

OIST-RIKEN Joint Symposium, Series 1

Green and Blue Planet How Can Ecological Research Shape Our Future?



April 6th-7th (Tue-Wed) 2021

Venue

Symposium, Poster session

OIST Auditorium, Conference Center

Schedule

Day 1

April 6th (Tue) 2021 Time: 8:40-19:00

Venue: Auditorium, Conference Center

8:40 - 9:00	Registration	
9:00 - 9:10	OIST Provost, Dr. Mary COLLINS	Opening Remarks
Chair: Jun KIKUCHI		
9:10 -10:30	Session 1 (3 speakers)	
	OIST Professor Dr. Noriyuki SATOH	Genome scientific approach towards coral reef preservation in Okinawa
	RIKEN Team Leader Dr. Shigehiro KURAKU	Underwater ecology of marine vertebrates unveiled by biodiversity genomics
	OIST Assistant Professor Dr. Filip HUSNIK	What can we learn about the origin of mitochondria and plastids from much younger endosymbioses?
10:30 - 10:45	Tea Break	
Chair: OIST Prof. Evan ECONOMO		
10:45 - 12:05	Session 2 (3 speakers)	
	RIKEN Team Leader Dr. Jun KIKUCHI	AI-based prediction of aquatic ecology, aquaculture and aqua-engineering
	OIST Professor Dr. Vincent LAUDET	The endocrinology of local adaptation in coral reef fishes
	RIKEN Team Leader Dr. Hideki ABE	For Molecular Design of Polymer Materials Biodegraded in Marine Environment
12:05 – 12:50	Lunch & Luncheon Meeting	
Chair: Takemasa MIYOSHI		
12:50 – 14:35	Session 3 (4 speakers)	
	RIKEN Team Leader Dr. Ryuhei NAKAMURA	Bio-Geo Catalysis for Sustainability
	OIST Professor Dr. Evan ECONOMO	Measuring, tracking, and understanding biodiversity change in a human-dominated world
	RNC Team Leader Dr. Hiroyuki ICHIDA	Heavy-ion beam mutagenesis and its molecular characteristics in plants
	OIST Science and Technology Gr. Associate Dr. Reina KOMIYA	Diverse non-coding RNAs involved in plant reproductive system

Schedule

Day 1

April 6th (Tue) 2021 Time: 8:40-19:00

Venue: Auditorium, Conference Center

14:35 – 14:55	Coffee Break	
Chair: Noriyuki SATOH		
14:55 – 16:40	Session 4 (4 speakers)	
	RIKEN Chief Scientist/Team Leader Dr. Takemasa MIYOSHI	Weather Predictability and Data Assimilation: Perspectives Toward General Theory of Prediction
	OIST Professor Dr. Timothy RAVASI	Adaptation and Acclimation of Coral Reef Fish as a Response to Global Warming
	RIKEN Team Leader Dr. Taro TOYOIZUMI	Edge of Chaos and Avalanches in Neural Networks with Heavy-Tailed Synaptic Weight Distribution
	OIST Assistant Professor Dr. Sam REITER	An ecological approach to understanding the brain
16:40 – 16:50	RIKEN Executive Director, Dr. Hidetoshi KOTERA	Closing Remarks [here or after Poster Session]
17:00 – 18:30	Poster Session and Networking	
	1: Marine genomics 2: Environment and Ecology 3: Evolution, Biodiversity and Bio-resources 4: Climate change 5: Computational science 6: Others (related to the theme of symposium)	

Schedule

Day 2

April 7th (Wed) 2021 Time: 9:00-12:00

Venue:TBD

9:00 – 12:00

Mini workshop (Concurrently)

Theme 1: Protection of Environment

- Discussion Leader: Hideki ABE (RIKEN)

Theme 2: Ecosystems & Biodiversity

- Discussion Leader: Evan ECONOMO (OIST)

Theme 3: Climate Change & Geoscience

- Discussion Leader: Yuko MOTIZUKI (RIKEN)

Theme 4: Data Science & Neuroscience

- Discussion Leader: Sam REITER (OIST)

Wrap up at the end.

Session 1



Marine Genomics Unit, OIST

Professor, Noriyuki Satoh

Genome scientific approach towards coral reef preservation in Okinawa

Coral reefs are the most biodiverse marine ecosystems. Because they nurture edible marine species and contribute to culture, communities and governments are calling for their preservation. However, many coral reefs including Great Barrier Reef and Okinawa are currently experiencing severe, cumulative disturbances, including coral bleaching and massive outbreaks of crown-of-thorns starfish (COTS). For the past decades, our group has adopted genome scientific approach towards better understanding of coral-reef biology, which might provides future plans of coral reef preservation in Okinawa. The approach includes decoding of genomes of 15 *Acropora* corals (Shinzato et al. 2020. *Mol. Biol. Evol.* Msaa216), four clades of coral-symbiotic dinoflagellates (Shoguchi et al. 2020. *Genome Biol. Evol.* in press), and COTS (Hall et al. 2017. *Nature* 544: 231-234). Taking advantages of the genomic information, we are now conducting several analyses to understand coral-reef preservation biology at Okinawa.



Laboratory for Phyloinformatics, RIKEN Center for Biosystems Dynamics Research

Team Leader, Shigehiro Kuraku

Underwater ecology of marine vertebrates unveiled by biodiversity genomics

High-throughput DNA sequencing has been fueled by continuous technical advances and has largely contributed to more consolidated molecular biology. Its utility is, however, not limited to laboratory experiments but is expanding the possibility of elucidating biological questions in nature. Despite the growing concerns of the marine environment and endangered wildlife, molecular-level analysis especially of large marine animals is highly limited by low accessibility to live materials. As an exploratory extension of traditional life science researches in RIKEN, my lab in Kobe conducts a minimally invasive investigation of marine vertebrates, including whole genome DNA sequencing, transcriptomic profiling of reproductive status, fecal DNA metabarcoding for diet analysis, and environmental DNA detection for habitat monitoring. This presentation will mainly cover recent achievements of my lab on shark genomics (Hara, et al., 2018. *Nat. Ecol. Evol.*, 2: 1761-1771) with a reference to the potential of this country with the unique fauna and flora in the recent world-wide trend of biodiversity genomics.



Evolution, Cell Biology, and Symbiosis Unit, OIST

Assistant Professor, Filip Husnik

What can we learn about the origin of mitochondria and plastids from much younger endosymbioses?

Whether mitochondria and plastids originated by endosymbiosis is no longer questioned, but we still do not understand the actual process of integration. Other, younger endosymbiotic systems are, however, extremely common. In this talk, I will present our data from endosymbiotic bacteria in insects and protists suggesting how some of these younger endosymbionts proceed along the path to cellular integration. The processes underlying these associations appear to be not so different from organelles after all. New models for endosymbiotic associations emphasize the importance of transient stages, conflict more than cooperation, and population genetics forces that lead to genome reduction. These processes restrict most endosymbionts to one of a few possible evolutionary pathways, commonly ending with extinction, and rarely in the origin of a new cellular organelle.



Session 2



Environmental Metabolic Analysis Research Team,
RIKEN Center for Sustainable Resource Science

Team Leader, Jun Kikuchi

AI-based prediction of aquatic ecology, aquaculture and aqua-engineering



Ecosystem homeostasis can be evaluated by fluctuation of these analytical parameters, then data science method can contribute to classify normal versus abnormal status of ecosystem, as well as biomarker (or environmental diagnostic marker) might be extracted by multivariate analysis and machine-learning computation [1]. To do this, we focused to analyze environmental complexity in terms physical, chemical and biological parameters. Therefore experimental analytical parameter can be supported to gain better prediction accuracy by incorporation of machine-learning approach [2]. Then, we have been promoted data science for evaluation and prediction of ecosystem, such as environmental water[3], sediment[4], natural algae[5], natural fishes[6] as well as aquaculture [7].

REFERENCES

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- [2] Date, Y. & Kikuchi, J. *Anal. Chem.* 90, 1805-1810 (2018); Asakura, T. et al., *Anal. Methods* (2018) 17, 16-26; Asakura, T. et al., *Anal. Chim Acta.* 1037, 230-236 (2018).
- [3] Ogawa, D. et al., *PLoS One* 9, e110723 (2014); Oita, A. et al., *Sci. Total Environ.* 636, 12-19 (2018).
- [4] Asakura, T. et al. *Anal. Chem.* 86, 5425-5432 (2014).
- [5] Date, Y. *Polymer J.* 44, 888-894 (2012); Ito, K et al., *Anal. Chem.* 86, 1098-1105 (2014); Wei, F. et al., *Anal. Chem.* 87, 2819-2826 (2015).
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- [7] Mekuchi, M. et al. *Sci. Rep.* 7, 9327 (2017); Mekuchi, M. et al. *PLoS One* 13, e0197256 (2018).



Eco-Evo-Devo Unit, Okinawa Institute of Science and Technology, Japan
and Institute of Cellular and Organismic Biology, Academia Sinica, Taiwan

Professor, Vincent Laudet

The endocrinology of local adaptation in coral reef fishes



The vast majority of coral reef fish have a life cycle with a pelagic larval phase, where the fish develops and grows as a planktonic organism, followed by juvenile and adult phases during which it settled in the reef. The larval phase stage is essential for the survival of adult populations, as it ensures a regular supply of new individuals and promotes dispersal and therefore significant genetic mixing, both key factors for their adaptation to a constantly changing environment. Our previous work has shown, using the Manini *Acanthurus triostegus* that the transformation of a larvae to a juvenile is a metamorphosis is controlled by thyroid hormones. These hormones not only trigger and coordinate this transformation, but they also determines the future "quality" of the juveniles produced, i.e. their ability to feed efficiently and to escape predators. Metamorphosis therefore constitutes a major step in the fish life cycle, controlling the success of juveniles in integrating adult populations and ensuring the dynamics of fish stocks. We are now testing using clownfishes and Manini, in several natural and anthropized environments how these hormones play a pivotal role in the local adaptation of juvenile populations in their various habitats.

Session 2



Bioplastic Research Team, RIKEN Center for Sustainable Resource Science

Team Leader, Hideki Abe

For Molecular Design of Polymer Materials Biodegraded in Marine Environment

Bioplastics, biodegradable and biomass-based polymers, have increasingly become important for development of environmentally benign materials. They can provide a solution to problems concerning energy resources, the global environment and solid waste management. Research on biodegradable and biomass-based polymers has been carried out worldwide with the aim of achieving a balance between human activities and the natural environment.

Poly(hydroxyalkanoate)s (PHAs) have emerged as a family of aliphatic polyesters produced by a number of bacteria and attracted much attention as biodegradable biomass-based plastics to solve the waste disposal challenge. Since PHA materials are decomposed in natural environments by the function of extracellular PHA-degrading enzymes secreted from microorganisms, we have investigated the reaction between PHA and purified PHA-degrading enzyme.

In this presentation, I would like to introduce the relationships between the structures and the biodegradability of PHA materials. In addition, the molecular design of novel biodegradable polymeric materials in marine environment is proposed based on those findings, and the further remaining issues will be discussed.



Session 3



Biofunctional Catalyst Research Team, RIKEN Center for sustainable resource science

Team Leader, Ryuhei Nakamura

Bio-Geo Catalysis for Sustainability



The goal of our team is to understand the elegance and beauty in biological and geological energy-conversion processes in order to develop a sustainable energy production strategy which is in harmony with nature. To this end, we are working on the development of biologically inspired catalysts and their application for chemical synthesis. Specifically, the solar-powered chemical synthesis in photosynthetic organisms has inspired us to develop innovative water splitting catalysts using only earth-abundant elements. This is a critical prerequisite necessary to use water as a resource for chemical synthesis. In parallel with our study on the solar-powered ecosphere, the team has also focused on replicating the unique chemical energy-harvesting systems found in the deep sea. The lack of sunlight has led these systems to develop intricate and elegant strategies for the interconversion of chemical, thermal, and electrical energy, thus allowing chemical synthesis using earth-abundant elements. We expect that understanding unique systems, such as those found in the dark depths of the oceans, will inspire new avenues of research in chemistry and technology - just as photosynthesis was the major inspiration for solar energy conversion.



Biodiversity and Biocomplexity Unit, OIST

Professor, Evan P. Economo

Measuring, tracking, and understanding biodiversity change in a human-dominated world



Biodiversity is under increasing threat due to the direct and indirect effects of human activities. However, while this crisis is well recognized, mapping, tracking, and monitoring the trajectories of biodiversity at different scales remains a major challenge, particularly so for poorly studied but functionally important invertebrate species. At the same time, new technologies and data streams give us ever-increasing ability to study and understand natural systems. In this talk, I present research on ant biodiversity at three scales, using ants as a model system. Ants are ecologically dominant, economically important, and relatively well studied (for an insect group), thus are an informative model for millions of understudied invertebrate species. First, on a global scale, I present our efforts to build a master database of ant species distributions, which is necessary to help identify where hotspots of species richness and endemism around the world and prioritize. Second, I discuss a project unraveling changes biodiversity on a regional scale, the ant community of the archipelago of Fiji. Here, we used a community genomics approach to reconstruct population demography over the last 2000 years, highlighting the roles of human colonization and invasions of new species. Finally, I present work on how the dynamics of ant communities are changing on a landscape scale in Okinawa with changes in land use, using OIST's island-wide observation system. The studies highlight both challenges and opportunities for monitoring and understanding biodiversity changes in the Anthropocene.

Session 3



*1 Plant Genome Evolution Research Team and

*2 Ion Beam Breeding Team, RIKEN Nishina Center for Accelerator-Based Science

Team Leader, Hiroyuki Ichida*¹ and Tomoko Abe*²

Heavy-ion beam mutagenesis and its molecular characteristics in plants

Mutagenesis is a fundamental tool with which to investigate gene functions and create new cultivars in plant and microbial breeding. RIKEN's Nishina Center develops and operates state-of-the-art heavy-ion accelerators, including the superconducting cyclotron. Heavy-ion beams are classified in high-linear energy transfer (LET) radiations, and, unlike classical low-LET radiations including X- and γ -rays, it induces double-strand breaks of DNA along with its track, which results in a variety of mutations from single nucleotide substitutions, insertions, and deletions to chromosomal rearrangements. Heavy-ion beams have been widely utilized as an effective random mutagen for mutation breeding in plant and microbial species, but the induced mutation spectrum is not fully understood at the genome-scale. We developed a cost-efficient whole-exome sequencing technique and analyzed the mutation spectrum of carbon-ion beam-induced mutations in unselected M2 populations in rice. The results indicated heavy-ion beams induced a moderate number of mutations in the rice genome, therefore good for further modification of elite cultivars without affecting their good characteristics and productivity.



Science and Technology Group, OIST

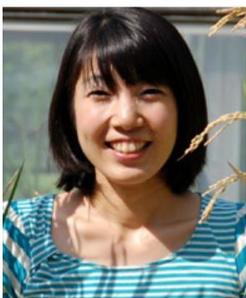
Associate, Reina Komiya

Diverse non-coding RNAs involved in plant reproductive system

Non-coding RNAs transcribed from NON-PROTEIN coding regions, not GENES, have been identified in many organisms. However, most biological functions remain unknown in plants and animals.

We identified 1300 kinds of reproductive long non-coding RNAs with microRNA2118 (miR2118) recognition site. Rice miR2118 cleaves these long non-coding RNAs and induces the production of secondary small RNAs derived from these long non-coding RNAs (Komiya *et al.*, 2014; Komiya 2017). This biogenesis of small RNAs via miR2118 cleavage is widely conserved in land plants.

In the recent few years, we have successfully generated more than 50 variant mutant rice by genome editing. Intriguingly, these mutants have shown sterility (no seeds), suggesting that non-coding RNAs are crucial for reproduction in rice (Araki *et al.*, 2020; unpublished data). In this symposium, I introduce the reproductive system about long non-coding RNAs/miR2118/secondary small RNAs in plants.



Session 4



RIKEN Center for Computational Science, Cluster for Pioneering Research, and RIKEN Interdisciplinary Theoretical and Mathematical Sciences Program (iTHEMS)

Chief Scientist/Team Leader, Takemasa Miyoshi

**Weather Predictability and Data Assimilation:
Perspectives Toward General Theory of Prediction**



Numerical weather prediction (NWP) has been improved consistently with computing, sensing, and information/communications technologies. Here, predictability and data assimilation are the key. The knowledge obtained in NWP may be useful in different areas. We started exploring a general theory of prediction and control for big complex problems.



Marine Climate Change Unit, Okinawa Institute of Science and Technology, Japan and ARC Centre of Excellence for Coral Reef Studies, James Cook University, Australia

Professor, Timothy Ravasi

Adaptation and Acclimation of Coral Reef Fish as a Response to Global Warming



Anthropogenic activities are leading to global climate change at an unprecedented rate. A plethora of studies have suggested that these anomalies in climate can lead to severe consequences to the marine environment, especially for poikilotherm species that constitute them. Further, there is evidence that an increase in concentration of atmospheric CO₂ will lead to severe disruption of key processes such as calcification, development during larval stages, predator and prey recognition, among others. However, most of these studies do not take into the capacity for marine organisms to adapt and acclimate to such fast changes. Thus, surveys have identified populations exposed to extreme conditions that have adapted to environmental oscillations, revealing the genes and metabolic pathways associated with the ability to cope with such changes. A growing body of research also exemplifies how species can acclimate to unusual settings if individuals are exposed at early life stages, and how tolerance attained during their lifetime can be inherited by its progeny via epigenetic mechanisms. Understanding the mechanisms of how marine species cope with environmental shifts is imperative to understand their fate in a changing planet. Further, in this talk, I will address the contribution of mechanisms of rapid evolution/phenotypic plasticity to the adaptive response of coral reef fish to changing environments.

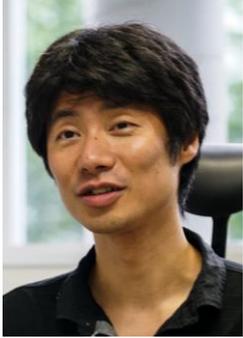
Session 4



Laboratory for Neural Computation and Adaptation, RIKEN Center for Brain Science

Team Leader, Taro Toyoizumi

Edge of Chaos and Avalanches in Neural Networks with Heavy-Tailed Synaptic Weight Distribution



We propose an analytically tractable neural connectivity model with power-law distributed synaptic strengths. When threshold neurons with biologically plausible number of incoming connections are considered, our model features a continuous transition to chaos and can reproduce biologically relevant low activity levels and scale-free avalanches, i.e., bursts of activity with power-law distributions of sizes and lifetimes. In contrast, the Gaussian counterpart exhibits a discontinuous transition to chaos and thus cannot be poised near the edge of chaos. We validate our predictions in simulations of networks of binary as well as leaky integrate-and-fire neurons. Our results suggest that heavy-tailed synaptic distribution may form a weakly informative sparse-connectivity prior that can be useful in biological and artificial adaptive systems.



Computational Neuroethology Unit, OIST

Assistant Professor, Sam Reiter

An ecological approach to understanding the brain



Understanding the activity of the brain is a central unsolved problem in biology. We now have the technological ability to record and manipulate the activity of every neuron in the brain of certain animals. However, few would argue that we now understand the brain. Here I will argue that progress can be made by looking to ecology and evolution. Studying the evolution of the nervous system, in particular by examining simple extant species, highlights the central importance of behavior. In studying animal behavior, there has traditionally been a tradeoff between the complexity of the behavior + environment under study and experimental precision. Using the study of cuttlefish camouflage as an example, I will show how recent developments in machine learning make it possible to rigorously study more complex behaviors in richer, more natural, environments. And I will explain why I think this more ecologically inspired approach to neuroscience offers a path forward.