



Sciences biologiques,  
Écologie et Environnement  
**CONFÉRENCES  
JACQUES-MONOD**



**Roscoff (France), 22-26 Juin 2015**

**Biologie Marine Eco-systémique**

***Marine Eco-system Biology***

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**Rapport sur la Conférence**  
***Conference Report***

## « Biologie Marine Eco-systémique »

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La conférence Jacques Monod « Biologie Marine Eco-systémique » (présidente Catherine Boyen, Station Biologique de Roscoff ; vice-Président, Jed Fuhrman, University of Southern California, Los Angeles) s'est tenue à Roscoff du 22 au 26 juin 2015. L'objectif majeur était de tirer parti de l'engouement actuel dans le domaine de l'« éco-biologie des systèmes » appliquée au marin en stimulant le dialogue entre les principaux acteurs scientifiques du domaine. Cette conférence, tout à fait opportune, avait également pour but d'inspirer une nouvelle génération de jeunes scientifiques en biologie intégrative. La conférence a rassemblé 24 orateurs invités, experts de niveau international (6 USA, 8 France, 1 Australie, 3 Allemagne, 1 Autriche, 1 Espagne, 1 Suède, 1 Italie, 1 Monaco et 1 Arabie Saoudite), et 40 participants (24 France, 4 USA, 3 Italie, 2 Espagne, 1 Allemagne, 1 Danemark, 1 Israël, 1 Inde, 1 Australie, 1 Portugal et 1 Hongrie) qui ont présenté leurs travaux sous forme de communications orales sélectionnées (13) et d'affiches (27).

Nous aurions souhaité avoir plus de participants mais le sujet est sans doute encore trop émergent et nouveau pour rassembler actuellement une plus large communauté. L'aspect positif est que ce format plus modeste a réellement favorisé les échanges et les discussions scientifiques au cours des sessions de présentation, ainsi que pendant les pauses et les deux sessions de poster. Il a semblé à tous les participants que cela a permis un meilleur brassage des disciplines et approches depuis des problématiques centrées sur des organismes marins modèles jusqu'à des études des communautés océaniques. Notre volonté initiale était de susciter la participation de jeunes scientifiques et effectivement 6 doctorants et 10 jeunes chercheurs post-doctorants ont participé à la conférence essentiellement au travers de la présentation de leurs travaux sous forme de posters. L'atmosphère tout au long de la semaine a été très chaleureuse et stimulante. Les participants ont grandement apprécié le support logistique irréprochable apporté par Nathalie Babic et Philippe Creignou ainsi que l'excellente qualité des repas et du service de l'équipe du Gulf Stream. Enfin nous avons eu la chance de bénéficier d'une météo tout à fait bienveillante qui a permis aux chercheurs de prolonger les discussions en soirée aux terrasses des cafés sur le vieux port de Roscoff et pour ceux qui le souhaitaient de faire une excursion ensoleillée à l'île de Batz. Le premier soir de la semaine, nous avons eu la chance de pouvoir proposer aux participants qui le souhaitaient de visiter la goëlette Tara qui faisait une courte escale à Roscoff. Les membres de l'équipage de Tara ont d'ailleurs dîné ensuite avec les congressistes au Gulf Stream.

La majorité des présentations étaient d'excellente qualité et il est à signaler que nombreuses d'entre elles étaient issues de la valorisation du tsunami de données du projet TARA Ocean et plus particulièrement des articles du numéro spécial de la revue Science publié le 22 mai 2015. Plusieurs exposés ont mis en avant l'intérêt et la nécessité d'appréhender les systèmes dans toute leur complexité au travers par exemple de l'étude des holobiontes marins ou du fonctionnement des écosystèmes océaniques. Enfin de nombreux travaux qui ont été présentés ont montré la puissance de la métagénomique, de la métabolomique et de la modélisation à plusieurs échelles pour comprendre l'interaction de la biodiversité marine avec son environnement biotique et abiotique dans un contexte changeant.

La conférence a été structurée en six sessions visant à couvrir les différents aspects de la recherche actuelle en biologie marine éco-systémique. Les thèmes ont été choisis afin d'illustrer

les différents systèmes expérimentaux utilisant des organismes marins et de représenter un large éventail d'écosystèmes marins, tout en mettant en exergue l'interdisciplinarité des approches. Les sessions étaient les suivantes :

- I- Interactions entre organismes
- II- Couplage des échelles écologiques et évolutives
- III- Dynamiques évolutives des interactions au sein des communautés
- IV- Interactions organismes-environnement
- V- Réponses aux environnements changeant : du génotype au phénotype
- VI- Des gènes aux communautés jusqu'à la distribution de la biodiversité à l'échelle globale

Au cours de la discussion générale finale les participants ont exprimé leur enthousiasme pour reconduire la conférence sur le sujet si possible dès 2017 et ont fait des propositions pour améliorer le programme et augmenter la visibilité de l'évènement afin d'avoir plus de participants. Jed Fuhrman et Angela Falciatore se sont proposés pour être respectivement le prochain président et la prochaine co-présidente et constituer un dossier de candidature auprès du CNRS.

## Summary

The Marine Eco-Systems Biology conference (Chairman: Catherine Boyen, Station Biologique de Roscoff, France; Vice-Chairman: Jed Fuhrman, University of Southern California, Los Angeles, USA) was held in Roscoff, France from 22 to 26 June 2015. The main objective of the conference was to draw on current enthusiasm in the field of marine eco-systems biology and bring together the main catalysts in the field. This conference was very timely and sought to attract a wide community, and in particular, a new generation of young integrative biologists. The conference hosted 24 invited speakers, all international-level experts (6 USA, 8 France, 1 Australia, 3 Germany, 1 Austria, 1 Spain, 1 Sweden, 1 Italy, 1 Monaco and 1 Saudi Arabia), and 40 participants (24 France, 4 USA, 3 Italy, 2 Spain, 1 Germany, 1 Denmark, 1 Israel, 1 India, 1 Australia, 1 Portugal and 1 Hungary) who presented their work in oral communications (13 selected talks) or posters (27). We were successful in stimulating the participation of young scientists: 6 doctoral students and 10 post-doctoral young researchers presented posters.

We initially hoped for more participants, but the topic is probably still in an emergence phase and thus too new to draw a larger audience. However, a positive aspect of a relatively small audience is that it facilitated interaction and scientific discussions during the presentation sessions, during breaks and during the two poster sessions. All participants agreed that this format promoted better mixing among disciplines and approaches, ranging from marine-model-centered issues to ocean-communities studies. The atmosphere throughout the week was very friendly and stimulating. The conference benefited from flawless organization, thanks to Nathalie Babic and Philippe Creignou, and excellent food service, provided by the staff at the Gulf Stream. Furthermore, we enjoyed magnificent weather during the conference, which was highly conducive to evening discussions on the cafe terraces at the old harbor of Roscoff and, for those who so desired, a sunny trip to the Island of Batz. The first night of the conference, we offered a visit on-board the *Tara* schooner that was in Roscoff for a short stopover. Members of the *Tara* crew joined the participants at the Gulf Stream for dinner on Monday evening.

The majority of the presentations were of excellent quality and it is noteworthy that many of them involved the tsunami of data from the Tara Oceans project and, in particular, relating to the articles of the special issue of *Science* published on 22 May 2015. Several presentations highlighted the value and importance of understanding eco-systems in all their complexity, for example, through the study of marine holobionts or the functioning of ocean ecosystems. Moreover, many of the presented studies demonstrated the power of metagenomics, metabolomics and modeling at multiple scales for a deeper understanding the interaction of marine biodiversity with its biotic and abiotic environment in a context of global change.

The conference was structured around six sessions covering various aspects of current research in marine eco-systems biology. The themes of each session were chosen to illustrate the different experimental systems that use marine organisms and to incorporate a wide range of marine ecosystems and interdisciplinary approaches. The six sessions included:

I- Organism-Organism Interactions

II- Coupling Ecological and Evolutionary Scales

III- Evolutionary Dynamics and Community Interactions

IV- Organism-Environment Interactions

V- Response to Variable Environments: Genotype to Phenotype

VI- From Genes to Communities to Global Biodiversity Patterns

During the final general discussion, participants expressed their enthusiasm for another conference on the same topic, if possible, in 2017 and made suggestions for improving the event

and increasing its visibility to attract more participants. Jed Fuhrman and Angela Falciatore volunteered to be respectively the next Chairman and Vice-Chairman and co-submit an application to the CNRS Jacques Monod Conference committee.

## **Scientific report**

Context:

Eco-systems biology is a new discipline that has emerged following technological breakthroughs in biology and ecology. Biology is moving beyond the reductionist view of cellular functions towards the consideration of an organism as an ecosystem with a holistic point of view. Ecology is now embracing new high-throughput bioimaging and DNA sequencing technologies to understand causality in ecosystem functioning with a mechanistic perspective. Both biology and ecology are at the crossroads of systems analysis in space and time and can address gene function, genotype-phenotype interactions and community structure.

Marine environments are a rich source of ecosystems that are amenable to interdisciplinary approaches. In particular, planktonic ecosystems collectively represent 95% of the marine biosphere and have been of central importance for ecosystem functioning and evolution throughout the history of life on Earth. Other marine systems, such as coral reefs or mangroves, are at the heart of some of the richest and most productive ecosystems and are nonetheless driven by the co-evolution of just a few keystone holobionts. Macroalgae-hosted ecosystems, primitive metazoans uniquely present in marine environments, and deep-sea communities represent additional examples of ecosystems of special interest that are tractable to multi-scale systems-level analysis.

Given these assets of marine systems, a new generation of scientists is working to describe a range of ecosystems within a cross-disciplinary framework, empowered by parallel methodological advances in oceanography, sampling and environmental monitoring in marine habitats, automated bioimaging and DNA sequencing, -omics, remote sensing, bioinformatics and mathematical modeling. Current research is revealing tremendous ecological diversity of genes, genomes, and organisms that will ultimately lead to the understanding of organism function within the context of their biotic and abiotic interactions across kingdoms. This approach is the foundation for comprehensive knowledge on marine eco-systems and eco-evolutionary responses to environmental change.

The conference started on Monday 22 June in the evening with an enlightening and inspiring one-hour opening lecture by Virginia Armbrust (University of Washington, Seattle, WA, USA) who showed the huge potential of combining tools and approaches, such as shipboard flow cytometry, model laboratory co-culture systems, metabolomics, metatranscriptomics and metagenomics for depicting synergistic and antagonist interactions between two dominant members of microbial ocean systems: diatoms and heterotrophic bacteria. She also illustrated how phytoplankton communities respond to current ocean conditions and how they will help shape future ocean conditions. This presentation effectively set the stage for a stimulating conference.

On Tuesday morning, the introduction was given by the Chairman, Catherine Boyen who thanked CNRS for supporting a conference on marine eco-systems biology, as well as all the staff of the Jacques Monod Conference committee for their valuable help in organizing the event. She also acknowledged the generous sponsors: Tara Expeditions, BioGenouest, Euromarine, and EMBRC-FR.

**Session I**, chaired by Jed Fuhrman, focused on interactions between organisms and more specifically on interactions between macro-organisms such as corals, cnidarians, sponges, algae, etc. and their associated microbiomes. Christine Ferrier-Pages (Centre Scientifique de Monaco, Monaco) opened the session by introducing a new isotope model used to trace nutrient exchanges between coral polyps, their endosymbiotic dinoflagellates *Symbiodinium* and their associated bacteria. The model showed that the amount of photosynthates transferred from the symbiont to the host decreases under stress conditions and that coral health is not necessarily correlated to symbiont abundance. We then had a talk by Sebastian Fraune (University of Kiel, Germany) on the important role of the microbiome in the development of cnidarian model organisms (*Nematostella* and *Hydra*). Using transgenesis and genomic approaches, he investigated the *in vivo* function of commensal microbiota and showed that their composition is influenced by host development, host biogeography, and environment and that commensal bacteria are essential for the inhibition of host-pathogen infections. Torsten Thomas (University of New South Wales, Sydney, Australia) gave a very clear and educational presentation on sponge holobionts. Using an approach combining metagenomics and phylogenetic analysis, he presented a global survey of microbial diversity associated with marine sponges. TT particularly highlighted the role of eukaryotic-like proteins (ELPs) found in the sponge microbiome and acquired via horizontal gene transfer from the host: ELPs modulate sponge phagocytosis, thereby allowing symbionts to bypass the sponge's filter-feeding system. The fourth talk of the session was given by Catherine Boyen (Station Biologique de Roscoff) who presented the results of a metabarcoding-based inventory of bacteria associated with the filamentous brown alga *Ectocarpus* cultivated in different salinity conditions. She showed that microbial communities affect the acclimation and physiological response of algae to different environments. The session ended with two very interesting short talks. Using an Imaging FlowCytobot, Heidi Sosik (Woods Hole Oceanographic Institution, MA, USA) was able to establish high-resolution time-series of plankton images and quantify the occurrence of a parasite that contributes to controlling a coastal diatom bloom. She also showed that parasite abundance is correlated to water temperature. Then Harald Hasler-Sheetal (University of Southern Denmark, Odense, Denmark) presented an environmental metabolomics approach to the response of seagrass (*Zostera marina*) ecosystems to abiotic variation (light and oxygen limitation). These results highlighted the value of integrating metabolomics data with ecological and biogeochemical results for exploring ecosystem functioning.

Most of the presentations in this session drew on pioneering studies, with several of them underlining how the holobiont concept has modified our vision of the biology and ecology of marine organisms.

**Session II**, entitled "Coupling Ecological and Evolutionary Scales" and chaired by Chris Bowler, focused on the ecology and evolution of contemporary marine ecosystems based on biogeochemical, fossil and climatic records. The session was opened with a keynote lecture given

by Andy Knoll (Harvard University, Cambridge, MA, USA) who in a vivid talk illustrated how knowledge on past oceans is essential for understanding modern marine ecosystem structure and functioning. He introduced the concept of Mesozoic ecosystem change and emphasized the impact of the [adaptive?] radiation of continental shelf primary-producers (coccolithophores, dinoflagellates, and diatoms) on the trophic pyramid. Then, Colombar de Vargas (Station Biologique de Roscoff) gave the first talk of the week on Tara Oceans results. Applying a massive metabarcoding approach, it was possible for the first time to assess the entire diversity of marine eukaryotes, which is significantly and unexpectedly greater than bacterial diversity. Eukaryotes also appear to play a fundamental role in structuring the plankton net mainly through biotic and positive interactions. The third and final talk of this session was given by Pedro Cermeno (CSIC, Barcelona, Spain) who showed that the diversification and geographic expansion of marine diatoms coincide with periods of increased continental weather fluxes and silicic acid input in the oceans. Overall, these presentations highlighted the close relationship between the evolution and diversification of marine life and the evolution of the Earth's surface environments.

**Session III** on "Evolutionary dynamics of community interactions" chaired by Colombar de Vargas was introduced by Gwenaël Piganneau (Laboratoire Arago, Banyuls, France) who presented the results of a population genomics analysis performed on *Ostreococcus* communities in the Mediterranean. She provided evidence of unexpected heterogeneity in polymorphism along *Ostreococcus* chromosomes and suggested for instance that the observed genetic diversity is linked to virus susceptibility. Then, Damien Eveillard (University of Nantes, France) showed the results from a computational analysis of environmental and metagenomics data gathered during the Tara Oceans expedition. Specifically, he applied a co-occurrence network (and subnetwork) analysis to investigate mathematical interactions among and between complex microbial communities and their environment. This approach demonstrated, for instance, that overlooked taxa such as Radiolaria, alveolate parasites, and bacterial pathogens, as well as *Synechococcus* and their phages, are highly connected and appear to be key drivers of the biological carbon pump in these marine communities. The final short communication by Daniella Schatz (Weizmann Institute of Science, Rehovot, Israel) was about the life strategies of the double-DNA virus infecting the coccolithophore *Emiliana huxleyi* and helping to regulate the massive *E. huxleyi* blooms that occur in the oceans. She investigated the cellular mechanisms that govern the replication cycle of the virus and showed that an autophagy-like process is central to the host-virus dynamics.

**Session IV**, entitled "Organism-environment interactions" and chaired by Catherine Boyen, addressed interactions between organisms and their environments and started with an impressive talk by Kristin Tessmar-Raible (University of Vienna, Austria) who clearly demonstrated the high interest of marine models for investigating the impact of light on the physiology and behavior of animals. Internal timers are essential for animals to be able to anticipate, regulate and synchronize biological processes. The circadian clock is well known, but KTR focuses her studies on the effect of the moon and tidal cycles on complementary marine models: the worm *Platynereis dumerii* and the marine midge *Clunio marinus*. Using a very elegant approach that combines transgenesis, TALEN and CRISPR-mediated genome engineering, genetics, conditional specific cell ablation and genomic resources, she presented preliminary results indicating that the circadian period is not required for the functioning of

circalunar clock in *Platynereis*, although the circalunar clocks influence circadian period length, and daily timing is genetically controlled in *Clunio*. Then, Georg Pohnert (University of Jena, Germany) gave an inspiring and vibrant presentation on chemically mediated interactions of diatoms with their biotic and abiotic environment. Two interesting and relevant examples showed the effectiveness of comparative metabolomics and co-culturing methods. The study identified the pheromone (L-diproline) that controls the chemical attraction of mating type + in the diatom *Seminavis robusta* and emphasized the role of allelochemicals in favoring the growth of co-cultured diatoms. This pioneering work clearly paves the way to a better understanding of chemical interactions in plankton ecology and physiology. Then, Florian Weinberger (GEOMAR, Kiel, Germany) presented an interesting study on determining the success of the invasive red alga *Gracilaria vermiculophyta*. He demonstrated that the invasive species is more resistant than the native species to temperature increases and grazers, and using metabolomics approaches, he suggested that the invasive *Gracilaria* is more successful than the local species due to the release of chemical "weapons" such as C20:4 fatty acids and their derivatives. Alexandra Worden (Monterey Bay Aquarium Research Institute, USA) then explored the connections between phytoplankton diversity and adaptive strategies for dealing with the limitation of nutrients such as phosphates. The development of a chemostat combined with a comparative proteomics approach helped identify about 20 highly abundant unknown proteins related to phosphate limitation in various *Micromonas* clades, half of which are unique to *Micromonas*. The sessions continued with three short talks. Christian Jeanthon (Station Biologique Roscoff) gave an overview on the work he has been doing on the assemblage of aerobic anoxygenic photoheterotrophic (AAP) bacteria in illuminated marine environments. A clustering analysis of marine samples from diverse environments showed that salinity is the major environmental determinant of these communities' composition. CJ emphasized the concept of "Ecoclades" and the importance of the links between phylogeny and habitats. Elva Toulza (University of Perpignan, France) investigated the drivers of thermal tolerance in the tropical coral *Pocillopora damicornis* using a multi-scale integrative study combining genome-wide transcriptomics, metagenomics and epigenomics approaches on clonal corals. Her conclusion is that coral may learn to cope with thermal stress: changes are rapidly fixed in the genome/methylome. Ingrid Obernosterer (Laboratoire Arago, Banyuls, France) reported results from ecosystem response to large-scale iron fertilization in the Southern Ocean and showed that carbon fluxes observed in an ecosystem are tightly correlated with plankton community composition.

**Session V** entitled "Response to Variable Environments: Genotype to Phenotype" and chaired by Alessandra Carbone, covered the topics of coral bleaching and other adverse reactions to environmental stress as well as diatom responses to environmental signals. Virginia Weis (Oregon State University, Corvallis, OR, USA) introduced her coral-model-based approach for depicting the cellular and molecular mechanisms underlying the establishment, maintenance and breakdown of the symbiosis between an anemone host and dinoflagellate symbiont. Coral bleaching results from the perturbation of a complex host innate immunity system involving signaling cascade (NF $\kappa$ B and sphingolipid rheostat) and apoptosis mechanisms. VW showed how, in the case of bleaching, the innate immune system of the host is re-engaged leading to increased nitric oxide levels, host-cell apoptosis and a collapse of symbiosis. New perspectives are now possible with the first available genome of a dinoflagellate, that opens perspectives for the assisted evolution of coral. VW underlined the need to evaluate the risks and benefits of this line of research and advocated a systems-biology approach for better understanding the biology of the coral holobiont. We then switched to a different topic: diatom-phytochrome (DPh)



photoreceptors and their potential role in sensing biotic and abiotic signals. Using a sophisticated approach combining over-expression mutants, transcriptomics data and computational modeling, Angela Falciatore (UPMC, Paris, France) presented her pioneering work on the identification and characterization of the first far-red light phytochromes in the marine model diatoms *Phaeodactylum tricornutum* and *Thalassiosira pseudonana*. The postulate is that diatoms use DPh for external versus internal (autofluorescence) light-signal perception. Then, Samuel Dupont (University of Gothenburg, Sweden) widened the perspective and emphasized the new challenge facing us: assessing the effect of multi-stress drivers on multi-species systems for analyzing the impact of global change on marine ecosystems and for making predictions under various scenarios. Adaption of sea urchins to acidification was used as a model system to illustrate this issue. A complex experimental biology study showed for instance that the extra energy cost required to decrease internal pH induces a shift in the energy budget resulting in a deleterious effect on the growth of sea urchin embryos. SD concluded his talk by stressing the importance of developing new approaches combining laboratory experiments and mesocosm studies for validating theoretical models. Then, we boarded the *Tara* again, this time with Chris Bowler (Ecole Normale Supérieure de Paris, France), who gave a brilliant presentation on a global metabarcoding approach for the study of marine eukaryotic diversity, inferred from *Tara Oceans* data. CB focused his analysis on diatom distribution in the global ocean and addressed the issue of how diatom composition and diversity change around the planet and why. Through the analysis of a huge V9-rRNA diatom ribotype database across 47 sampling stations all over the global ocean, he identified specific biogeographical patterns of diatom diversity and demonstrated that diatoms are as diverse and abundant in the open ocean as on the coast. However, "everything is not everywhere"! Data computing shows clear relationships between diatom ribotypes and environmental variables (e.g. carbon flux) and led to the identification of nine clusters. CB concluded by introducing the next challenge: further depicting the correlations between diatom diversity and environmental parameters. The session went on with three short talks. Tristan Biard (Station Biologique Roscoff) gave an overview of a worldwide survey of Rhizaria, an overlooked super-group of fragile unicellular marine protists that are difficult to collect and preserve. Using an *in situ* underwater vision profiler, he demonstrated the substantial contribution of Rhizaria biomass to plankton marine diversity and showed their abundance in oligotrophic tropical regions. TB concluded by stressing the importance of this thus-far neglected taxon for understanding ocean functioning and shared very beautiful pictures from the Plankton portal. Then, Julie Reveillaud (IUEM, Brest, France) gave a presentation on sub-seafloor microbial communities in hydrogen-rich vent fluids from two hydrothermal sites along the Mid-Cayman Rise. Using a combination of chemical measurements, energy modeling, enrichment cultures and metagenomics sequencing, a comparison of the two sites showed that the unexpected functional microbial diversity was not tightly correlated with heat-vent fluid chemistry. Back to *Tara Oceans*, Daniele Luidicone (Stazione Zoologica, Naples, Italy) emphasized the importance of multidisciplinary approaches for coupling physics and biology systems and for understanding the plasticity of marine ecosystems with climate change. DL illustrated this holistic view by an end-to-end experiment based on *Tara Oceans* sampling followed by metagenomics and metatranscriptomics functional analysis of a natural iron fertilization region in tropical waters.

The final **Session (VI)**, entitled "From Genes to Communities to Global Biodiversity", chaired by Andy Knoll, aimed to go beyond individual observations and attempt to develop a general synthesis by examining global biodiversity patterns. Jed Fuhrman (University of Southern

California, Los Angeles, USA) began the session with an enlightening presentation on association networks in marine plankton communities. Using the comprehensive microbial long-term series collected at the USC Microbial Observatory in the Santa Catalina Islands, associations and potential interactions between bacteria, virus, archaea and protists were inferred from natural co-occurrence patterns. JF showed the complexity of such holistic studies resulting from the diversity of interactions (competition, parasitism, symbiosis, grazing) and actors, combined with seasonal and local perturbations. The main conclusions were the remarkable resilience of the average microbial community, the importance of time-scale and seasonal variability and the recommendation for using high phylogenetic resolution, finer than standard OTUs. Then Xabier Irigoien (Red Sea Research Center, Thuval, Saudi Arabia) presented a large comparative metatranscriptomics analysis of viral infection in neustonic zooplankton during a bloom of the nitrogen-fixing cyanobacteria *Trichodesmium* in the hot and oligotrophic waters of the Red Sea. The study revealed differential gene expression before, during and after the bloom. XI hypothesized that *Trichodesmium* affects the immune system of copepods, thus facilitating viral infection. The overall conclusion is that the system is more complex than initially thought. We switched then to a more theoretical approach with the presentation of Mick Follows (MIT, Cambridge, MA, USA) who introduced a virtual ocean numerical modeling study on marine plankton populations. Applying a multi-traits approach that integrates body size and trophic strategy, the virtual ocean model simulations suggested that phagotrophic mixotrophy is a common trophic strategy in the oceans. This strategy enhances mean body size and enhances the efficiency of community nutrient use and carbon export. The next step of this research will be to test or constrain the model with observation data. Markus Weinbauer (Observatoire Océanologique de Villefranche, France) then took the audience to the dark ocean, i.e. the ocean at depths without photoautotrophic production. A still-unsolved paradox of the deep sea is the high abundance of viruses with a strong decrease in host abundance with depth. Using metagenomics approaches, MW explored depth-related trends in prokaryotic and viral abundance. The main conclusion of the talk is that there is a strong seasonal variability in microbe and virus abundance in this zone and that surface viral diversity differs from that found at great depths. Moreover, viral infection, through viral lysis-mediated carbon flow, can influence ecosystem functions as well as biogeochemical cycles. Again, the system is more complex than initially thought. Alessandra Carbone (UPMC, Paris) finished the morning part of the session with a rich and clear talk on computational biology, more specifically on a global protein-domain consensus model designed to better identify the marine communities' functional preferences. The CLADE pipeline includes a database of probabilistic domains allowing to identify potential domains and to select the best ones. An analysis of a metatranscriptomic data set from various open ocean regions (including polar regions) illustrated the power of CLADE, for example through the identification of new bacteriorhodopsin-like proteins. As a conclusion, AC advocated the development of new strategies for functional annotations of a large amount of marine molecular data and stressed the limits of the phylogenetic-closeness hypothesis for very divergent sequences. The session continued with four short talks. Based on a Shannon-index analysis of Tara Oceans protist (18S ribotypes) data, Silvia de Monte (Ecole Normale Supérieure, Paris, France) investigated the patterns of rarity in marine microorganisms and suggested that rare marine species provide less information than those of intermediate abundance. Yann Moalic (IUEM, Brest) used a holistic network analysis approach for modeling the co-occurrence patterns of bacterial communities associated with different *Caulerpa* green seaweeds species in the Mediterranean Sea. A strong specificity exists between the algal host and its endophytic bacterial communities, suggesting the tight dynamics of the relationship are related to the

environment conditions. Then, Zackary Johnson (Duke University, Beaufort Marine Lab, NC, USA) presented results of *in vitro* steady-state and temperature-shift experiments on various *Prochlorococcus* strains. By comparing these results to patterns of photosynthesis and activity of *Prochlorococcus* ecotypes from different ocean regions, he proposed that temperature is a key factor in balancing the diversity and activity of cyanobacteria in the open ocean. The last talk of the session and of the conference was given by Flora Vincent (Ecole Normale Supérieure, Paris) on an ecological network-based approach to study diatom communities. Using Tara Oceans metabarcoding data, FV explored biotic interactions of diatoms in marine ecosystems. Based on inferred networks, a global photic plankton interactome was established followed by a zoom of diatom interactions with other organisms (pathogens, predators, and grazers). The next issue is to link the abundance profile to the type of interaction.

### **Discussion session: conclusions and recommendations**

The last short session on Friday morning was devoted to general discussion. Overall, participants gave very positive feedback on the conference, which led us to conclude that it was a true success from a scientific and organizational point of view, including the food at the Gulf Stream, the weather, and the location. Nathalie Babic's professionalism and efficiency were warmly acknowledged. Participants particularly enjoyed the cross-disciplinarity of the presentations as well as the mingling of different scientific sub-communities. For instance, biologists who work with marine-model-organisms, oceanographers, and computational scientists had the opportunity to talk together and exchange new ideas and questions. Marine eco-systems biology is an emerging new field and the conference fostered a stimulating, pioneering atmosphere. The participants were unanimously in favor of renewing the conference in 2017 or 2018 to continue to build the community. Jed Fuhrman and Angela Falciatore volunteered to be respectively the next Chairman and Vice-Chairman and submit an application to a CNRS-JMC call in the near future. Main suggestions and recommendations for improving the conference included the following:

- allow more time for discussion after talks;
- include working sessions in small groups (e.g., ground-breaking areas, goals we can achieve together, etc.);
- invite scientists from other fields, such as the social sciences, theoretical sciences, terrestrial ecology;
- hold more educational talks to provide an introduction to new sub-topics;
- hold more talks on coastal zone-related topics, on marine mammals;
- avoid insofar as possible over-scheduling days: Thursday's session with 16 talks was much too long;
- avoid overlapping with the Gordon Research Conferences (e.g., Marine Microbes).