRAM



6th OCTOBER

Conference room

8h30 **Registration**

9H00 **Welcome**

Catherine Boyen, Director of the Station Biologique de Roscoff

Session 1. «Major advances at the SBR over the past 40 years»

Moderator: Mirjam Czjzek

09h05 **Marine Biological Stations: 150 years seeking knowledge by the sea**

Ibon Cancio, Plentzia Marine Station, University of the Basque Country, Plentzia, Spain

09h35 **What do marine metazoans tell us about cellular and molecular mechanisms in ourselves?**

Patrick Cormier, Station Biologique, Roscoff, France

10h05 **The Seaweed revolution during 150 years at Station Biologique de Roscoff**

Philippe Potin, Station Biologique, Roscoff, France

10h35 -11h05 // Coffee break

11h05 **A brief history of Plankton in Roscoff**

Daniel Vaultot, Station Biologique, Roscoff, France

11h35 **Roscoff and deep-sea hydrothermal vents: a 40 years story**

François Lallier, Station Biologique, Roscoff, France

12h05 **From natural history outpost to marine genomics core facility at SBR (1980-2022)**

Jeanine Olsen, University of Groningen, The Netherlands

13h -14h30 // Lunch break

Session 2. « Evolution and life cycle »

Moderator: Fabrice Not

- 14h30** **A 20-year journey uncovering the private life of brown algae**
Susana Coelho, Max Planck Institute for Developmental Biology, Tübingen, Germany
- 15h00** **Molecular focus on the microbial world: from oceans to the Earth's biomes**
Puri López-García, Institut d'Ecologie et Evolution du Vivant (IDEEV),
Université Paris-Saclay, France
- 15h30** **From gene regulatory networks to cell type evolution: lessons from sea urchins**
Maria Ina Arnone, Stazione Zoologica Anton Dohrn, Napoli, Italy

16h00-16h30 // coffee break

- 16h30** **Genome Evolution and lifecycle in picophytoplankton**
Gwenael Piganeau, Observatoire océanologique de Banyuls, Banyuls sur mer, France
- 17h00** **The evolution of ploidy: from algae to sex chromosomes**
Thomas Lenormand, Institut des Sciences de l'Evolution de Montpellier,
Montpellier, France
- 17h30** **Evolution of a transmissible cancer in marine mussels**
Nicolas Bierne, Institut des Sciences de l'Evolution de Montpellier, Montpellier, France

Dinner at 19h30, Gulf Stream

7th OCTOBER

Conference room

« Exploring and understanding marine biodiversity »

Session 3. «Interactions in the marine environment»

Moderator: Eric Thiébaud

- 09h00** **Exploring microbial dark matter in sponge symbioses**
Ute Hentschel Humeida, Geomar Helmholtz Centre for Ocean Research Kiel, Germany
- 09h30** **Chemical signaling shapes the complex microbial consortia of the plankton**
Georg Pohnert, Friedrich Schiller University, Max Planck Institute for Chemical Ecology, Jena, Germany
- 10h00** **Pairing up in the plankton: insights on the ecology, genomic diversity, and activity of planktonic symbioses**
Rachel A. Foster, Department of Ecology, Environment and Plant Sciences, Stockholm University, Stockholm, Sweden

10h30 -11h00 // Coffee break

Session 4. « Understanding marine biodiversity at different scales »

Moderator: Catherine Leblanc

- 11h00** **Exploration of marine microbiome by merging “omics” and culturing approaches**
Sylvia Acinas Gonzales, Institut de Ciències del Mar (ICM), Barcelona, Spain
- 11h30** **Algae control carbon cycling and carbon sequestration in the ocean**
Jan-Hendrik Hehemann, Max Planck Institute for marine microbiology, Bremen, Germany
- 12h00** **eDNAbyss: A DNA-based exploration of the largest biome on Earth**
Sophie Arnaud Haond and the eDNAbyss consortium, Marine Biodiversity, Exploitation & Conservation (MARBEC), Sète, France

13h00 - 14h30 // Lunch Gulf Stream

14h30 **Genetic diversity and connectivity of the Mediterranean seagrass *Posidonia oceanica***

Gabriele Procaccini, Stazione Zoologica Anton Dohrn, Napoli, Italy

15h00 **Macroecology & macroevolution of the oceanic plankton**

Hélène Morlon, Institut de Biologie de l'École Normale Supérieure (IBENS), Paris, France

15h30 -16h00 // Coffee break

Session 5. « Biodiversity and global change »

Moderator: Stéphane Egée

16h00 **Marine introduced species and the Ocean Sprawl: What did we learn from DNA-based studies?**

Frédérique Viard, Institut des Sciences de l'Evolution de Montpellier, Montpellier, France

16h30 **Marine Biodiversity and Climate Change: 70 years tracking intertidal species around the UK and northern France**

Nova Mieszkowska, Marine Biological Association, Plymouth, UK

17h00 **Measures to limit climate change and its impacts, and to rebuild marine life**

Jean-Pierre Gattuso, Institut de la mer de Villefranche (IMEV), Villefranche sur Mer, France

17h30 - 17h45 // Closing words

Session 1.

«Major advances at the SBR over the past 40 years»

Marine Biological Stations: 150 years seeking knowledge by the sea

Ibon Cancio, Plentzia Marine Station, University of the Basque Country, Plentzia, Spain

Lacaze-Duthiers would be proud!

The sea is no habitat for humans and during most of our history it has been just the corridor, or the void, in between lands. In that way, the organisms that inhabit the oceans and their characteristics have been mostly unknown. We have had the need to develop skills and sometimes infrastructures in the form of shelter places for researchers and equipment permanently placed in the seashores (after all, it rains a lot in the intertide in Roscoff) for the study of coastal biodiversity. Such study and the valorisation of marine bioresources has been in fact the mission of marine biological stations since their conception in the 19th century.

Marine biological stations were created both as “rest stop sites” and “visiting hubs” for scientists and students, offering then protection, a research environment and on-site trained background knowledge. In these 175 years long journey since the first station opened in Ostend, Belgium and 150 years after the birth of Station Biologique de Roscoff, oceans have provided avenues for basic science at the forefront of biomedical research through the utilization of marine model organisms.

With marine stations science at the frontiers of knowledge reached the periphery and France is a clear example with 15 marine stations working by 1910 out of the roughly 50 functioning in Europe. It was important for Universities in the periphery to compete with Paris and attract trained scientists in the new wonders of physiology, embryology, experimental zoology... On bioresources and with fisheries research Nations began to invest in science, creating for the first time national research programs and funding schemes in the late 1900s. Additionally, basic fisheries research, or aquaculture and oceanography, fostered transnational collaborative research, building upon the collaborative spirit already in practice for biodiversity research in marine stations. All this occurred because “Knowledge is Power” and through the understanding among authorities that research is not an expenditure but an investment. Now, in the 21st century, marine stations continue providing tools to achieve that “Power”. Rocket science at the frontiers of technological advances occurs inside and outside their walls and the development of “Blue Biotechnology” holds the promise to contribute to the socioeconomic development of maritime regions. Roscoff is a proof of these sentences over three different centuries!!!

What do marine metazoans tell us about cellular and molecular mechanisms in ourselves?

Patrick Cormier, Station Biologique, Roscoff, France

Whether we are experienced scientists or not, we are fascinated by marine metazoans' diversity of forms and lifestyles during a low tide excursion to the seashore. Furthermore, back to the workbench, it is also amazing to realize how metazoans we encountered represent established or emerging models used in comparative and experimental biology. We illustrate here how these models have contributed to our understanding of the general mechanisms that govern the life of cells and multicellular organisms, including humans. In addition, we show that, in parallel to basic and applied research, the knowledge derived from these models represents a fundamental base in the academic training of our students to prepare them for future challenging questions. In the coming years, it will be exciting to see the number and the diversity of marine metazoans studied by cell biologists expand as outstanding questions are addressed.

The Seaweed revolution during 150 years at Station Biologique de Roscoff

Philippe Potin, Station Biologique, Roscoff, France

During 150 years, the research at Station Biologique de Roscoff (SBR) has led to breakthroughs in the understanding of seaweed biology, ecology, systematics, biochemistry, genetics, and biotechnology. The possibility in staying in Roscoff to identify seaweed and their biology contributed at the turn of the XIXth century, to the first local flora encompassing more than 500 species. Renowned SBR's visitors pioneered the use of culture techniques to unravel life histories of not only brown algae but red and green seaweed. Others contributed to establish strong knowledge about kelp physiology or calcareous red algae. Since the turn of the XXth century, the increasing number of SBR permanent researchers contributed largely to a transformative period in studies of the evolution and functioning of seaweed groups, associated microbiota and their potential for novel applications, wrought by high-throughput 'omic', genetic methods and system biology. The research at SBR has provided major contributions covering the ecosystemic importance of seaweed communities, the origin of algal groups, advanced understanding of the seaweed holobiont and the link between phenotype and genotype, deciphered algal sex determination and explored the roots of algal multicellularity. The use of seaweed for food, feed, nutraceuticals, agro-solutions, green chemicals, or therapeutics was also promoted thanks to the development of glycobiology, 'omic' and microbial tools.

A brief history of Plankton in Roscoff

Daniel Vaultot, Station Biologique, Roscoff, France

In contrast to other field of Marine Biology and different from what happened in other French marine stations in particular Villefranche-sur-Mer, the study of plankton in Roscoff is relatively young. It really started in the 60s with in particular the work of Jean-René Grall et Guy Jacques. However, it was really in the mid-eighties with the arrival of Alain Sournia and Serge Poulet, working respectively on the phyto- and zoo-plankton, that the discipline expanded. Two techniques really helped develop the field in the three ensuing decades: flow cytometry that allowed to quantify very accurately the abundance of different phytoplankton populations and molecular biology. In these two areas, Roscoff played a pioneering role, developing novel approaches and protocols that are now widely used in the field. During this period, the «Plankton group» expanded from a few researchers to almost 50 people, counting Master, PhDs, engineers, researchers and university personnel. Initially it focused on the smallest size fraction of the plankton, the picoplankton, whose importance was only recognized in the 80s and which dominates in the more oligotrophic regions of the world. This led in particular to develop a very strong line of research on unicellular oceanic cyanobacteria such as *Prochlorococcus* or *Synechococcus* and on phototrophic picoeukaryotes. However, throughout the years, new researchers joined the «Plankton Group» and developed novel interest in groups or phenomena that had been little studied before. For example, there is now a strong line of research on radiolarians, a group of large planktonic organism and many studies on parasitism (e.g. on dinoflagellates or by viruses). The last decade has seen tremendous development of approaches such as metagenomics and metabarcoding that allow to map organisms at oceanic scales and strong research in comparative genomics and transcriptomics that give access to their function. Again the «Plankton Group» plays a key role in these developments which allow us to predict that Roscoff will continue to be a world leader on plankton biology for many years.

Roscoff and deep-sea hydrothermal vents: a 40 years story

François Lallier, Station Biologique, Roscoff, France

The discovery of deep-sea hydrothermal vents and their biota in 1977 is certainly one of the major paradigmatic change of the XXth century for our understanding of global ecology. In addition to photosynthesis, there was chemosynthesis supporting an entirely new kind of ecosystem in the abyss. No plants, no sunlight. Just microbes converting carbon dioxide in the ocean into organic compounds—for themselves and for their hosts. Indeed, relative to the majority of the deep sea, the areas around hydrothermal vents are biologically more productive, often hosting complex communities fueled by the chemicals dissolved in the vent fluids. Chemosynthetic bacteria and archaea form the base of the food chain, supporting diverse animals, the most abundant being closely associated with them in intimate symbiosis.

Adaptation of these organisms to these extreme and unusual environments has prompted

many investigations on their physiology and evolution. The distribution of deep-sea hydrothermal vents along oceanic ridges and other special places also offered interesting models for population genetics, connectivity and biogeographic studies.

All these disciplines have been explored by researchers in Roscoff starting as early as the mid 80's and continuing until now. A lot of people from Roscoff have participated and often lead multidisciplinary oceanographic cruises to these remote environments, in close collaboration with our Ifremer colleagues in Brest. Some of their most striking scientific adventures into the deep will be reported.

From natural history outpost to marine genomics core facility at SBR (1980-2022)

Jeanine Olsen, Professor Emeritus, University of Groningen—GELIFES, The Netherlands

In this presentation, I look back at sequencing technology advances, the changing way of “doing” science, and offer a preview the ‘omics’ challenges for the coming decade.

First-generation DNA sequencing and the development of PCR (early 1990s) launched a new era for biodiversity research and its central role in ecosystem function. The 2000s brought genomics into our vocabulary with the completion of the first human genome (2003). Unfortunately, genome size, cost, slowness and rationale were still major hurdles. Sequencing the wine grape could be justified, a seaweed was a much harder sell.

SBR Director, Bernard Kloareg, had the early vision to see that a genomics trajectory was the way forward for the station, and Catherine Boyen's leadership of the EU Network of Excellence, Marine-Genomics-Europe (2003-2008) set the European standard with 44 top-level labs participating. Major omics projects followed, e.g., PhaeoExplorer, Idealg and Tara Oceans.

This past decade has witnessed a tsunami of advances on the omics front. The Earth BioGenome Project: a moonshot project to sequence two million eukaryotes is about to get underway. And how is that likely to change our conceptions of life, evolution and function?

Session 2.

« evolution and life cycle »

A 20-year journey uncovering the private life of brown algae

Susana Coelho, Max Planck Institute for Developmental Biology, Tübingen, Germany

While struggling through the tangles of brown seaweeds clinging to your legs when bathing in Atlantic waters, you may find it hard to understand my passion for these fascinating organisms. Models for plant embryogenesis until the late 90's, they have emerged recently as a unique group to study the evolution of multicellularity and reproduction. I will describe my 20-year journey studying the biology of these wonderful and mysterious organisms, starting in Porto, through Yerseke, Plymouth and Tübingen, with an emphasis on the research carried out at the Station Biologique de Roscoff.

Molecular focus on the microbial world: from oceans to the Earth's biomes

Puri López-García, Institut d'Ecologie et Evolution du Vivant (IDEEV), Université Paris-Saclay, France

During its 150 years of history, the Station Biologique de Roscoff has witnessed immense progress in marine, and particularly, biological sciences. This progress has been most outstanding in the study of single-celled organisms, first through optical and electron microscopy observations combined with classical cultural approaches. This led to the characterization of a wide diversity of unicellular eukaryotes or, generally, protists but also to the intuition that prokaryotes composing the picoplankton were a key oceanic component. However, it was the development of molecular biology and molecular phylogeny during the second half of the twentieth century that actually opened the so-far black box of the microbial world. From the first universal phylogenies based on highly conserved genes and the discovery of the Archaea to the study of the dominant but unseen uncultured microbial majority, the molecular revolution has had profound consequences on our understanding of biological evolution and ecology. Oceans pioneered those studies before these molecular approaches were systematically applied to other ecosystem types. Metagenomics, single-cell omics and other molecular approaches have thus uncovered a wide diversity of microbial lineages previously unknown to science in natural ecosystems. These newly discovered archaeal, bacterial and, to a lesser extent, protist lineages often represent deep-branches in the tree of life and their study may help to reconstruct trait evolution throughout natural history. They can also have previously unsuspected ecological roles. I will illustrate this with specific examples.

From gene regulatory networks to cell type evolution: lessons from sea urchins

Maria Ina Arnone, Stazione Zoologica Anton Dohrn, Napoli, Italy

One intriguing and still open fundamental question in biology is how different embryonic structures or distinct organs, originating from the same embryonic tissue, developed and evolved in different animals. The answer to these questions most likely lies in the complex nature of the developmental gene regulatory networks (GRNs) that functionally connect transcription factors (TFs) to the terminal differentiation genes of a specific cell type. Developmental GRNs well describe the causal progression in embryonic space and time of the regulatory states (unique combinations of TFs and signaling molecules) that are necessary to specify different cell types in the embryo. Moreover, modifications in developmental GRNs topologies are believed to be at the basis of the emergence of new cell types and embryonic structures. By using a combination of different omics methods, information on the chromatin availability, cis-regulatory region locations, putative TF binding sites as well as gene expression profiles of individual cells, tissues and embryos, we are now able to uncover the components of developmental GRNs and their interactions in the sea urchin larva at unprecedented resolution. We are currently developing new tools combining molecular and morphological comparative analyses of cell types for the understanding of how the diversity of animal cells has evolved.

Evolutionary and Environmental Genomics-Picoplancton

Gwenael Piganeau, Observatoire océanologique de Banyuls, Banyuls sur mer, France

Marine phytoplanktonic green algae are ubiquitous in the sunlit ocean. Among the smallest sized phytoplankton, *Mamiellophyceae* comprise ~20 described species. They have haploid compact genomes and a diploid stage has never been reported, raising the question about asexual evolution in this lineage. Our lab has developed indirect approaches to detect sexual reproduction in these picoeukaryotes by taking advantage of the molecular signatures of meiosis in sequence data. I will present our inference of the frequency of sexual reproduction in natural populations from population genomics data in two *Ostreococcus* species. Comparative genomics of all Mamiellophyceae genomes sequenced so far enabled us to identify a candidate large mating type locus, suggesting very ancient origin of this mating type loci in this lineage.

The evolution of ploidy: from algae to sex chromosomes

Thomas Lenormand, Institut des Sciences de l'Evolution de Montpellier, France

In this presentation, I will try to trace the history, issues and perspectives related to the evolution of ploidy. This is a major theme in theoretical population genetics, as it deals with a salient feature of the biology of higher eukaryotes (which are essentially diploid). This questioning is also at the heart of the biology of algae whose life cycles are, in terms of ploidy, much more varied than those of plants and animals. It is a theme of study which has and remains a major theme studied at the Biological Station of Roscoff. This theme of ploidy has since gone far beyond the question of life cycles, because diploid expression of genes is also a particular state, at the origin of the recessivity of deleterious mutations and of all the consequences of this phenomenon, including inbreeding depression, a central factor in the evolution of reproductive systems. Finally, diploid expression is also a dynamic phenomenon that can rapidly evolve, as is often observed in sex chromosomes. This anniversary seems to me to be an excellent opportunity to look back on 30 years of research on ploidy, a theme so dear to many scientists of Roscoff Biological Station.

Evolution of a transmissible cancer in marine mussels

Nicolas Bierne, Institut des Sciences de l'Evolution de Montpellier, France

The ocean is home to unique biological entities that are unlike anything else in the tree of life and which we did not know anything about before their recent discovery: Bivalve Transmissible Neoplasias (BTN). Transmissible cancers are malignant cell lineages that have evolved the ability to colonize new individuals by transmission of the cancer cells themselves. Since 2015 eight BTNs have been reported in several species of marine bivalves and new ones are continually reported. Everything needs to be investigated about these new parasitic forms that emerged from the cell of a sexually reproducing multicellular host to switch into a clonally reproducing unicellular parasite lifestyle. I will focus on a transmissible cancer that infects *Mytilus* mussels. I will present the results we obtained about the distribution and prevalence of this cancer in European mussel populations, its evolutionary origin and history, its mode of dispersal, as well as its effect on its hosts and the host response to cancer cell invasion. In addition to being unique and intriguing biological entities that allow us to study cancer from an original evolutionary viewpoint, transmissible cancers could well represent ideal biological models for many fundamental questions in biology.

Session 3.

« interactions in the marine environment »

Exploring microbial dark matter in sponge symbioses

Ute Hentschel Humeida, Geomar Helmholtz Centre for Ocean Research Kiel, Germany

The recognition that all higher organisms live in symbiotic association with microorganisms has opened new perspectives in biology. Marine sponges are excellent examples of such holobionts, because many species harbor enormously dense and diverse communities of symbiotic microorganisms in their tissues. More than 40 bacterial phyla and candidate phyla as well as two archaeal lineages representing potentially thousands of symbiont lineages per sponge individual have been recorded. This diverse array of microbial and viral communities has received considerable research attention over the last two decades and the mechanisms of host-microbe interactions within the sponge holobiont and with its environment are beginning to be understood. Collectively, this effort has not only exposed the biodiversity aspects of sponge-microbe symbioses but more fundamentally how they function, evolve, and influence marine habitats. This presentation will focus on recent insights into sponge symbioses, ranging from discoveries in the deep-sea to efforts to develop sponges as experimental models for ancient host-microbe interactions.

Chemical signaling shapes the complex microbial consortia of the plankton

Georg Pohnert, Friedrich Schiller University, Max Planck Institute for Chemical Ecology, Jena, Germany

Unicellular algae and their associated bacteria, viruses, and pathogens in the plankton have established chemical means to interact. These processes contribute to the observed highly dynamic species successions and community structures. Algal exudates can mediate algal / algal interactions but also structure the entire surrounding microbial community. This talk introduces an approach based on the combination of ecological, metabolomic, and imaging investigations to address such chemically mediated interactions. We introduce that algae exhibit high plasticity of metabolite production and uptake and identify key regulators of interactions. We conduct laboratory bioassays and mesocosms to prove their function and show that single chemical signals can predictably manipulate plankton communities. Given the enormous abundance and activity of microalgae in the plankton, we can also link the identified chemical mediators, which regulate an intricate network of interactions, to global element cycling. Consequences for future investigations of plankton ecology, algal physiology, and chemical interactions are discussed.

Pairing up in the plankton: insights on the ecology, genomic diversity, and activity of planktonic symbioses

Rachel A. Foster, Department of Ecology, Environment and Plant Sciences, Stockholm University, Stockholm, Sweden

Some of the most enigmatic components of the plankton are the microalgal groups, which carry intimately associated cyanobacteria and other plastids as symbionts. These partnerships can persist as temporary to more stable obligate relationships, and are found in vast expanses of sunlit zones in most aquatic environments. In some relationships the role and identity of each partner has been clearly resolved, but in many, our understanding is still limited. Combining several different methodologies, intriguing aspects for several of these planktonic partnerships will be presented.

Session 4.

« Understanding marine biodiversity at different scales »

Exploration of marine microbiome by merging “omics” and culturing approaches

Sylvia Acinas Gonzales, Institut de Ciències del Mar (ICM), Barcelona, Spain

Bacteria and Archaea are relevant components of the ocean's food networks; they are key players in all marine biogeochemical cycles. They are accounting with 10^{29} cells in the global ocean but only few thousands of species of marine prokaryotes have been described to date despite that there is estimation of about 10^{12} prokaryotes species in our planet. To fully understand which are the ecologically relevant microorganisms in the ocean, a combination of different approaches is needed to fully cover the whole spectrum of microbial diversity targeting both, the highly abundant and rare microbial taxa. To that end, microbial metagenomics are crucial to enable to reconstruct microbial genomes, what it is called Metagenomic-Assembled Genomes (MAGs). In parallel, single cell genomes through the analyses of Single Amplified Genomes (SAGs) is an alternative approach to target uncultured abundant individual genomes without cultivation. Finally, cultured isolates are also important to fully cover the whole spectrum of microbial diversity and to perform physiological experimental analyses to confirm some functional or metabolic processes. During this talk, I will explain how merging “omics” with isolation would be helpful to dig into important questions in microbial ecology, how MAGs and SAGs are used to reconstruct and describe novel and uncultured microbial species, and why bacterial isolates not always represent members of the rare biosphere.

Algae control carbon cycling and carbon sequestration in the ocean

Jan-Hendrik Hehemann, Max Planck Institute for marine microbiology, Bremen, Germany

eDNAbyss: A DNA-based exploration of the largest biome on Earth

Sophie Arnaud Haond and the eDNAbyss consortium, Marine Biodiversity, Exploitation & Conservation (MARBEC), Sète, France

The largest biome on Earth is by far the deep sea floor, yet the biodiversity it encompasses and the way it contributes to large biogeochemical cycles remain largely unknown. Technical challenges associated to its remote access, to the amount of material needed, and to integrate inventories based on distinct sampling strategies and performed by different experts in distinct areas of the world prevent a comprehensive appraisal of benthic biodiversity in the deep sea floor. The relatively small amount of material required to perform metabarcoding and metagenomics assessments based on eDNA, and the level of standardization they allow offered new promises to advance toward complementary and interoperable biodiversity assessment and improve our understanding of the extent and drivers of deep sea biodiversity. It may also allow unravelling completely unknown lineages, the so-called “dark matter”, which identification requires challenging bioinformatics analysis to separate wheat from the chaff. In the framework of the projects *Pourquoi Pas les Abysses* (2016-2019), launched by Ifremer in 2016 and *eDNAbyss* (2018-ongoing) supported by France Génomique, we developed a series of standard protocols from sampling to bioinformatics analysis, to assess benthic diversity of the deep sea floor across the tree of life. These protocols were applied to a diversity of ecosystems already, allowing to foresee the ability to gather concerted efforts across the international community, to gain a global holistic appraisal of the large reservoir of biodiversity in the deep ocean.

Genetic diversity and connectivity of the Mediterranean seagrass *Posidonia oceanica*

Gabriele Procaccini, Stazione Zoologica Anton Dohrn, Napoli, Italy

The seagrass *Posidonia oceanica* is endemic of the Mediterranean Sea, where it forms dense meadows distributed all along the coasts of the basin, from the surface to up to 35 meters' depth. *Posidonia* meadows fulfill highly valuable ecosystem services and host a complex and diverse associated community. Sexual reproduction is not regular and slow growing rhizomatous individuals can persist in meadows for hundreds of years, shaping populations with very different levels of genetic and genotypic diversity. Dispersal and connectivity among meadows is ensured by the floating fruits and by the stochastic detachment of vegetative propagules, that can be transported by marine currents over long distances. Population genetic studies in the last 10 years have provided a quite comprehensive picture of *Posidonia* population diversity and connectivity all along the distribution of the species, across latitudinal and longitudinal gradients. Variability of genetic indices has been analyzed in relation to local disturbance, in order to relate genetic diversity with population resilience. Basin and local-scale genetic structure has been correlated with potential and realized connectivity among populations, as assessed by Lagrangian dispersal modelling and gene flow estimates, respectively. A differential response to global and local environmental challenges among locally adapted populations has

been highlighted. An effort is ongoing for providing GPS genetic diversity maps that could be at the service of protection and restoration plans in the Mediterranean Sea.

Macroecology & macroevolution of the oceanic plankton

Hélène Morlon, Institut de Biologie de l'École Normale Supérieure (IBENS), Paris, France

Plankton are a core component of marine ecosystems with exceptional taxonomic and ecological diversity, yet their global distribution patterns, as well as the historical and contemporary processes driving these patterns, remain poorly understood. I will present research in my group using *Tara Oceans* metabarcoding data aimed at better characterizing the patterns and drivers of ocean plankton diversity. I will first present a global study of eukaryotic plankton biogeography comparing the biogeography of 70 major groups of eukaryotic plankton and showing how body-size and ecological function shape biogeography through the joint roles of transport and the environment. Next, I will present phylogenetic methods that allow understanding how historical events of speciation, extinction and trait evolution shaped present-day diversity patterns, as well as some applications on planktonic groups. I will highlight the difficulties and promise of carrying these types of analyses on the oceanic plankton.

Session 5.

« Biodiversity and global change »

Marine introduced species and the Ocean Sprawl: What did we learn from DNA-based studies?

Frédérique Viard, Institut des Sciences de l'Evolution de Montpellier (ISEM), Montpellier, France

The development of infrastructures along the coast, and in the open sea, known as the "Ocean Sprawl", provides novel habitats to diverse species, notably sessile species specialized on rocky hard substrates. The species assemblages found on these artificial structures (ports, offshore platforms, aquaculture facilities, etc.) are unique, and often composed of a mixture of native and introduced species. In the last decades, DNA-based studies had been increasingly used to document and study ecological and evolutionary processes in these artificial habitats. This will be illustrated by research, conducted at the Station Biologique de Roscoff, that focused on ports in Brittany and showed 1) the potential of metabarcoding to document the important contribution of non-native species to marina biological communities, 2) the unpredictability of connectivity patterns of species inhabiting these artificial habitats, and 3) the (still too neglected) importance of hybridization due to secondary contacts between native and non-native species. These case studies highlight that marine invasions and coastal urbanization, two facets of global change, have cumulative impacts that cause new ecological interactions and have major evolutionary consequences.

Marine Biodiversity and Climate Change: 70 years tracking intertidal species around the UK and northern France

Nova Mieszkowska, Marine Biological Association, Plymouth, UK

The MarClim project is the largest spatio-temporal long-term intertidal time-series globally. Sustained observations of rocky intertidal species in the UK were started in the 1950s by Professors Crisp and Southward, in collaboration with Fischer-Piette in France. Prof. Lewis and his team undertook surveys on the distribution and abundance of rocky intertidal invertebrates around the UK in the 1980s, extending the scope to include newly developed quantitative surveys for topshells and limpets and investigations of reproductive cycles in these species. Prof. Lewis also realized that intertidal species were 'sentinels' of changes to the marine climate and resultant ecosystem-level shifts, and published a seminal scientific paper on how coastal

species could be used to track global climate change. Prof. Hawkins began recording in the 1980s during his PhD with Southward, and initiated the MarClim project in 2002.

MarClim focuses on a robust set of eighty two temperature-sensitive, readily observed, intertidal climate indicator species of invertebrates and macroalgae for which long-term data sets and monitoring sites are available. The MarClim species list includes boreal coldwater and lusitanian warmwater origins, and invasive non-native species that are, or may pose a potential threat to native biodiversity. These species are surveyed annually at around 100 sites in UK Regional Seas and the Brittany coastline. The data have shown shifts in trailing and leading range edges of species across a wide range of taxa. These changes are amongst the fastest recorded globally and up to ten times faster than those recorded in terrestrial systems.

Measures to limit climate change and its impacts, and to rebuild marine life

Jean-Pierre Gattuso, Institut de la mer de Villefranche (IMEV), Villefranche sur Mer, France

The global ocean is warming, acidifying and losing oxygen, and sea level is rising. As a result, keystone species and key ecosystems such as warm-water coral reefs, seagrass meadows and kelp forests will face high to very high risks by the end of this century even under low carbon dioxide (CO₂) emissions (IPCC, 2019). Moreover, low-lying coastal settlements will face moderate to high sea-level rise risks by the end of the century, even under full and timely implementation of the Paris Agreement, unless comprehensive and intense adaptation efforts are undertaken. This calls for a dramatic scaling up of efforts towards ambitious mitigation and adaptation.

The ocean offers opportunities to reduce the causes and consequences of climate change, globally and locally, as shown by The Ocean Solutions Initiative and other recent reports. However, countries have poorly used ocean-based measures for tackling climate change and its impacts, in their Nationally Determined Contributions (NDCs) under the Paris Agreement. The process towards the revision of NDCs, culminating at the 26th Conference of the Parties of UNFCCC, offers an opportunity for countries to adopt more ocean-inclusive mitigation and adaptation strategies.

In this presentation, I assess ocean-based measures to support climate policies and the revision of NDCs in the areas of mitigation and adaptation. Recovery rates of marine populations, habitats and ecosystems following past conservation interventions suggest that substantial recovery of the abundance, structure and function of marine life could be achieved by 2050, if major pressures—including climate change—are mitigated. Rebuilding marine life represents a doable Grand Challenge for humanity, an ethical obligation and a smart economic objective to achieve a sustainable future.

References

Duarte C. M., Agustí S., Barbier E., Britten G. L., Castilla J. C., Gattuso J.-P., Fulweiler R. W., Hughes T. P., Knowlton N., Lovelock C. E., Lotze H. K., Predragovic M., Poloczanska E.,

Roberts C. & Worm B., 2020. Rebuilding marine life. *Nature* 580:39-51.

Gattuso J.-P., Magnan A. K., Bopp L., Cheung W. W. L., Duarte C. M., Hinkel J., Mcleod E., Micheli F., Oschlies A., Williamson P., Billé R., Chalastani V. I., Gates R. D., Irisson J.-O., Middelburg J. J., Pörtner H.-O. & Rau G. H., 2018. Ocean solutions to address climate change and its effects on marine ecosystems. *Frontiers in Marine Science* 5:337.

Gattuso J.-P., Williamson P., Duarte C. & Magnan A. K., 2021. The potential for ocean-based climate action: negative emissions technologies and beyond. *Frontiers in Climate* 2:575716.



150 ANS

Nous remercions nos partenaires pour les 150 ans de la Station Biologique de Roscoff



BIOTHERM

Brittany Ferries



GOËMAR

