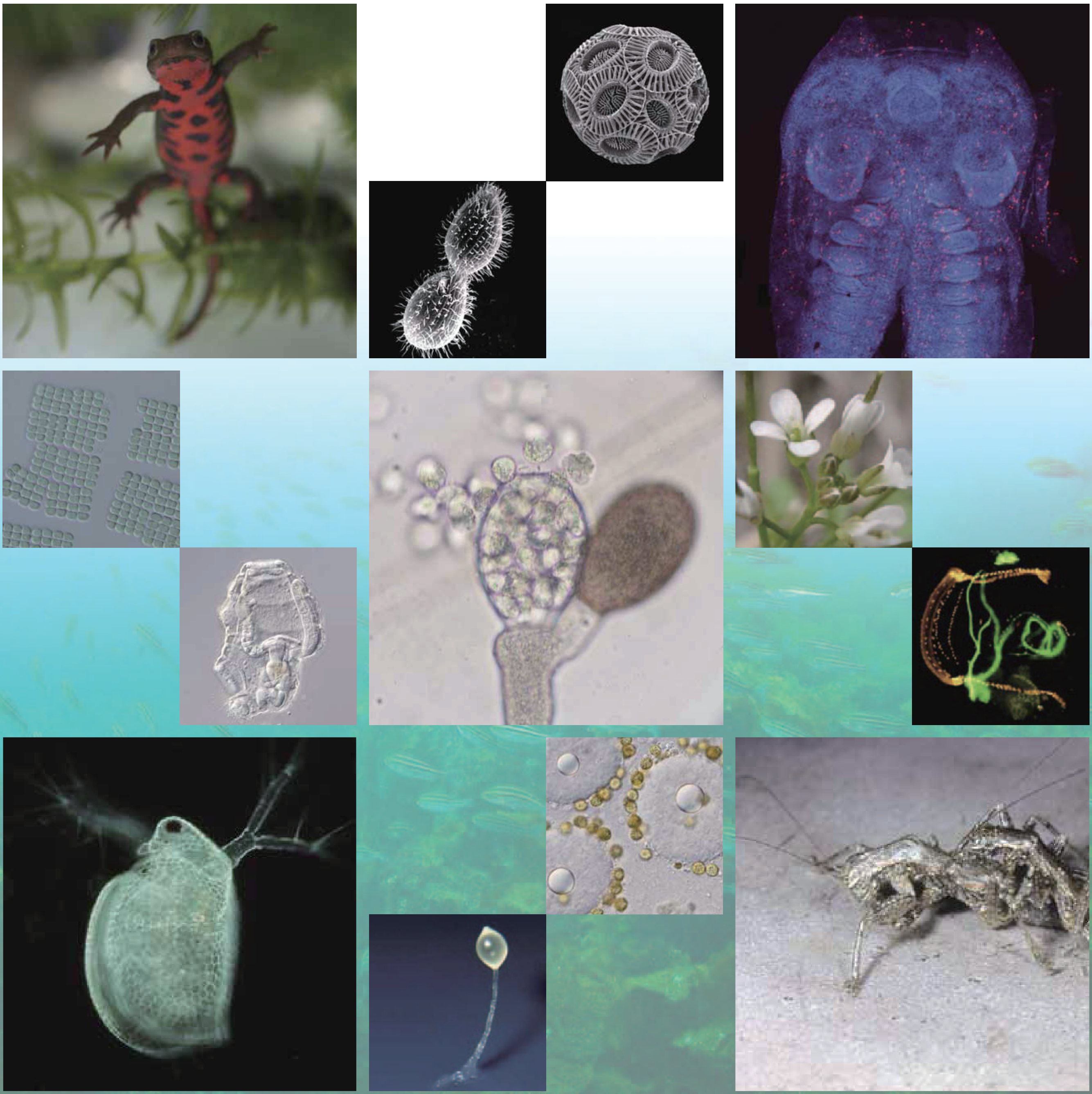
University of Tsukuba

Graduate School of Science and Technology
Degree Programs in Life and Earth Sciences

Biology



Sylvain Agostini

Ecophysiology of hermatypic corals

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Hermatypic corals are on the fore front of climate change. Rising temperature has resulted in increased mass bleaching and disease occurrence in the tropics, but it has also favor a poleward shift/expansion of corals in Japan and other parts of the world. In order to understand the future extent of this expansion and the possibility that high latitudes provides a future refuge for corals, a better understanding of the effect of environmental parameters on coral ecology and physiology is required.

Monitoring and diverse surveys including citizen surveys of coral communities around Izu and the Izu Islands were established to study the competition with macroalgae, the bleaching occurrence and the growth and diversity of high latitude corals under different pH conditions. The effects of pH on natural coral communities is studied at the recently discovered CO_2 seep in Shikine Island. Laboratory experiments complement the investigation of the stress response of corals. The physiological mechanisms of the effects of high and low temperature stresses and of ocean acidification are studied under controlled conditions in the laboratory.

Porites heronensis is a dominant species of hermatypic corals in high latitude of Japan. It forms dense patchy communities around Shimoda and Izu. It cohabit and compete with a diverse community of macroalgae. Low temperature often cause important bleaching and mortality during winter.

Publications

1. Agostini, S., Fujimura, H., Higuchi, T., Yuyama, I., Casareto, B.E., Suzuki, Y., and Nakano, Y. (2013). The effects of thermal and high-CO2 stresses on the metabolism and surrounding microenvironment of the coral Galaxea fascicularis. Comptes Rendus Biologies *336*, 384–391.
2. Agostini, S., Wada, S., Kon, K., Omori, A., Kohtsuka, H., Fujimura, H., Tsuchiya, Y., Sato, T., Shinagawa, H., Yamada, Y., et al. (2015). Geochemistry of two shallow CO2 seeps in Shikine Island (Japan) and their potential for ocean acidification research. Regional Studies in Marine Science.
3. Agostini, S., Fujimura, H., Hayashi, H., and Fujita, K. (2016). Mitochondrial electron transport activity and metabolism of experimentally bleached hermatypic corals. Journal of Experimental Marine Biology and Ecology *475*, 100–107.
4. Higuchi, T., Agostini, S., Casareto, B.E., Suzuki, Y., and Yuyama, I. (2015). The northern limit of corals of the genus Acropora in temperate zones is determined by their resilience to cold bleaching. Scientific Reports *5*, 18467.

Casco Martin

Regenerative Physiology

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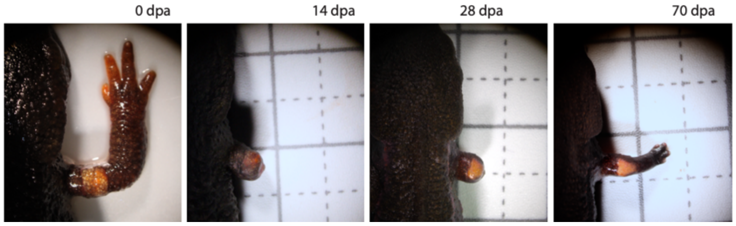
Keywords: newt, tissue, regeneration, patterning



Urodele amphibians such as the newt are the only known adult vertebrates to carry out scar less tissue regeneration in multiple tissues (heart, jaw, brain, limb, retina, and lens) following a traumatic event. Humans on the other hand undergo scar formation. Scar formation (or fibrosis) in humans is a serious medical setback that can have health consequences to patients. Multiple human diseases are associated with scar formation in various tissue types. Therefore, understanding the newt’s scar less regeneration provides hope that medical applications can be developed for human patients. Great advancements have been made in this field using a transgenic approach to study the underlying mechanisms of newt tissue regeneration. To understand scar less tissue regeneration we use multidisciplinary approach.

Selected Publications

1. Roman Casco-Robles, Akihiko Watanabe, Ko Eto, Kazuhito Takeshima, Shuichi Obata, Tsutomu Kinoshita, Takashi Ariizumi, Kei Nakatani, Tomoaki Nakada, Panagiotis Tsonis, Casco-Robles MM, Keisuke Sakurai, Kensuke Yahata, Fumiaki Maruo, Fubito Toyama, and Chikafumi Chiba. (2018) Novel erythrocyte clumps revealed by an orphan gene Newtic1 in circulating blood and regenerating limbs of the adult newt. *Scientific Reports,* 8 (1):7455.
2. Casco-Robles MM, Islam MR, Inami W, Tanaka Hibiki, Kunahong A, Yasumuro H, Hanzawa S, Casco-Robles RM, Toyama F, Maruo F, and Chiba C. (2016) Turning the fate of reprogramming cells from retinal disorder to regeneration by Pax6 in newts. *Scientific Reports,* 6:1-9.
3. Tanaka HT, Yin Ng NC, Yu ZY, Casco-Robles MM, Maruo F, Tsonis PA, and Chiba C. (2016) A developmentally-regulated switch from stem cells to dedifferentiation for limb skeletal muscle regeneration in newts. *Nature Communications,* 7: 1-8.
4. Casco-Robles MM, Miura T, and Chiba C. (2014). The newt (*Cynops pyrrhogaster*) RPE65 promoter: molecular cloning, characterization and functional analysis. *Transgenic Research*, 24:463-473.
5. Casco-Robles MM, Yamada S, Miura T, Nakamura K, Haynes T, Maki N, Del Rio-Tsonis K, Tsonis, PA and Chiba, C. (2011). Expressing exogenous genes in newts by transgenesis. *Nature Protocols*, 6:600-608. Selected for the Journal cover.

Google Scholar: https://scholar.google.com/citations?user=_pJkOsEAAAAJ&hl=en

Chikafumi Chiba

Regenerative Physiology

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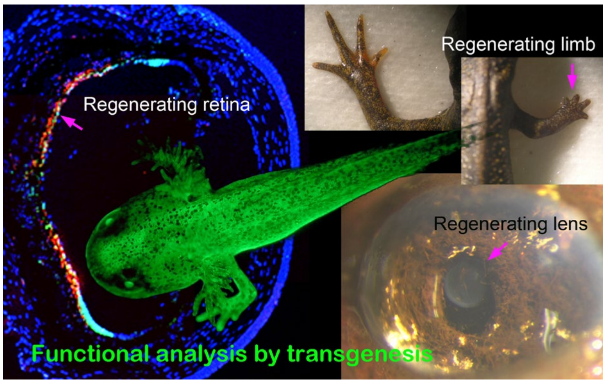
Keywords: **regeneration, scar formation, reprogramming, stem cell, newt**

My research purpose is to save the lives of people who suffer traumatic injuries, through the application of newts' strategy for regeneration of body-parts in medical treatments. Thus, I am now trying to uncover the cellular and molecular mechanisms of newt body-parts regeneration (a biological mystery over two centuries) while comparing them with mammalian wound healing and tissue repair mechanisms as well as with their pathogenic or oncogenic processes after traumatic injuries.



The newt is the master of regeneration. No other animal can parallel its regenerative abilities in body-parts such as the limbs, the tail and spinal cord, parts of the eye (such as the retina and the lens), the brain, the heart and the jaws. This regeneration is mediated by dedifferentiation or transdifferentiation of fully matured somatic cells at the site of injury, making this process relevant to a number of important issues, such as the involvement of stem cells in wound healing, reprogramming, differentiation, patterning, and the restoration of physiological function.

Selected publications

1. Casco-Robles, R. M. et al. (2018) Novel erythrocyte clumps revealed by an orphan gene Newtic1 in circulating blood and regenerating limbs of the adult newt. *Scientific Reports* 8:7455.
2. Casco-Robles, M. M. et al. (2016) Turning the fate of reprogramming cells from retinal disorder to regeneration by Pax6 in newts. *Scientific Reports* 6:33761.
3. Tanaka, H. V. et al. (2016) A developmentally regulated switch from stem cells to dedifferentiation for limb muscle regeneration in newts. *Nature Communications* 7:11069.
4. Chiba, C. (2014) The retinal pigment epithelium: An important player of retinal disorders and regeneration. *Experimental Eye Resarch* 123:107-114.
5. Casco-Robles, M. M. et al. (2011) Expressing exogenous genes in newts by transgenesis. *Nature Protocols* 6:600-608.
6. Tsonis, P. A. et al. (2011) Controlling gene loss of function in newts with emphasis on lens regeneration. *Nature Protocols* 6:593-599.

Tomoki Chiba, Ph. D.

Molecular Biology

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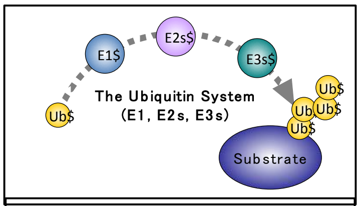
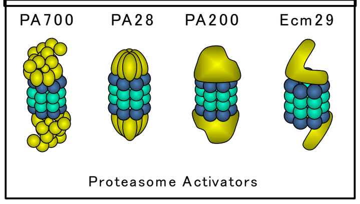
In our body, proteins are in a dynamic state, and the speed of protein synthesis and degradation is tightly regulated. The degradation of protein is individually regulated by the "Ubiquitin and the Proteasome System" which plays critical roles in many biological aspects such as embryogenesis, immune system, and memory.
The major goal of our laboratory is to understand;
(1) The component and regulation of intracellular protein degradation at molecular level.
(2) The physiological roles of selective protein degradation in our body.



The Ubiquitin System.
Ubiquitin acts as a degradation signal and its attachment to the substrate is tightly catalyzed by a cascade reaction composed of E1, E2s and E3s enzymes.
(Keywords; Cullin, NEDD8, signalosome)



Proteasome Activators
Proteasome is a barrel-shaped multisubunit protease complex that captures and degrades ubiquitinated proteins. The activitiy of the proteasome is regulated by multiple proteasome activators.
(Keywords; Proteasome, PA28, PA200, Ecm29)

My lab is focusing on;
(1) The regulation and function of Cullin-RING-type Ubiquitin ligases.
(2) The regulation and function of proteasome activators using multiple knockout mice.

Publications

1. Huang L, *et al*. Proteasome activators, PA28γ and PA200, play indispensable roles in male fertility. ***Sci. Rep.*** *2016, 6: 23171.*
2. Kigoshi Y, *et al.* CACUL1/CAC1 regulates the antioxidant response by stabilizing Nrf2. ***Sci. Rep.*** *2015, 5: 12857.*
3. Ebina M, *et al.* Myeloma overexpressed 2 (Myeov2) regulates L11 subnuclear localization through Nedd8 modification. ***PLoS ONE*** *2013, 8: e65285.*
4. Qian MX, *et al.* Acetylation-Mediated Proteasomal Degradation of Core Histones during DNA Repair and Spermatogenesis. ***Cell*** *2013, 153: 1012-1024.*
5. Takashima O, *et al.* Brap2 regulates temporal control of NF-kB localization mediated by inflammatory response. ***PLoS ONE*** *2013, 8: e58911.*
6. Kigoshi Y, *et al.* Ubiquitin Ligase Activity of Cul3-KLHL7 Protein Is Attenuated by Autosomal Dominant Retinitis Pigmentosa Causative Mutation. ***J. Biol. Chem****. 2011 286: 33613-33621.*

Yoko Chiba

Metabolic Biochemistry and Evolution

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Keywords: **Microorganism, Thermophile, Enzymology, Origin of Life**

Our scientific goal is to understand the diversity of metabolism and evolutionary principles of existing organisms in order to clarify the nature of primitive life and "to what" and "how" the metabolism of each organism has adapted. Specifically, we will identify novel central metabolic pathways and enzymes, and conduct comparative analysis of enzymes and metabolism by integrating biology and physicochemistry.

Elucidation of **metabolic evolution** by identifying novel **amino acid biosynthetic pathways**

The emergence of an autotroph and CO_2 fixation pathway is essential for the creation of a sustainable biosphere. However, the oldest $CO2_2$ fixation pathway remains unidentified.

The biosynthetic pathways of glycine and serine (amino acids) are interesting in that they are closely related to CO_2 fixation pathway. Furthermore, the glycine and serine synthetic pathways in existing organisms are diverse, are some of them remain unidentified. Therefore, we will identify the novel amino biosynthetic pathways, and use the knowledge to estimate the evolution of CO_2 fixation pathways.

Identification of **enzyme optimizing factors** by **integrating biochemistry and catalysis**

Enzymes that catalyze the same reaction but have different origins (functional homolog) suggest that each organism selects a suitable type of enzyme in the process of evolution, however, the selective pressure is unknown. We are developing a new methodology to compare the physicochemical parameters of the enzymes to discuss how and to what they have adapted to explain the diversity of enzymes and evolutionary principles.

Selected publications

1. Chiba Y., Miyakawa T., Shimane Y., Takai K., Tanokura M., Nozaki T. (2019) Structural comparisons of phosphoenolpyruvate carboxykinases reveal the evolutionary trajectories of these phosphodiester energy-conversion enzymes. *J Biol Chem* 294:19269-19278.
2. Chiba Y., Yoshida A., Shimamura S., Kameya M., Tomita T., Nishiyama M., Takai K. (2019) Discovery and analysis of a novel type of the serine biosynthetic enzyme phosphoserine phosphatase in *Thermus thermophilus*. *FEBS J* 286:726-736.
3. Kim K., Chiba Y., Kobayashi A., Arai H., Ishii M. (2017) Phosphoserine phosphatase is required for serine and one-carbon unit synthesis in *Hydrogenobacter thermophilus. J Bact* 199:e00409-e00417.
4. Chiba Y., Oshima K., Arai H., Ishii M., Igarashi Y. (2012) Discovery and analysis of cofactor-dependent phosphoglycerate mutase homologs as novel phosphoserine phosphatases in *Hydrogenobacter thermophilus*. *J Biol Chem* 287:11934-11941.

Yousuke Degawa

Mycology

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Keywords: **fungi, biodivesity, natural history, phylogeny, yeast, slime mold**

Biodiversity of the Kingdom Fungi. Top row, left to right: Chytridiomycota (zoospores discharged from zoosporangium of *Chytriomyces*), Mucoromycota (sporangiophores of *Pilobolus*), and Zooagomycota (zygospores of *Basidiobolus*). Bottom row, left to right: Ascomycota (conidiophores of the anamorphic hyphomycete *Kumanasamuha*), Ascomycota (apothecium of *Trichaleurina*), Basidiomycota (basidiocarp of *Pluteus*).

The Kingdom Fungi is one of the most important on Earth. At present there are 100,000 known species, but the total number is estimated to be over 5 million. Our Laboratory of Mycology is situated in the Japan Alps in the Sugadaira Highland, at an elevation of about 1300 m. It has 30 ha of well-preserved natural fields, including grasslands and *Pinus–Quercus* forests. The lab has been managed by the late Emer. Prof. H. Indoh (1908–2003), the late Emer. Prof. K. Tubaki (1924–2005), and Emer. Prof. S Tokumasu (1945–).

The Kingdom Fungi is regarded a sister group of the Kingdom Animalia in the supergroup Opisthokonta. But how did fungi originate and diversify? In our laboratory, we are studying the natural history (taxonomy, phylogeny, and ecology) of a wide range of fungal taxa and its relatives (slime molds and pseudofungi), using living natural materials. Our focus is 1) the biodiversity of the Chytridiomycota and basal lineages of fungi, in order to elucidate the origin of fungi; 2) the biodiversity of the Zygomycota (Mucoromycota, Zoopagomycota), to examine the terrestrialization of fungi considered based on the interactions between fungi and other organisms; 3) the biodiversity and life histories (teleomorph–anamorph connections) of the Ascomycota and Basidiomycota.

Selected publications

1. Matsuzaki, R., Takashima, Y., Suzuki, I., Kawachi, M., Nozaki, H., Nohara, S., and Degawa, Y. (2021). The enigmatic snow Microorganism, *Chionaster nivalis*, is closely related to *Bartheletia paradoxa* (Agaricomycotina, Basidiomycota). *Microbes and environments* 36:ME21011.
2. Hashimoto, A., Masumoto, H., Endoh, R., Degawa, Y., and Ohkuma, M. (2021) Revision of Xylonaceae (Xylonales, Xylonomycetes) to include *Sarea* and *Tromera*. *Mycoscience* 62:47-63
3. Masumoto, H. and Degawa, Y. (2020). *Bryoclavula phycophila* gen. et sp. nov. belonging to a novel lichenized lineage in Cantharellales (Basidiomycota). *Mycological Progress* 19:705-714. https://doi.org/10.1007/s11557-020-01588-2
4. Takashima, Y., Degawa, Y., Nishizawa, T., Ohta, H. and Narisawa, K. (2020). Aposymbiosis of a Burkholderiaceae-related endobacterium impacts on sexual reproduction of its fungal host. *Microbes and environments* 35:ME19167.
5. Seto. K., Van den Wyngaert, S., Degawa, Y., Kagami, M. (2020). Taxonomic revision of the genus *Zygorhizidium*: Zygorhizidiales and Zygophlyctidales ord. nov. (Chytridiomycetes, Chytridiomycota). *Fungal Systematics and Evolution* 5:17-38.

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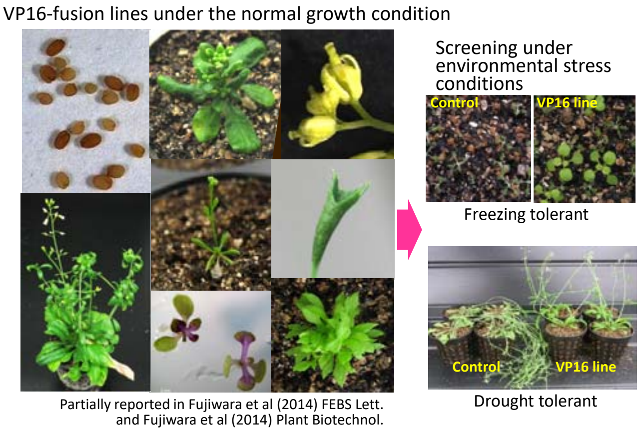
Plant growth and functions are controlled by the dynamic regulation of gene expression by transcription factors. We work on functional analyses and utilization of such transcription factors that are promising to solve many problems we are facing, such as food shortage, energy issues, and global warming. Our current projects include: 1) basic studies of transcriptional regulation mechanisms, 2) identifications and analyses of transcription factors that can be utilized for the development of useful plants, and 3) research and development of useful plants by modifications of transcription factors.



Partially reported in Fujiwara et al (2014) FEBS Lett. and Fujiwara et al (2014) Plant Biotechnol.

To understand the functions of transcriptional repressors and isolate candidates for the targets of super-plant production, we generated approx. 300 Arabidopsis transgenic lines in which a transcriptional repressor fused with an activation domain (VP16) is constitutively expressed. In these lines, the genes whose transcription is usually repressed by the transcriptional repressor are expected to be highly transcribed which could result in causing strong phenotypes. We grew all of them and found many lines showing unique phenotypes or useful traits such as stress tolerance or higher yield.

Select Publications

1. Fujiwara, S., Sakamoto, S., Kigoshi, K., Mitsuda, N., Suzuki, K., and Ohme-Takagi, M. (2014) VP16 fusion induces the multiple-knockout phenotype of redundant transcriptional repressors partly by Med25-independent mechanisms in Arabidopsis. FEBS Lett. *588*, 3665-3672
2. Fujiwara, S., Kigoshi, K., Mitsuda, N., Ohme-Takagi, M., and Suzuki, K. (2014) VP16 fusion efficiently reveals the function of transcriptional repressors in Arabidopsis. Plant Biotechnol. *31*, 123-132
3. Wang, L., Fujiwara, S., and Somers, D.E. (2010) PRR5 regulates nuclear import and subnuclear localization of TOC1 in the Arabidopsis circadian clock. EMBO J., *29*, 1903-1915
4. Fujiwara, S., Oda, A., Yoshida, R., Niinuma, K., Miyata, K., Tomozoe, Y., Tajima, T., Nakagawa, M., Hayashi, K., Coupland, G., and Mizoguchi, T. (2008) Circadian Clock Proteins LHY and CCA1 Regulate SVP Protein Accumulation to Control Flowering in Arabidopsis. Plant Cell *20*, 2960-2971
5. Kim, W.Y.*, Fujiwara, S.*, Suh, S.S., Kim, J., Kim, Y., Han, L., David, K., Putterill, J., Nam, H.G., and Somers, D.E. (2007) ZEITLUPE is a circadian photoreceptor stabilized by GIGANTEA in blue light. Nature *449*, 356-360 (*: equal contribution)

Ben Harvey

Global Change Marine Ecology

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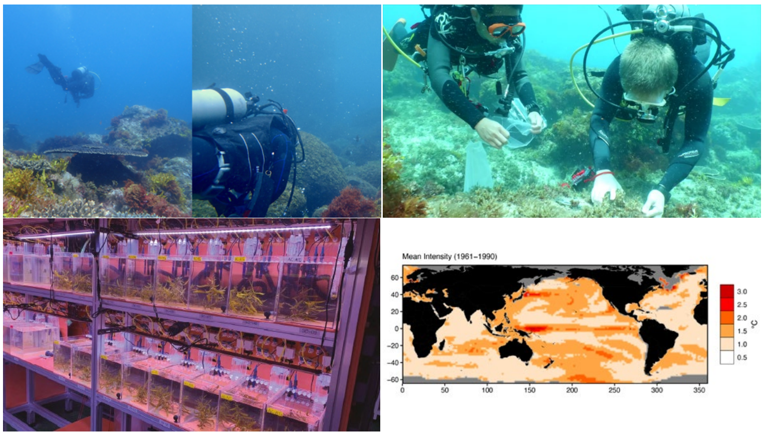
Keywords: **ocean acidification, climate change, community structure, ecosystem functioning**

Oceans help regulate the global climate system, and support the environmental, economic, and social needs of the global population. Over three billion people are dependent on the marine and coastal biodiversity of our oceans for their livelihood. However, continued exploitation over many years has led to the increasing degradation of marine ecosystems at an often-alarming rate. Any loss or deterioration of coastal ecosystems can compromise their ability to provision functioning, goods, and services; thereby affecting human wellbeing. The decline of coastal ecosystems has already begun but is expected to greatly accelerate with future ocean acidification and climate change.

Our research group seeks to understand how changes in environmental conditions (focussing on ocean acidification, ocean warming, and marine heatwaves) will change our oceans, with particular focus on marine communities and ecosystems.



Our research is multidisciplinary, combining field-based surveys and experiments using CO_2 seeps, aquarium-based manipulative experiments, and modelling approaches. Taken together, this will allow us to better understand the impacts of global climate change on coastal ecosystems worldwide.

Selected publications

1. Harvey, B. P. et al. 2021a. Feedback mechanisms stabilise degraded turf algal systems at a CO_2 seep site. *Communications Biology* 4:219.
2. Harvey, B. P. et al. 2021b. Ocean acidification locks algal communities in a species-poor early successional stage. *Global Change Biology* 27:2174–2187.
3. Harvey, B. P. et al. 2021c. Predicting responses to marine heatwaves using functional traits. *Trends in Ecology & Evolution*. https://doi.org/10.1016/j.tree.2021.09.003
4. Agostini, S., Harvey, B. P. et al. 2021. Simplification, not "tropicalization", of temperate marine ecosystems under ocean warming and acidification. *Global Change Biology*. https://doi.org/10.1111/gcb.15749
5. Cornwall, C. E., Harvey, B. P., et al. (2021). Understanding coralline algal responses to ocean acidification: Meta-analysis and synthesis. *Global Change Biology*. https://doi.org/10.1111/gcb.15899

Tetsuo Hashimoto

Molecular Evolution of Microbes

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The central focus of our research is to gain insight into the origin and early evolution of eukaryotes. This is currently the most important open problem in evolutionary biology. We are using molecular and cellular biological methods, including comparative 'omics' analyses and molecular phylogeny, to approach the evolutionarily interesting issues presented by diverse eukaryotic microorganisms.

One of the goals of our research is to reconstruct a reliable eukaryotic tree. We are continuing to perform phylogenomic analyses using high-performance computing to elucidate the early phase of eukaryotic evolution. By using a refined tree of the organisms of interest, we compare genomic, transcriptomic, and proteomic data so as to trace the evolutionary history of the divergence of cellular functions and molecular mechanisms. Our recent focus is elucidation of the reductive evolution of mitochondria in a diverse anaerobic organismal group, the Fornicata, all of which contain no typical mitochondria but have mitochondrion-related, reduced organelles.

Giardia intestinalis is a flagellated organism belonging to a diverse anaerobic group, the Fornicata. It is a mammalian parasite that colonizes and reproduces in the small intestine, causing giardiasis. Tiny double membrane–bound organelles called mitosomes are present in the cell; these are considered to be reduced mitochondria.

(Photo by N. Yubuki)

Select Publications

1. Arisue, N., Hashimoto, T., Mitsui, H., Palacpac, N.M.Q., Kaneko, A., Kawai, S., Hasegawa, M., Tanabe, K., and Horii, T. (2012). The *Plasmodium* apicoplast genome: conserved structure and close relationship of *P. ovale* to rodent malaria parasites. Mol Biol Evol, in press.
2. Takishita, K., Kolisko, M., Komatsuzaki, H., Yabuki, A., Inagaki, Y., Cepicka, I., Smejkalová, P., Silberman, J.D., Hashimoto, T., Roger, A.J., and Simpson, A.G.B. (2012). Multigene phylogenies of diverse Carpediemonas-like organisms identify the closest relatives of 'amitochondriate' diplomonads and retortamonads. Protist *163*, 344-355.
3. Kamikawa, R., Inagaki, Y., Tokoro, M., Roger, A.J., and Hashimoto, T. (2011). Split introns in the genome of a divergent eukaryote *Giardia intestinalis* are excised by spliceosome-mediated trans-splicing. Curr Biol *21*, 311-315.

Yoshiki Hayashi

Developmental Genetics

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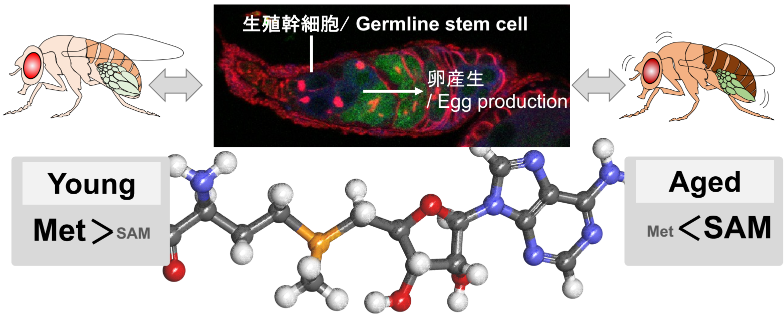
Keywords: **Tissue stem cells, Germline, Aging, Metabolism, Extra-Cellular-Matrix**

Understanding of development & aging of tissue stem cells and primordial-germ-cells.

The research focus of our group is to understand the **development and aging processes of tissue stem cells** that is crucial for tissue maintenance. We also intensively study the **developmental process of primordial-germ-cells** that have unique cellular characteristics having potential multipotency. Recently we are focusing on the role of **cellular metabolism** in above processes. Since cellular metabolism plays important role in regulation of cancer development and animal's life span, we hope we could shed the light to those fields from our basic life science. ***Drosophila melanogaster***, our favorite animal is easy to be used and to have the advantage for genetic experiments and aging analysis, and we have good techniques for gene expression, epigenome, and cellular metabolism analysis. We are tackling the above research aims by combining our advantages.



Selected publications

1. **Hayashi*** et al. (2021). The heparan sulfate proteoglycan molecules, syndevan and perlecan have distinct role in the maintenance of germline stem cell in *Drosophila melanogasiter*. ***Dev. Growth Differ.*** 63:295-305.
2. **Hayashi*** et al (2020). The regulation of *Drosophila* ovarian stem cell niches by signaling cross talk. ***Curr. Opin. Insect Sci.*** 37:23-29.
3. **Hayashi** et al. (2012). Glypicans regulate JAK/ STAT signaling and distribution of Unpaired morphogen. ***Development*** 139:4162-4171. ***# Evaluated by Faculty of 1000***
4. **Hayashi** et al. (2009). *Drosophila* glypicans regulate the germline stem cell niche. ***J. Cell Biol.*** 187:473-480. ***# Cited in the "Molecular Biology of the Cell"***
5. **Hayashi** et al. (2004). Nanos suppresses somatic cell fate in *Drosophila* germline. ***Proc. Natl. Acad. Sci. USA*** 101:10338-10342. ***# Cited in the "Gilbert, Developmental Biology"***

Yoshihisa Hirakawa

Molecular Biology and Evolution

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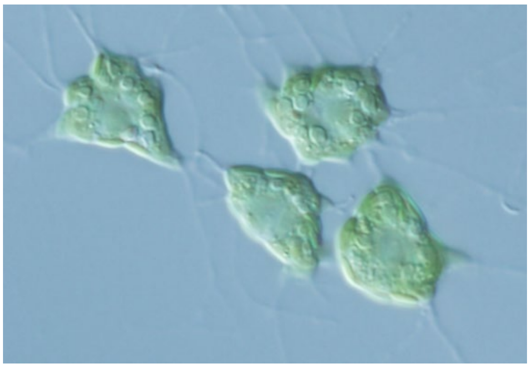
Keywords: **endosymbiosis, microalgae, organelle, plastid, pyrenoid**

Photosynthetic organelles, plastids (chloroplasts), were evolved through endosymbioses. In the long history, endosymbiotic events have occurred many times between a photosynthetic organism and a phagotrophic eukaryote host. In my lab, we use the marine unicellular algae "chlorarachniophytes" that obtained their complex plastids by the uptake of green algae.



We are currently investigating about plastid targeting proteins, plastid division machinery, and plastid carbon concentration mechanism in chlorarachniophytes. My major research interest is to understand the diversity and evolution of plastid functions.

Current research topics: "Study on the pyrenoid construction in algal plastids", "Study on the algal plastid division mechanism", "Study on the development of genetic transformation system".

Selected publications

1. Hirakawa Y. Senda M., Fukuda K., Yu H. Y., Ishida M., Taira M., Kinbara K., Senda T. (2021) Characterization of a novel type of carbonic anhydrase thta acts without metal cofactors. *BMC Biology* 19: 105
2. Fukuda K., Cooney E.C., Irwin N.A.T., Keeling P.J., Hirakawa Y. (2020) High-efficiency transformation of the chlorarachniophyte *Amorphochlora amoebiformis* by electroporation. *Algal Research* 48:101903
3. Hirakawa Y. (2017) Secondary endosymbioses. *Advance in Botanical Research* volume 84, Academic press.
4. Hirakawa Y., Ishida K. (2015) Prospective function of FtsZ proteins in the secondary plastid of chlorarachniophyte algae. *BMC Plant Biology* 15: 276
5. Hirakawa Y., Burki F., Keeling P.J. (2012). Dual targeting of aminoacyl-tRNA synthetases to the mitochondrion and plastid in chlorarachniophytes. *Journal of Cell Science* 125: 6176-6184

Mitsuru Hirota

Terrestrial Ecosystem Ecology

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We are seeking to improve process-based understanding of carbon dynamics in terrestrial ecosystems by investigating carbon fluxes and pools. By demonstrating such parameters and their relationships with various environmental factors, we will be able not only to estimate carbon sink capacity with high accuracy, but also to demonstrate the features of individual ecosystems. Current projects include

- ✓ Responses of alpine grassland carbon dynamics to recent environmental changes
- ✓ Relationship between biodiversity and ecosystem functioning in a highly diverse Tibetan grassland ecosystem
- ✓ Island ecosystem restoration focused on decomposition processes after the 2000 eruption on Miyake Island, Japan
- ✓ Reevaluation of the carbon sink capacity of old-growth forest ecosystems.

Select publications

1. Hirota M., Zhang P., Gu S., Shen H., Kuriyama T., Li Y., and Tang, Y. (2010). Small-scale variation in ecosystem CO_2 flux in an alpine meadow depends on plant biomass and species richness. Journal of Plant Research *123*, 531-541.
2. Hirota M., Zhang P., Gu S., Du M., Shimono A., Shen H., Li Y., and Tang. Y. (2009). Altitudinal variation of ecosystem CO_2 fluxes in an alpine grassland from 3600 to 4200 m. Journal Plant Ecology *2*, 197-205.
3. Hirota, M., Senga, Y., Seike, Y., Nohara, S., and Kunii, H. (2007). Fluxes of carbon dioxide, methane and nitrous oxide in two contrastive fringing zones of coastal lagoon, Lake Nakaumi, Japan. Chemosphere *68*, 597-603.
4. Hirota, M., Tang, Y., Hu, Q., Kato, T., Hirata, S., Mo, W., Cao, G., and Mariko, S. (2006). Carbon dioxide dynamics and controls in a deep-water wetland on the Qinghai-Tibetan Plateau. Ecosystems *9*, 673-688.
5. Hirota, M., Tang, Y., Hu, Q., Kato, T., Hirata, S., Mo, W., Cao, G., and Mariko, S. (2005). The potential importance of grazing to the fluxes of carbon dioxide and methane in an alpine wetland on the Qinghai-Tibetan Plateau. Atmospheric Environment *39*, 5255-5259.
6. Hirota, M., Tang, Y., Hu, Q., Hirata, S., Kato, T., Mo, W., Cao, G., and Mariko, S. (2004). Methane emissions from different vegetation zones in a Qinghai-Tibetan Plateau wetland. Soil Biology and Biochemistry *36*, 737-748.

Masanao Honda

Taxonomy, Phylogeny and Conservation Biology

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Keywords: **reptiles, amphibians, birds, alien species, Ryukyu Archipelago**

Our researches focus on molecular phylogenetics and conservation genetics of reptiles. As to researches on the Kuroiwa's ground gecko distributed in the Central Ryukyus, we found the northern and southern populations of Okinawa Island, which were classified as the same subspecies, were genetically highly differentiated than the recognized subspecies. This points out that the current classification and conservation based on morphology underestimates the true diversity of species. Each population should be recognized as a unit to be conserved. Other interests include amphibians and birds. In the study of Anderson's crocodile newt in the Central Ryukyus, we found populations in the southern part of Okinawa Island lacked genetic diversity and were more vulnerable to environmental changes than would be expected from their population size.

Selected publications

1. Igawa, T., Sugawara, H., Honda, M., Tominaga, A., Oumi, S., Katsuren, S., Ota, H., Matsui, M. and Sumida, M. （2019）. Detecting inter- and intra-island genetic diversity: population structure of the endangered crocodile newt, *Echinotriton andersoni*, in the Ryukyus. *Conservation Genetics* 21: 13-26.
2. Honda, M. and Ota, H. (2017). On the live coloration and partial mitochondrial DNA sequences in the topotypic population of *Goniurosaurus kuroiwae orientalis* (Squamata: Eublepharidae), with description of a new subspecies from Tokashikijima Island, Ryukyu Archipelago, Japan. *Asian Herpetological Research* 8: 96-107.
3. Karasawa, S., Nagata S., Aoki J., Yahata K. and Honda, M. (2015). Phylogeographic study of whip scorpions (Chelicerata: Arachnida: Thelyphonida) in Japan and Taiwan. *Zoological Science* 32: 352-363.
4. Honda, M., Kurita, T., Toda, M. and Ota, H. (2014). Phylogenetic relationships, genetic divergence, historical biogeography and conservation of an endangered gecko, *Goniurosaurus kuroiwae* (Squamata: Eublepharidae), from the Central Ryukyus, Japan. *Zoological Science* 31: 309-320.
5. Honda, M., Matsui, M., Tominaga, A., Ota, H. and Tanaka, S. (2012). Phylogeny and biogeography of the Anderson's crocodile newt, *Echinotriton andersoni* (Amphibia: Caudata), as revealed by mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution* 65: 642-653.

Horie Takeo

Neural Circuit Development and Function in Ascidian Larvae

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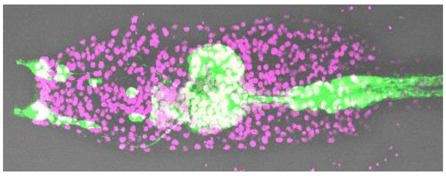
Keywords: **ascidian, neural circuit, single cell transcriptomics. optogenetics**

Animal behavior results fundamentally from the coordinated activity of neural circuits. Our laboratory is studying the relationships among neurons, neural circuits, and behavior in ascidian larvae. These larvae have a very simple central nervous system (CNS) consisting of only about 100 neurons. Despite its simplicity, the CNS of ascidian larvae shares several properties with those of vertebrates. The small number of neurons in these larvae enables us to describe neural circuits at the single-cell level. Our ability to manipulate the activity of individual neurons makes it possible to elucidate how neural circuits function. We are using a combination of optogenetics, in vivo Ca^{2+} imaging, proteomics, and behavioral genetics in the ascidian *Ciona intestinalis* to gain an understanding of the operating principles of the neural circuits underlying animal behavior. Cilia are microtubule-based organelles that extend from basal bodies and form on the apical surfaces of cells. We are also studying the developmental role and physiological functions of the cilia present in the nervous system of ascidian larvae.



The CNS of the ascidian larva.
Green: neurons Magenta: nuclei

Selected publications

1. Zhao, D+., Chen, S+., Horie, T+., Gao, Y., Bao, H and Liu, X. (2020). Comparison of differentiation gene batteries for migratory mechanosensory neurons across bilaterians. Evolution & Development 54: 438-450.
2. Horie, T+*., Horie, R+., Chen, K+., Cao C+., Nakagawa, M., Kusakabe, TG., Satoh, N., Sasakura, Y* ann Levine, M*. (2018) . Regulatory cocktail for dopaminergic neurons in a proto-vertebrate identified by whole embryo single cell transcriptomics. Genes & Development 32: 1297-1302.
3. Horie, R., Hazbun, A., Chen, K., Cao, C., Levine, M and Horie, T*. (2018). Shared evolutionary origin of vertebrate neural crest and cranial placodes. Nature 560: 228-232.
4. Li, Y+., Zhao, D+., Horie, T+., Chen, G+., Bao, H., Chen, S., Liu, W., Horie, R., Liang, T., Dong, B., Feng, Q., Tao, Q and Liu, X. (2017). Conserved gene regulatory module specifies lateral neural borders across bilaterians. Proceedings of the National Academy of Sciences of the United States of America 114: E6352-6360.
5. Horie, T*., Shinki, R., Ogura, Y., Kusakabe, TG., Satoh, N and Sasakura Y (2011). Ependymal cells of chordate larvae are stem-like cells that form the adult nervous system. Nature 469: 525-528.

Tsuyoshi Hosoya

Biodiversity of Fungi

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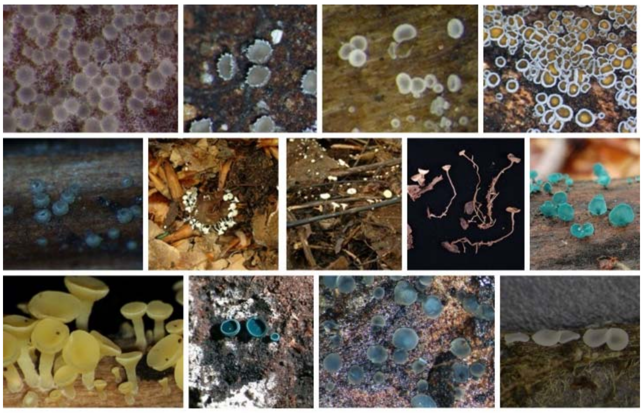
My research is focused on the biodiversity of the order Helotiales, phylum Ascomycota, Kingdom of Fungi. Fungi is one of the largest group of organisms in the world, estimated to consisted of more than 1.5 millions of species. Ascomycota is the largest group of fungi, and Helotiales is one of the most diverse group in Ascomycota. The members of Helotiales produces small saucer to nail-shaped mushroom, called apothecia. The majority of the members of Helotiales were thought to be weak saprophytes occurring on decaying plant substrates. Recently, however, the majority of plant root endophytes (fungi that live in plant symbiotically or without showing any symptoms) turned out to be Helotiales. Helotiales were more versatile than we imagined! Then which species are there? Actually, we cannot tell which species by names, because the taxonomy of Helotiales is so poor, and we are not sure how many species exactly are there in Japan, either.



We use molecular barcoding technique and conventional taxonomic technique (morphology and isolation) to evaluate the biodiversity of species. Enumeration of all the Helotiales in Japan is one of the goal. Another issue is the comparisons with previously known European species. Our predecessors have identified Japanese species based on European literature. However, the present knowledge suggests that Japanese species may be different from that in Europe. We have to critically examine the identity using molecular technique. Finally, we also use isolates to help understanding the lifecycles.

[Selected Publications]

1. Zhao YJ, Hosaka K, Hosoya T (2016) Taxonomic re-evaluation of the genus Lambertella Rutstroemiaceae, Helotiales) and allied stroma-forming fungi. Mycological Progress 15:1215-1228.
2. Hosoya T, Jinbo U, Tanney J (2015) "MolliBase", a new sequence database including unidentified Mollisia and its allied genera. Ascomycete.org 7:311-314.
3. Gross A, Hosoya T, Zhao, Y.-J., Baral, H.-O. (2015) Hymenoscyphus linearis sp. nov.: another close relative of the ash dieback pathogen H. fraxineus. Mycological Progress 14:1-15.
4. Han JG, Hosoya T, Sung GH, Shin HD (2014) Phylogenetic reassessment of Hyaloscyphaceae sensu lato (Helotiales, Leotiomycetes) based on multigene analysses. Fungal Biology 118:150-167.
5. Hosoya T, Hosaka K, Saito Y, Degawa Y, Suzuki R (2013) Naemacyclus culmigenus, a newly reported potential pathogen to Miscanthus sinensis, new to Japan. Mycoscience 54:433-443.

Kazuo Inaba

Cell Biology of Sperm, Cilia and Flagella

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Our research goal is to explore the biological significance of sperm and eukaryotic cilia and flagella by using several marine organisms, including tunicates, sea urchins, sea snails, comb jellies, spiny lobsters, flounder and marine algae. The main projects in my lab are as follows:
Biology of sperm: Molecular characterization of sperm flagella; molecular mechanism and regulation of flagellar motility; sperm activation and chemotaxis by egg-derived substances; genomics and proteomics analyses of testis-expressed genes and proteins; ocean acidification and sperm function; molecular mechanisms of spermatogenesis; the structure and function of gastropod parasperm; and the molecular diversity of sperm protein.
Biology of cilia and flagella: Structure and function of dynein motors; regulation of flagellar motility by protein kinases and protein phosphatases; molecular architecture of the axoneme and comb plate; cDNA and proteomics analysis of axonemal proteins; novel Ca^{2+}-binding protein and photoreceptor protein; in vitro assembly of the axoneme; phylogenetic analysis of ciliary and flagellar proteins; and eukaryotic evolution and diversity of cilia and flagella.

Select Publications

1. Miyata H et al. (2015). Sperm calcineurin inhibition prevents mouse fertility with implications for male contraceptive. Science *350* 442-445.
2. Inaba K. (2015). Calcium sensors of ciliary outer arm dynein: functions and phylogenetic considerations for eukaryotic evolution. Cilia. *4*:6.
3. Mizuno K et al. (2012). Calaxin drives sperm chemotaxis by Ca^{2+}-mediated direct modulation of a dynein motor. Proc Natl Acad Sci U S A. *109*:20497-20502.
4. Inaba K. (2011). Sperm flagella: comparative and phylogenetic perspectives of protein components. Mol Hum Reprod. *17*, 524-538.
5. Konno A et al. (2010). Distribution and structural diversity of cilia in tadpole larvae of the ascidian Ciona intestinalis. Dev Biol. *337*, 42-62.
6. Satouh Y et al. (2005). Molecular characterization of radial spoke subcomplex containing radial spoke protein 3 and heat shock protein 40 in sperm flagella of the ascidian Ciona intestinalis. Mol Biol Cell *16*, 626-636.
7. Murata Y et al. (2005) Phosphoinositide phosphatase activity coupled to an intrinsic voltage sensor. Nature *435*, 1239-1243.

Yuji Inagaki

Molecular Evolution of Microbes

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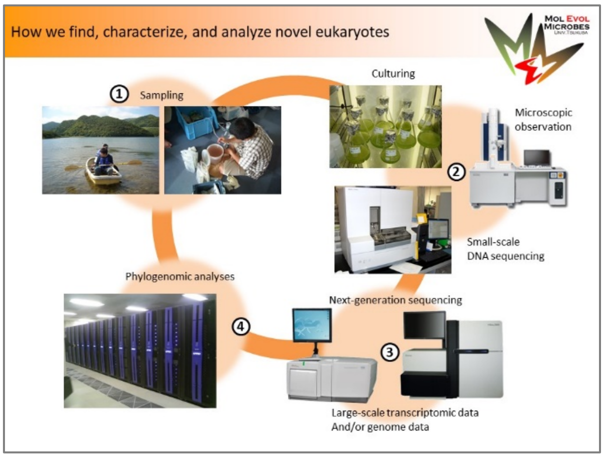
https://sites.google.com/site/yujiswebsite/Home

Keywords: **eukaryotic phylogeny, genomes, transcriptomes, phylogenomics, organelles, endosymbiosis**



We endeavor to understand the evolutionary path of eukaryotes by inferring their phylogenetic relationships and performing comparative genomic analyses based on nucleotide and amino acid sequences of existing species. We are investigating “novel” organisms in the natural environment, which are evolutionarily important but have not yet been investigated, to search for the key to solving various problems in eukaryotic evolution. We are also interested in the origin and evolution of organelles established through endosymbioses and obligate bacterial endosymbionts in eukaryotes.

Molecular phylogenetic analysis requires statistical processing using the maximum likelihood method, and computers are used for this purpose. To accurately infer the relationship between major eukaryotic phylogenetic groups that may have diverged in the distant past, it is necessary to analyze large amounts of sequence data. We are obtaining transcriptome and genome data and using supercomputers to handle large-scale sequence data.

Selected publications

1. Yazaki, E et al. (2020). Barthelonids represent a deep-branching matamonad clade with mitochondrion-related organelles predicted to generate no ATP. *Proc Royal Soc B* 287:20201538.
2. Sarai, C et al. (2020). Dinoflagellates with relic endosymbiont nuclei as models for elucidating organellogenesis.. *Proc Nat Acad Sci USA* 117:5364-5375.
3. Brown, MW et al. (2018). Phylogenomics places orphan protistan lineages in a novel candidate super-group. *Genome Biol Evol* 10:427-433.
4. Leger, MM et al. (2017). Organelles that illuminate the origins of *Trichomonas* hydrogenosomes and *Giardia* mitosomes.. *Nat Ecol Evol* 1:00092.
5. Nakayama, T et al. (2014). Complete genome of a nonphotosynthetic cyanobacterium in a diatom reveals recent adaptations to an intercellular lifestyle. *Proc Nat Acad Sci USA* 111:11407-11412.

You can find the list of my publications at Google Scholar.
https://scholar.google.ca/citations?hl=en&user=ZjRo4uMAAAAJ&view_op=list_works

Louis J Irving

Plant Ecophysiology

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Keywords: **parasitic plant, nutrient uptake, biomass allocation, growth**

Parasitic plant ecophysiology

Parasitic plants cause millions of dollars of damage to agriculture annually. However, the mechanisms by which this damage is caused are not well understood.

Our group aims to investigate the influence of environmental factors (particularly nutrition) on the host / parasite relationship, focusing on methods to suppress the negative impacts of parasitism on the host plant. We use a range of techniques focusing on photosynthesis, isotope labelling, nutrient measurements, and biomass allocation to understand how the parasite damages the host, and how the host can resist the parasite.

Plant competition for resources

Plants compete for resources both above and belowground. Root proliferation in nutrient—rich patches is thought to help them compete with other plants, while aboveground plants compete for light, mainly by changing leaf area and thickness. However, the mechanisms by which plants "decide" whether to invest resources in new leaves or roots are not clear. Our goal is to understand how plants make decisions, and the influence of these decisions on plant competition.

A maize plant parasitized by *P. japonicum*

Selected publications

1. Irving, LJ. and Mori, S. (2021). Effect of light, N and defoliation on biomass allocation in *Poa annua*. *Plants* 10(9):1783.
2. Irving, LJ. and Zhang, HX. (2021). Modelling the effect of salt and PEG on water uptake in wheat seeds. *Agronomy* 11(8):1660.
3. Irving, LJ. et al. (2019). Host nutrient supply affects the interaction between the hemiparasite *Phtheirospermum japonicum* and its host, *Medicago sativa*. *Environmental and Experimental Botany* 162:125-132.
4. Irving, LJ. et al. (2019). Differential carbon allocation to nitrogen-rich patches in *Poa annua* precedes root proliferation but has no immediate benefit to N uptake. *Journal of Plant Physiology* 234:54-59.
5. Jokinen, JI. and Irving, LJ. (2019). Effects of light level and nitrogen supply on the red clover – *Orobanche minor* host – parasite interaction. *Plants* 8(6):146.

Ken-ichiro Ishida

Plant Systematics and Evolution

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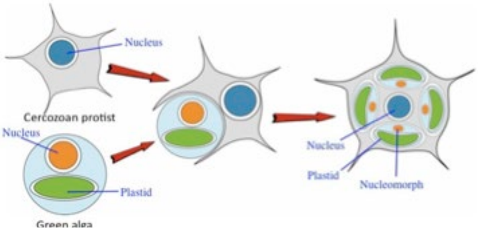
Keywords: **algae, protists, endosymbiosis, evolution, algal biomass**

Research interest in my lab is to elucidate the diversity and evolution of photosynthetic protists (algae) and their non-photosynthetic relatives. Following three major subjects are the current focuses in my research.

1. **Cellular evolution in the endosymbiotic acquisition of plastids:** Plastids were born by a primary endosymbiosis and transferred to the different eukaryotic lineages by several secondary endosymbioses. We are interested in how a photosynthetic endosymbiont was integrated into a host cell as an organelle. This mystery is being uncovered by various approaches, such as genomics, cell biology, electron microscopy and molecular phylogenetics.
2. **Classification and evolution of protists:** We look for new protist species, especially the ones that can connect missing links in the tree of life. We collect protists from the nature, establish clonal cultures, observe them under light and electron microscopes and perform molecular phylogenetic analyses. We are the protist hunters.
3. **Search for useful protists for bio-fuel production:** We are studying how to look for oil-producing algae and protists in the nature and establish cultures of high-performance strains.



Establishment of the Chlorarachniophytes, a photosynthetic protist group with green secondary plastids. A cercozoan protist engulfed a green alga and kept it as a plastid. The plastids of the Chlorarachniophytes still have a vestigial nucleus (nucleomorph) from the endosymbiotic green alga.

Selected publications

1. Shiratori, T., Yabuki, A. and Ishida, K. (2020). Morphology, ultrastructure and phylogeny of two novel species of *Ventrifissura* (*V. oblonga* n. sp. and *V. velata* n. sp., Thecofilosea Cercozoa). *Protist* 171:125731.
2. Nomura, M., Kamikawa, R. and Ishida, K. (2020). Fine structure observation of feeding behavior, Nephroselmis spp.-derived chloroplast engulfment and mitotic process in the katablepharid *Hatena arenicola*. *Protist* 171:125714.
3. Shiratori, T., Suzuki, S., Kakizawa, Y. and Ishida, K. (2019). Phagocytosis-like cell engulfment by a planctomycete bacterium. *Nature Commun.* 10:5529.
4. Thakur, R., Shiratori, T. and Ishida, K. (2019). Taxon-rich multigene ohylogenetic analyses resolve the phylogenetic relationship among deep-branching Stramenopiles. *Protist* 170:125682.
5. Yabuki, A. and Ishida, K. (2018). An orphan protist *Quadricilia rotundata* finally finds its phylogenetic home in Cercozoa. *J. Euk. Microbiol.* 65:729-732.

Kaori Ishikawa

Mitochondrial Biology

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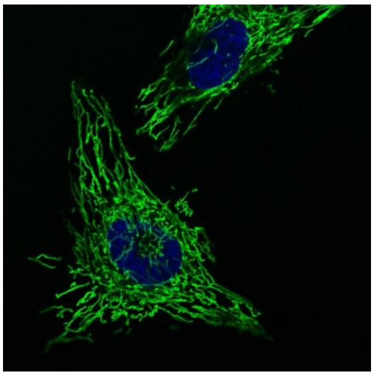
Keywords: **mitochondria, mtDNA (mitochondrial DNA), model mice, disease phenotype, mitochondrial dynamics**

Mitochondria are dynamic organelles which fuse and divide continuously, and they have evolved with eukaryotic cells, developing a symbiotic relationship and complementing each other. Understanding "normal" and "abnormal" mitochondrial functions is very important to uncover the mechanisms of human diseases.

We are studying the impact of mitochondrial DNA (mtDNA) mutations on cellular or tissue functions using *in vitro* and *in vivo* models.



◀ Mitochondria in human cells are visualized by green dye. Blue dye indicates nuclei. Mitochondria construct dynamic networks in cytosols.

Selected publications

1. Ishikawa K, Yamamoto S, Hattori S, Nishimura N, Matsumoto H, Miyakawa T, Nakada K. (2021). Neuronal degeneration and cognitive impairment can be prevented via the normalization of mitochondrial dynamics. *Pharmacol Res* 163:105246.
2. Ishikawa K, Yamamoto S, Hattori S, Nishimura N, Tani H, Mito T, Matsumoto H, Miyakawa T, Nakada K. (2019). Acquired Expression of Mutant Mitofusin 2 Causes Progressive Neurodegeneration and Abnormal Behavior. *J Neurosci* 39:1588-1604.
3. Ishikawa K, Toyama-Sorimachi N, Nakada K, Morimoto M, Imanishi H, Yoshizaki M, Sasawatari S, Niikura M, Takenaga K, Yonekawa H, Hayashi J. (2010). The innate immune system in host mice targets cells with allogenic mitochondrial DNA. *J Exp Med* 207:2297-2305.
4. Ishikawa K, Takenaga K, Akimoto M, Koshikawa N, Yamaguchi A, Imanishi H, Nakada K, Honma Y, Hayashi J. (2008). ROS-generating mitochondrial DNA mutations can regulate tumor cell metastasis. *Science* 320:661-664.

Yuzuru Ito

Stem Cell Engineering for Regenerative Medicine

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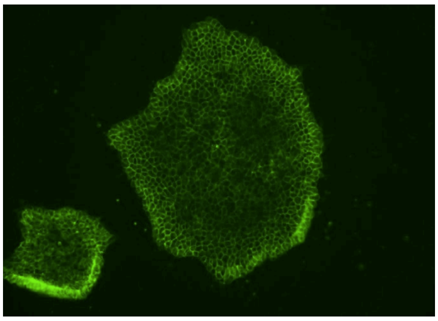
Keywords: **mesenchymal stem cell, iPS cell, process, quality control, regenerative medicine**

Human pluripotent stem cells (ES/iPS cells) and mesenchymal stem cell are expected as powerful tool for regenerative medicine in the world. However, those cells are likely to lose the useful ability for cell therapy during preparation (establishment, culture, cryopreservation etc.) Moreover, method for preparation of some organ cells is insufficient so safe and effective method of treatment isn't realized yet.
To establish the facile, economical and safe regenerative medicine, we should develop several supporting technology for quality control, safety administration and so on. We will promote the development of technology for supporting regenerative medicine.



Fluoresceinated rBC2LCN directly stains human iPS cell colonies. This new probe that we developed can detect good iPS/ES cells accurately, nondestructively and quickly. We can use this probe as "high-sensitive" and "low-toxic" technology for human ES/iPS cells to facilitate of quality control.

Selected publications

1. Oyane, A., Araki, H., Nakamura, M., Aiki, Y. and Ito Y. (2021). Storable bFGF-releasing membrane allowing continuous human iPSC culture. *Materials* 14:651.
2. Haramoto, Y., Onuma, Y., Mawaribuchi, S., Nakajima, Y., Aiki, Y., Higuchi, K., Shimizu, M., Tateno, H., Hirabayashi, J. and Ito, Y. (2020). A technique for removing tumourigenic pluripotent stem cells using rBC2LCN lectin. *Regen. Ther.* 14:306-314.
3. Oyane, A., Araki, H., Nakamura, M., Aiki, Y., Higuchi, K., Pyatenko, A., Adachi, M. and Ito Y. (2020). Controlled release of basic fibroblast growth factor from a water-floatable polyethylene nonwoven fabric sheet for maintenance culture of iPSCs. *Rsc Advances* 10:95-104.
4. Mawaribuchi, S., Aiki, Y., Ikeda, N. and Ito, Y. (2019). mRNA and miRNA expression profiles in an ectoderm-biased substate of human pluripotent stem cells. *Sci. Rep.* 9(1):11910.
5. Mawaribuchi, S., Onuma, Y., Aiki, Y., Kuriyama, Y., Mutoh, M., Fujii, G. and Ito, Y. (2019). The rBC2LCN-positive subpopulation of PC-3 cells exhibits cancer stem-like properties. *BBRC* 515(1):176-182.

Hiroaki Iwai

Plant Cell Wall Biology

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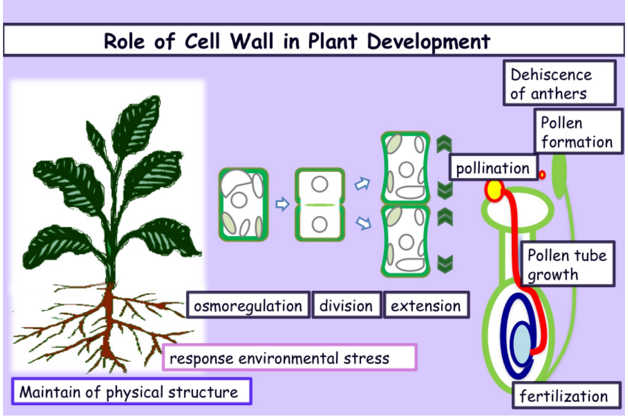
Keywords: **Cell wall, Pectin, Fruit ripening, Seed germination, Salinity response, Heavy metal response**

We are interested in understanding plants development and environmental responses. We focus on the cell wall because it is the most characteristic feature of vascular plants. The cell wall plays multiple roles, including determining cell shape and size, cell-cell adhesion, controlling cell differentiation and growth, and promoting abiotic and biotic stress tolerance. We are studying the function of the cell wall matrix and its regulation in plant growth and environmental responses.



Selected publications

1. Hasegawa K, Kamada S, Takehara S, Takeuchi H, Nakamura A, Satoh S, **Iwai H.** (2021). Rice Putative Pectin Methyltransferase Gene OsPMT10 is Required for Maintaining the Cell Wall Properties of Pistil Transmitting Tissues via Pectin Modification. Plant Cell Physiol (in press)
2. **Iwai H.** (2021). Cell Wall Functions in Plant Growth and Environmental Responses. J Plant Res. 134(6):1155-1158
3. Ohara T, Takeuchi H, Sato J, Nakamura A, Ichikawa H, Yokoyama R, Nishitani K, Minami E, Satoh S, **Iwai H.** (2021). Structural Alternation of Rice Pectin Affects Cell Wall Mechanical Strength and Pathogenicity for the Rice Blast Fungus under Weak Light Conditions. Plant Cell Physiol. 62: 641-649
4. Takebe N, Nakamura A, Watanabe T, Miyashita A, Satoh S, **Iwai H.** (2020). Cell wall Glycine-rich Protein2 is involved in tapetal differentiation and pollen maturation. J Plant Res. 133(6):883-895.
5. Hasegawa K, Kamada S, Takehara S, Takeuchi H, Nakamura A, Satoh S, **Iwai H.** (2020). Rice Putative Methyltransferase Gene OsPMT16 Is Required for Pistil Development Involving Pectin Modification. Front Plant Sci. 11:475
6. Nagayama T., Nakamura A., Yamaji N., Satoh S., Furukawa J., **Iwai H.** (2019). Changes in the Distribution of Pectin in Root Border Cells Under Aluminum Stress. Frontiers in Plant Science, 10: 1216

Akira Kikuchi

Stress Physiology in Higher Plants

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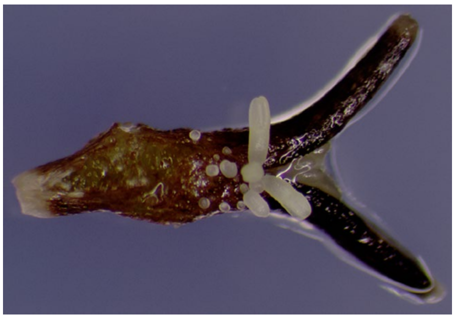
http://www.gene.tsukuba.ac.jp/Plant/GeneticDiversity/

Keywords: **abiotic stresses, somatic embryo, carrot, potato**

Stress tolerance in higher plants is an interesting phenomenon. Plants are immobile and must evolve defense systems that are uniquely suited to their ambient environmental stresses. Several genes associated with these defense systems have been identified. Our aim here is to generate genetic lines conferring abiotic stress tolerance and to verify their performance. We are also studying the impacts of transgenic plants on biological diversity so as to establish an environmental biosafety risk-assessment system for transgenic plants. In addition, we are trying to elucidate the mechanisms of abiotic stress tolerance in higher plants by using GM (genetically modified) techniques, and we are studying the induction of somatic embryogenesis by abiotic stress. In this way, while elucidating the mechanism of abiotic stress in higher plants, we are also working on the development of abiotic stress–tolerant GM plants that can be used for crop production.



Somatic embryogenesis induced in carrots by abiotic stress
In carrots, somatic embryo production can be induced from apical tip segments by application and removal of stress treatment. The somatic cells are converted to embryogenic cells by the stress treatment. After removal of the stress, the embryogenic cell begins to develop into a somatic embryo.

Select Publications

1. Shimazaki T., Endo T., Kazsuga M., Yamaguchi-Shinozaki K., Watanabe K., Kikuchi A. (2016) Evaluation of the yield of abiotic-stress-tolerant AtDREB1A transgenic potato under saline conditions in advance of field traials. Breeding science. 66:703-710.
2. Kikuchi A., Huynh D., Endo T., Watanabe K. (2015) Review of recent transgenic studies on abiotic stress tolerance and future molecular breeding in potato. Breeding science. 65:85-102.
3. Kikuchi A., Asahina M., Tanaka M., Satoh S., Kamada H. (2013) Acquisition of embryogenic competency does not require cell division in carrot somatic cell. J Plant Res, 126:243-250.
4. Shibukawa T., Yazawa K., Kikuchi A., Kamada H. (2009) Possible involvement of DNA methylation on expression regulation of Carrot *LEC1* gene in its 5'-upstream region. Gene *437*, 22-31.
5. Tanaka M., Kikuchi A., Kamada H. (2008) The *Arabidopsis* histone deacetylases HDA6 and HDA19 contribute to the repression of embryonic properties after germination. Plant Physiol *146*, 149-161.

Satoru Kobayashi

Molecular Mechanisms Regulating Germline Development

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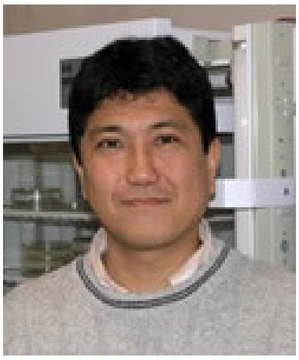
Germ cells are specialized cells that can transmit genetic materials from one generation to the next through sexual reproduction. All other cells of the body are somatic cells. This separation of germ and somatic cells is one of the oldest problems in developmental biology. In many animal groups, a specialized portion of egg cytoplasm, or germ plasm, is inherited by the cell lineage which gives rise to germ cells. This cell lineage is called germline. The germline progenitors eventually migrate into the gonads, where they differentiate as germline stem cells (GSC) to form eggs and sperm when the organisms are physically matured. Our laboratory aims to find the molecular mechanisms regulating germline segregation, germline sex determination, and GSC niche function in *Drosophila*.

Publications

1. Ohhara, Y., Shimada-Niwa, Y., Niwa, R., Kayashima, Y., Hayashi, Y., Akagi, K., Ueda, H., Yamakawa-Kobayashi, K. and Kobayashi, S. (2015) Autocrine regulation of ecdysone synthesis by β3-octopamine receptor in the prothoracic gland is essential for *Drosophila* metamorphosis. Proc. Natl. Acad. Sci., USA., *112*, 1452-1457.
2. Hashiyama, K., Hayashi, Y. and Kobayashi, S. (2011). *Drosophila Sex lethal* gene initiates female development in germline progenitors. Science *333*, 885-888.
3. Kitadate, Y. and Kobayashi, S. (2010). Notch and Egfr signaling act antagonistically to regulate germline stem cell niche formation in *Drosophila* male embryonic gonads. Proc. Natl. Acad. Sci. USA *107*, 14241-14246.
4. Kitadate, Y., Shigenobu, S., Arita, K. and Kobayashi, S. (2007). Boss/Sev signaling from germline to soma restricts germlinestem-cell-niche formation in the anterior region of *Drosophila* male gonad. Dev. Cell *13*, 151-159.
5. Hayashi, Y., Hayashi, M. and Kobayashi, S. (2004). Nanos suppresses somatic cell fate in *Drosophila* germline. Proc. Natl. Acad. Sci. USA. *101*, 10338-10342.
6. Asaoka-Taguchi, M., Yamada, M., Nakamura, A., Hanyu, K. and Kobayashi, S. (1999) Maternal Pumilio acts together with Nanos in germline development in *Drosophila* embryos. Nature Cell Biol. *1*, 431-437.
7. Kobayashi, S., Yamada, M., Asaoka, M., and Kitamura, T. (1996). Essential role of the posterior morphogen nanos for germline development in *Drosophila*. Nature *380*, 708-711.

Hidekazu Kuwayama



Molecular Mechanisms and Dynamics of Biological Self-organization

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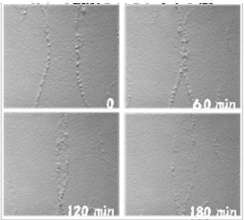
Self-reproduction or Self-organization is a characteristic observed in all biological organisms. In my Lab, we research self-organization using a cellular slime mold, *Dictyostelium discoideum*, as a model system, by a combination of experimental and theoretical methods. Our aim is to clarify the molecular systems that regulate cell orientation and to simulate its dynamics.

Dictyostelium discoideum is a solitary amoeboid microorganism that grows as a single cell, but during starvation it initiates chemotaxis towards a cAMP signal secreted by neighboring cells and constructs a multicellular "slug". This feature is simple but very useful for investigating how cells interact to construct multi-cellular organisms. At present, we are focusing on biological soliton phenomenon which was firstly discovered in my Lab, and chemotaxis which involves questions about how cells recognize their environment using molecular techniques. We are also interested in disease-causing genes related to biological self-organization.



Biological soliton phenomena in multi-cellular movement observed in *Dictyostelium* mutant.

Selected Publications

1. Kuwayama, H. (2021) Peptide nucleic acid as a template for Taq DNA polymerase. Biochemical and biophysical research communications, 579, 76-80
2. Kuwayama, H, Higashinakagawa, T. (2019) The Life Cycle of Dictyostelium discoideum Is Accelerated via MAP Kinase Cascade by a Culture Extract Produced by a Synthetic Microbial Consortium. Journal of Molecular Biology and Biotechnology, 29, 35-42
3. Kida, Y., Pan, K. and Kuwayama, H. (2019) Some chemotactic mutants can be progress through development in chimeric populations.
Differentiation., 105, 71-79.
4. Kuwayama, H., Kikuchi, H., Oshima, Y. and Kubohara, Y. (2016) Glutathione S-transferase 4 is a putative DIF-binding protein that regulates the size of fruiting bodies in *Dictyostelium discoideum*. Bioch., and Biophy., Reports, 8, 219-226.
5. Kuwayama, H. and Kubohara, Y. (2016) Differentiation-inducing factor 2 modulates chemotaxis via the histidine kinase DhkC-dependent pathway in *Dictyostelium discoideum*. FEBS Lett. *590*,760-768.
6. Kuwayama, H. et al. (2014) Cross-species functional complementation of cellulose synthase during the development of cellular slime molds. Dev. Growth and Diff., *56*, 526–533.
7. Kuwayama, H. et al. (2013) A RabGAP Regulates Life-Cycle Duration via Trimeric G-protein Cascades in *Dictyostelium discoideum*. PLoS One *8,* e81811.
8. Kuwayama, H. and Ishida, S. (2013) Biological soliton in multicellular movement. Scientific Reports, *3*, Article number: 2272.
9. Kuwayama, H. (2012). Arachidonic Acid Enhances Caffeine-Induced Cell Death via Caspase-Independent Cell Death. Scientfic Reports *2*, Article number: 577.
10. Kuwayama, H., Kikuchi, H., Oshima, Y. and Kubohara, Y. (2011). Artificial compounds differentially control *Dictyostelium* chemotaxis and cell differentiation. Cell Struct Funct *36*, 21-26.

Fumiaki Maruo

Developmental Biology of Stem Cells

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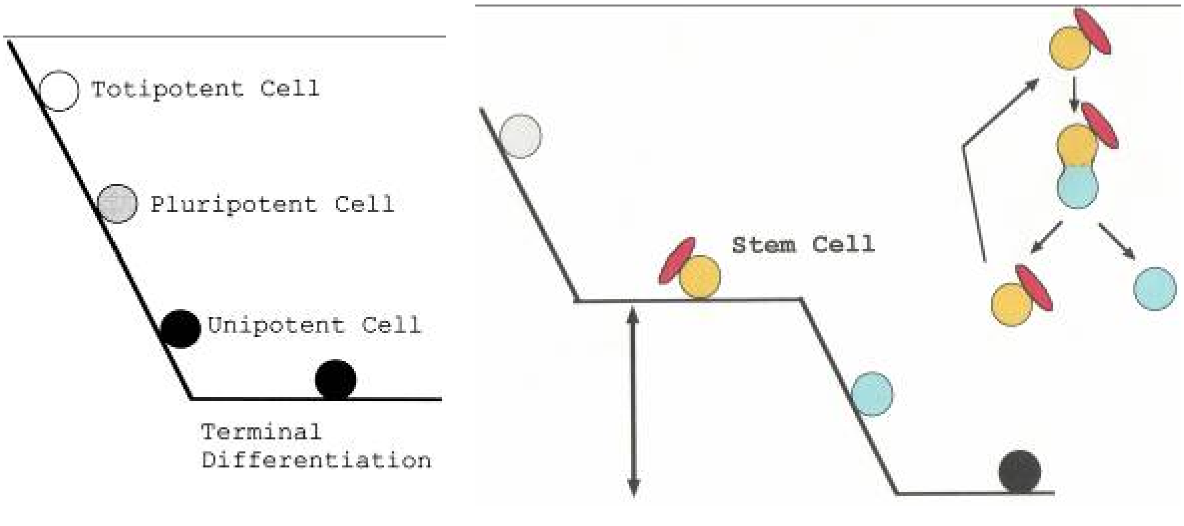
Stem cells and regeneration are currently hot research subjects in the life sciences and provide many possibilities for future treatments for major diseases, including organ damage and degenerative conditions. We are studying the mechanisms regulating stem cell maintenance, proliferation, and differentiation. Our experimental system uses the germline stem cells in *Drosophila* oogenesis. We also use neuronal stem cells in the regenerating newt retina and undifferentiated germline cells in developing newt gonads. Our approaches involve genetic, immunological, and molecular biological techniques.

Keywords on our research are “cell differentiation”, “regeneration”, “*Drosophila*”, “newt”, “germ cell”, and “stem cell”.

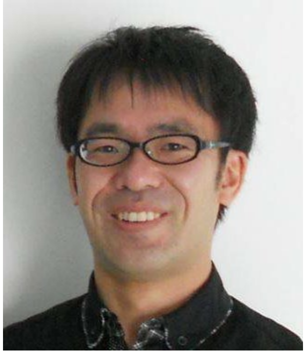


Steps in developmental potency (left), and a model mechanism of stem cell maintenance (right).

Select Publications

1. Chiba, C., Hoshino, A., Nakamura, K., Susaki, K., Yamano, Y., Kaneko, Y., Kuwata, O., Maruo, F., and Saito, T. (2006). Visual cycle protein RPE65 persists in new retinal cells during retinal regeneration of adult newt. The Journal of Comparative Neurology *495*, 391-407.
2. Maruo, F. (1996). Developmental genetics of oogenesis. In *Developmental Genetics* (ed. Okada, M.), pp. 35-68. SHOKABO, Tokyo. (in Japanese)

Hisanori Matsui



Translational Science in Drug Discovery

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Keywords: **Drug Discovery, Translational, Open Science**

Functional analysis of orphan GPCR was my first research area as a biologist in drug discovery research. Kisspeptin was one of the most impactful research topics for me, starting from the discovery of its physiological functions in relation to reproductive neuroendocrinology and its therapeutic application for prostate cancer. Through this program I gained experience and knowledge ranging from the drug target discovery to drug development as clinical studies. I then changed my research field from oncology to drug repurposing, expanded my research therapeutic areas and strengthened translational science. I am now leading External Neuroscience Research to deliver breakthrough medicine through innovative partnership. My experience of therapeutic area includes oncology, reproductive neuroendocrinology, inflammation, and neuroscience.

Drug discovery and development is a teamwork-oriented process where very diverse multi-functional professionals are working together. In addition, drug discovery and development cannot be achieved without external professional partners as well. I really like this multidisciplinary research approach because we can overcome hurdle after hurdle to eventually achieve our goals. Let's work together to make innovation happen.

Selected publications

1. Kimura M., Ishii N.M., Seki N., Sakai Y., Yamashita T., Awatsuji H., Kanda K., Matsumoto K., and Matsui, H. (2019). Reduction of Kiss1 expression in the anteroventral periventricular nucleus is associated with atrazine-induced attenuation of the luteinizing hormone surge in female rats. Biol Reprod. *100*, 41-48.
2. Muller, S, Ackloo S, Arrowsmith C, Bauser M, Baryza J, et al. (2018). Donated chemical probes for open science. eLife 7:e34311
3. Ishikawa K., Tanaka A., Kogame A., Watanabe T., Tagawa Y., and Matsui H. (2018). Usefulness of pharmacokinetic/efficacy analysis of an investigational kisspeptin analog, TAK-448, in quantitatively evaluating anti-tumor growth effect in the rat VCaP androgen-sensitive prostate cancer model. Eur. J. Pharmacol. *828*, 126-134.
4. Tanaka A., Nakata D., Masaki T., Kusaka M., Watanabe T., and Matsui H. (2018). Evaluation of pharmacokinetics/pharmacodynamics and efficacy of one-month depots of TAK-448 and TAK-683, investigational kisspeptin analogs, in male rats and an androgen-dependent prostate cancer model. Eur. J. Pharmacol. *822*, 138-146.
5. MacLean D.B., Matsui H., Suri A., Neuwirth R., and Colombel M. (2014). Sustained exposure to the investigational Kisspeptin analog, TAK-448, down-regulates testosterone into the castration range in healthy males and in patients with prostate cancer: results from two phase 1 studies. J Clin Endocrinol Metab *99*, E1445-1453.
6. Matsui H., Takatsu Y., Kumano S., Matsumoto H., and Ohtaki T. (2004). Peripheral administration of metastin induces marked gonadotropin release and ovulation in the rat. Biochem. Biophys. Res. Commun. *320*, 383-388.

Ayumi Minoda

Plant Molecular Physiology

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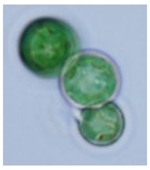
Keywords: **photosynthesis, environmental response, carbon metabolism, metal metabolism, green technology, algae, microorganisms**

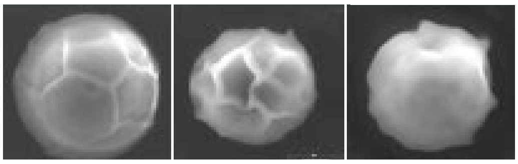
Regulation of photosynthesis and metabolism under extreme environment

A unicellular red alga, *Galdieria sulphuraria* is found in nature in acidic hot springs and soils where other organisms cannot live. In order to survive these environments, they have strong environmental tolerance to strong acids, high osmotic pressure, and high concentrations of metals. In addition, they are the only alga that can grow photoautotrophically under pure CO_2. However, little is known about how they are able to adapt to such extreme environments. To elucidate the mechanisms, we have found new regulatory mechanisms for photosynthesis and metal tolerance, and have identified unique factors such as multi-metal tolerance factors.

Green technology for sustainability

Microorganisms adapt and create the environment through biological and non-biological phenomena. By examining these phenomena with the latest technology, we are exploring sustainable green technology.





G. sulphuraria (right panel)
SEM images
(lower panel, from left):
Living cell, Lyophilized cell,
Au-adsorbed lyophilized
cell of *G. sulphuraria,*

Selected publications

1. Miyashita S, Ogura T, Fujii S, Inagaki K, Takahashi Y and Minoda A Recovery of Au from dilute aqua regia solutions via adsorption on the lyophilized cells of a unicellular red alga *Galdieria sulphuraria*: A mechanism study. 2021 J Hazard Mater in press
2. Miyashita S, Ogura T, Fujii S, Inagaki K, Takahashi Y and Minoda A Effect of lyophilization on the acid resistance of a unicellular red alga *Galdieria sulphuraria* during platinum recovery. 2021 J Hazard Mater Advances
3. Sakurai T , Aoki M, Ju X, Ueda T, Nakamura Y, Fujiwara S, Umemura T, Tsuzuki, M and Minoda A Profiling of lipid and glycogen accumulations under different growth conditions in the sulfothermophilic red alga *Galdieria sulphuraria.* 2016 Bioresource Technol. 200, 861-866.
4. Minoda A, Weber APM, Tanaka K and Miyagishima SY Nuclear independent control of Rubisco operon by the plastid-encoded transcription factor Ycf30 in the red alga *Cyanidioschyzon merolae* 2010 Plant Physiol, 154, 1532-1540.
5. Minoda A, Sonoike K, Okada K, Sato N and Tsuzuki M. Decrease in the efficiency of the electron donation to tyrosine Z of photosystem II in an SQDG-deficient mutant of *Chlamydomonas.* 2003 FEBS Lett., 553, 109-112

Kenji Miura

Plant Molecular Biology

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Keywords: **transient expression, genome editing, plant abiotic stress responses, plant biotechnology**

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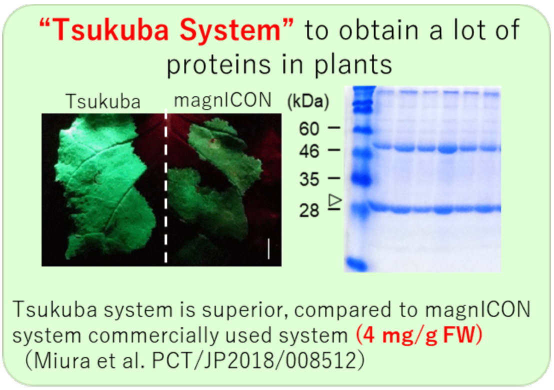
(1) “Tsukuba System” for high amount of protein production system in plants



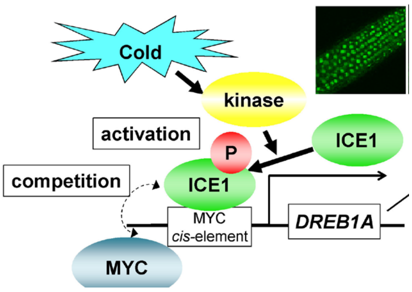
“Tsukuba System” to obtain a lot of proteins in plants

Tsukuba system is superior, compared to magnICON system commercially used system (4 mg/g FW)
(Miura et al. PCT/JP2018/008512)

We established high amount of protein production system in plants, termed “Tsukuba System”. The yield of protein production is compatible to other expression systems, such as *E. coli* and yeast. By using this system, we are now establishing the following application methodology;

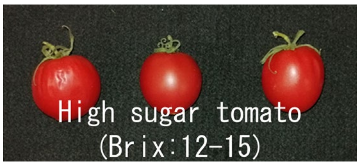
1. High amount of pharmaceutical protein production in plants for cost effectiveness. The targets are proteins for regenerative medicine, veterinary medicine, etc.
2. High amount of production of plant secondary metabolites by expression of enzymes.
3. Transient expression of Cas9 and sgRNA in plants to achieve plant genome editing without transformation.

(2) Elucidation of molecular mechanisms of abiotic stress signaling and sugar accumulation



Because sugar accumulation and abiotic stress responses are correlated, e.g. cold stress enhances sugar accumulation in plants, we are elucidating molecular mechanism of abiotic stress signaling and sugar accumulation. We are to identify interacting factors to control abiotic stress signaling. Several factors have already isolated, thus, we are checking functional role of these factors.

For sugar accumulation, we have already isolated high sugar tomato mutant (Brix: 12-15). The level of Brix is similar to that of grape. We are now identifying the mutation in this mutant and characterizing functional role of this mutation.



Selected publications

1. Nosaki, S. et al. (2021). Prevention of necrosis caused by transient expression in *Nicotiana benthamiana* by application of ascorbic acid. *Plant Physiology* 186: 832-835.
2. Miura, K. et al. (2020). The PHD finger of *Arabidopsis* SIZ1 recognizes trimethylated histone H3K4 mediating SIZ1 function and abiotic stress response. *Commun. Biol*. 3: 23.
3. Shimatani, Z. et al. (2017). Targeted base editing in rice and tomato using CRISPR-Cas9 cytidine deaminase fusion. *Nature Biotechnology* 35: 441-443.

Shinichi Miyamura

Cell Biology of Sexual Dimorphism in Green Plants

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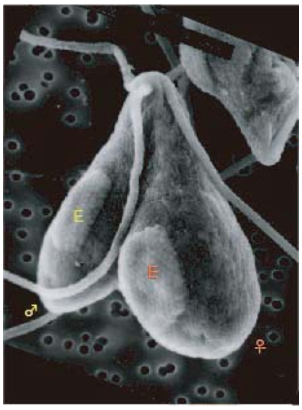
My lab is working on two projects: 1) the cellular and molecular mechanisms of sexual dimorphism of gametes in isogamous, anisogamous, and oogamous green algae; and 2) sexual reproduction in green algae, mosses, ferns, and gymnosperms. Marine green algae belonging to the Ulvophyceae, as well as the unicellular green alga *Chlamydomonas* and land plant sperm, are used mainly as our experimental systems.



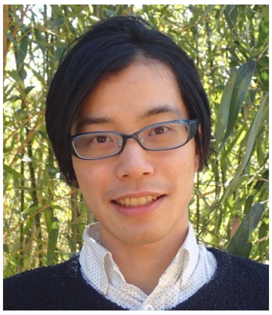
Sexual dimorphism of green algal gametes

We have been focusing on asymmetric placement of the mating structure (cell-fusion apparatus) in gametes as a feature of sexual dimorphism in green algae. The gamete of green algae belonging to the Chlorophyta has two flagella elongated from the cell apex and a mating structure that is a specialized plasma membrane near the flagellar apparatus. The spatial position of the mating structure differs between the sexes. In the male gamete, the mating structure is located on the opposite side to the eyespot (E), whereas it is located on the same side as the eyespot in the female gamete. As a result of this difference, the two eyespots align on the same side of the planozygote after fertilization. Our lab is trying to elucidate the cellular and molecular mechanisms of mating structure development and placement in green algal gametes. We also aim to elucidate the machanisms of gamete-type differentiation according to mating-type locus by using *Chlamydomonas* and ulvophycean green algae.

Select Publications

1. Miyamura, S. (2010). Cytoplasmic inheritance in green algae: patterns, mechanisms and relation to sex type. J Plant Res *123*, 171-184.
2. Miyamura, S., Sakaushi, S., Hori, T., and Nagumo, T. (2010). Behavior of flagella and flagellar root systems in the planozygotes and settled zygotes of the green alga *Bryopsis maxima* Okamura (Ulvophyceae, Chlorophyta) with reference to spatial arrangement of eyespot and cell fusion site. Phycol Res *58*, 258-269.
3. Miyamura, S., Mogi, Y., Mitsuhashi, F., Kawano, S., and Nagumo, T. (2009). Visualizing the spatial arrangement of flagella-eyespot-cell fusion sites in gametes and planozygotes of *Chlamydomonas reinhardtii* (Chlorophyceae, Chlorophyta) with high-resolution FE-SEM. Cytologia *74*, 409-415.
4. Mogi, Y., Kagami, Y., Kuwano, K., Miyamura, S., Nagumo, T., and Kawano, S. (2008). Asymmetry of eyespot and mating structure positiobs in *Ulva compressa* (Ulvales, Chlorophyta) revealed by a new field emission scanning electron microscopy method. J Phycol *44*, 1290-1299.
5. Miyamura, S. (2007). Inheritance pattern of chloroplast DNA is correlated with gamete types based on sex-specific arrangement of the cell fusion site in *Caulerpa* (Ullvophyceae, Chlorophyta). Phycol Res *55*, 47-57.

Yoshiaki Morino



Evolution and Development

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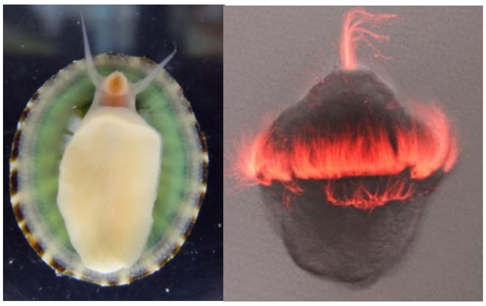
Keywords: spiralian, EvoDevo, transcriptome, transcription factor, NGS



Our research focuses on the early development of marine invertebrates, particularly spiralian (higher taxa including molluscs, and annelids and platyhelminthes), to reveal how animal development evolves. In order to get a better picture of the evolution of development, information from non-model animal is important. We use bidirectional approaches of bioinformatics and experimental embryology to extract as much evolutionary information as possible from non-model animals.

Examples of current research projects: "Role of lineage-specific transcription factors in spiralian development", "Search for genes controlling spiralian development", "Developmental system drift in spiralian development".

Selected publications *corresponding author

1. *Supanat Phuangphong, Jumpei Tsunoda, Hiroshi Wada, ***Yoshiaki Morino** (2021) "Duplication of spiralian-specific TALE genes and evolution of the blastomere specification mechanism in the bivalve lineage" ***EvoDevo*** 12:1, 1-16
2. ***Yoshiaki Morino**, Naoki Hashimoto, Hiroshi Wada (2017) “Expansion of TALE homeobox genes and the evolution of spiralian development” ***Nature Ecology and Evolution*** 1, 1942–1949
3. **Yoshiaki Morino**, Hiroyuki Koga, Hiroshi Wada. (2016) “The conserved genetic background for pluteus arm development in brittle stars and sea urchin” ***Evolution & Development*** 18, 2, 89-95.
4. **Yoshiaki Morino**, Kazunori Okada, Miyuki Niikura, Masanao Honda, Nori Satoh, *Hiroshi Wada (2013) “A genome-wide survey of genes encoding transcription factors in the Japanese pearl oyster, Pinctada fucata: I. Homeobox Genes” ***Zoological Science*** 30, 851-857.
5. ***Yoshiaki Morino**[1], Hiroyuki Koga[1], Kazunori Tachibana, Eiichi Shoguchi, Masato Kiyomoto, Hiroshi Wada (2012) “Heterochronic activation of VEGF signaling and the evolution of the skeleton in echinoderm pluteus larvae” ***Evolution & Development*** 14, 5, 428-436. [1]:Equal Contribution

Kisaburo Nagamune

How to Become a Parasite and Survive as One

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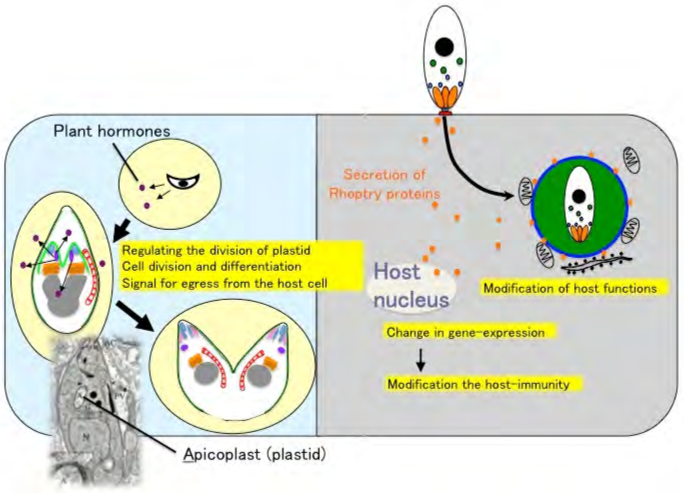
Apicomplexan parasites, including *Toxoplasma gondii* and malarial parasites, have an organelle called the apicoplast, which a kind of plastid and developed from a secondary symbiont of the ancestor of red algae. Apicomplexan parasites have lost their photosynthetic activity because they gained a new, parasitic ability during evolution. However, they still possess the apicoplast, which is essential for their survival. The biology of *T. gondii* and malarial parasites is therefore similar in some ways to that of plant systems because they still have a plant inside the cell. We are investigating the plant-like nature of apicomplexan parasites as a target for the development of anti-parasitic drugs. We are also focusing on the parasitic ability that replaced their photosynthetic ability, and studying how they highjack host functions for their survival.



Toxoplasma gondii produces plant hormones and regulates the progression of the cell cycle and division of plastids. It also secretes rhoptry proteins and highjacks gene expression and organelles in the host cell. Through this highjacking, *T. gondii* can escape the host immune response and take up essential molecules.

Select Publications

1. Toyama, T. *et al.* (2011). Gibberellin Biosynthetic Inhibitors Make Human Malaria Parasite *Plasmodium falciparum* Cells Swell and Rupture to Death. PLoS ONE *7*, e32246.
2. Nakatani, F. *et al.* (2011). Identification of a second catalytically active trans-sialidase in *Trypanosoma brucei*. Biochem Biophysic Res Comm *415*, 421-425.
3. Yamamoto, M. *et al.* (2011). ATF6β is a host cellular target of the *Toxoplasma* virulence factor ROP18. J Exp Med *208*, 1533-1546.
4. Hirakawa, Y. *et al.* (2009). Protein targeting into secondary plastids of chlorarachniophytes. PNAS *106*, 12820-12825.
5. Nagamune, K. *et al.* (2008). Abscisic acid controls calcium-dependent egress and development in *Toxoplasma gondii*. Nature *451*, 207-210.

Kazuto Nakada

Mitochondrial Biology and Medicine

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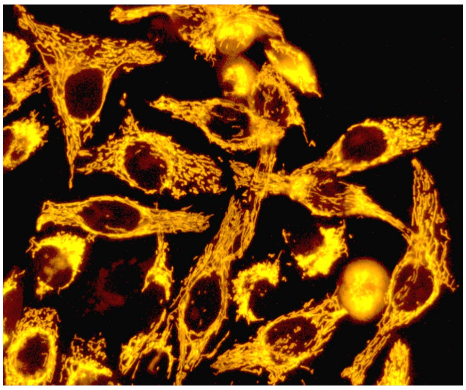
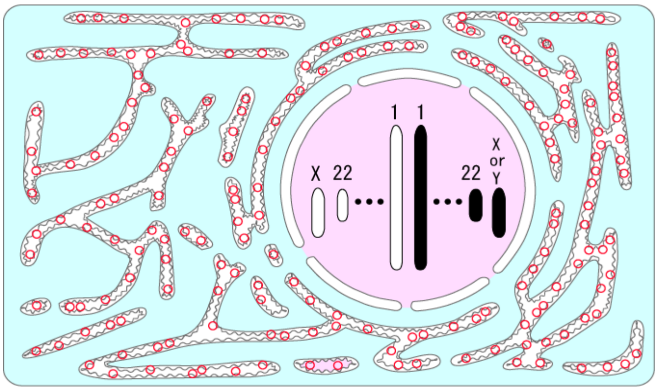
Keywords: mitochondrial DNA, mitochondria-based diseases, model mice

- Studies on biological and medical significance of mitochondrial fission, fusion, and quality control
- Studies on inheritance and gene expression of mitochondrial genome
- Generation of model mice for mitochondria-related diseases
- Studies on pathogeneses of mitochondria-related diseases using model cells and mice
- Studies on mitochondrial diabetes mellitus
- Studies on the mitochondrial theory of aging
- Therapeutic strategies for mitochondria-related diseases





Selected publications

1. Ishikawa K *et al*. Neuronal degeneration and cognitive impairment can be prevented via normalization of mitochondrial dynamics. **Pharmacol Res**, 63: 105246.(2021).
2. Ogasawara E *et al*. Distal control of mitochondrial biogenesis and respiratory activity by extracellular lactate caused by large-scale deletion of mitochondrial DNA. **Pharmacol Res**, 160: 05204 (2020).
3. Ishikawa K *et al*. Acquired Expression of Mutant Mitofusin 2 Causes Progressive Neurodegeneration and Abnormal Behavior. **J Neurosci**, 39: 1588-1604 (2019).
4. Ishihara T *et al*. Dynamics of mtDNA nucleoids regulated by mitochondrial fission is essential for maintenance of homogeneously active mitochondria during neonatal heart development. **Mol Cell Biol**, 35: 211–223 (2015).
5. Shimizu A *et al*. Transmitochondrial mice as models for primary prevention of diseases caused by mutation in the $tRNA^{Lys}$ gene. **PNAS**, 111: 3104-3109 (2014).
6. Hashizume O *et al*. A specific mitochondrial DNA mutation in mice regulates diabetes and lymphoma development. **PNAS**, 109: 10528-10533 (2012).
7. Ishikawa K *et al*. ROS-generating mitochondrial DNA mutations can regulate tumor cell metastasis. **Science**, 320: 661-664 (2008).
8. Nakada K *et al*. Mitochondria-related male infertility. **PNAS**, 103, 15148-15153 (2006).
9. Nakada K et al. Inter-mitochondrial complementation: mitochondria-specific system preventing mice from expression of disease phenotypes by mutant mtDNA. **Nature Med**, 7: 934-939 (2001).

Kouji Nakamura

It’s a Small RNA World

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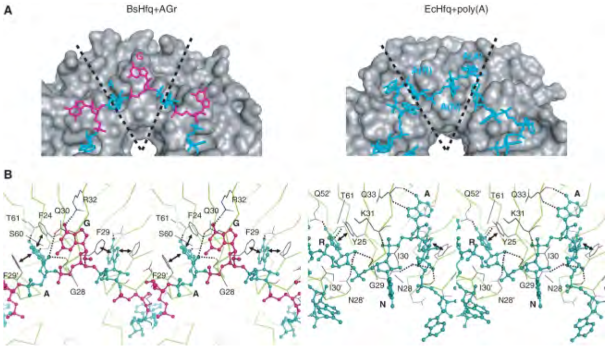
Until recently, gene expression was thought to be controlled mainly at the level of transcription initiation by repressor or activator proteins. It has now been revealed that other mechanisms can regulate gene expression and involve RNAs that might act as antisense RNAs, sequestering molecules, or thermosensors. Bacterial pathogens sense their environments, and in response, virulence genes are induced or repressed through spatial and temporal regulation. These pathogens are also subjected to stress conditions, which require appropriate responses. Recent research has revealed that RNAs are key regulators in pathogens. Small RNAs regulate the translation or stability of mRNAs that encode virulence proteins, namely proteins that are triggered by environmental cues and stresses. In most cases, these small RNAs act directly on target RNAs by an antisense mechanism.

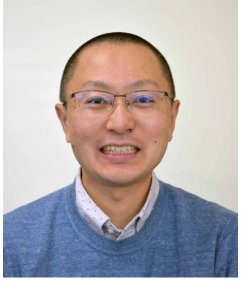


Molecular recognition of RNA by distal site of Hfq. (**A**) Left panel: surface representation of hexameric BsHfq (gray) with stick representation of A (cyan) and G (magenta) residues of AGr. Right panel: surface representation of hexameric EcHfq (gray) with stick representation of poly(A) (cyan). Subunit boundaries are indicated by dashed lines. (**B**) Stereo view of BsHfq–AGr and EcHfq–poly(A) (left and right panel, respectively). R is a purine nucleotide and N is any nucleotide [6].

Select Publications

1. Someya, T., Baba, S., Fujimoto, M., Kawai, G., Kumasaka, T., and Nakamura, K. (2012). Crystal structure of Hfq from *Bacillus subtilis* in complex with SELEX-derived RNA aptamer: insight into RNA-binding properties of bacterial Hfq. Nucleic Acids Research *40*, 1856-1867.
2. Kakeshita, H., Kageyama, Y., Endo, K., Tohata, M., Ara, K., Ozaki, K., and Nakamura,K. (2011b). Secretion of biologically-active interferon-β by *Bacillus subtilis*. Biotechnology letters *33*, 1847-1852.
3. Obana, N., and Nakamura, K. (2011a). A novel regulator, the CPE1446-1447 protein heterodimeric complex, controls toxin genes in *Clostridium perfringens*. J. Bacteriology *193*, 4417-4424.
4. Obana, N., Shirahama, Y., Abe, K., and Nakamura, K. (2010b). Stabilization of *Clostridium perfringens* collagenase mRNA by VR-RNA-dependent cleavage in 5’ leader sequence. Molecular Microbiology *77*, 1416-1428.
5. Abe, K., Obana, N., and Nakamura, K. (2010a). Effects of depletion of RNA-binding protein Tex on the expression of toxin genes in *Clostridium perfringens*. Bioscience, Biotechnology and Biochemistry *74*, 1564-1571.
6. Saito, S., Kakeshita, H., and Nakamura, K. (2009). Novel small RNA-encoding genes in the intergenenic regions of *Bacillus subtilis*. Gene *428*, 2-8.

Hiroaki Nakano



Evolutionary Zoology

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Keywords: **marine invertebrates, placozoa, *Xenoturbella*, acoel, diversity**

We are performing zoological studies on less studied marine invertebrates, currently focusing on placozoans, *Xenoturbella*, acoels, and sea slugs. Our laboratory is situated at Shimoda Marine Research Center, and the research animals are mostly collected at or around Shimoda. By studying the morphology, taxonomy, development, and ecology of these animals, we aim to gain new information on the evolution and diversity of metazoans and bilaterians.

Placozoa is an amoebae-like marine flat animal about 1mm in diameter, possessing one of the simplest body plans within the metazoans. It lacks tissues or organs, and even neurons or muscle cells. There are still no reports of their complete development.

Xenoturbella is a marine animal about 1 cm long lacking typical bilaterian traits such as anus, gonads, and coelomic cavities. We made the first report of its development, and described a new species, *X. japonica*, from Japanese waters.

Acoels share a similar body plan with *Xenoturbella*, and the two groups form the phylum Xenacoelomorpha. Although the phylum is widely believed to be important when considering the origins of bilaterians, the phylogenetic position of this phylum still remains unresolved.

from left

- placozoa
- *Xenoturbella*
- acoel

Selected publications

1. Miyazawa H., *et al.* (2021). Mitochondrial Genome Evolution of Placozoans: Gene Rearrangements and Repeat Expansions. Genome Biology and Evolution *13*, evaa213
2. Philippe H., *et al.* (2019) Mitigating anticipated effects of systematic errors supports sister-group relationship between Xenacoelomorpha and Ambulacraria. Current Biology *29*, 1818-1826.
3. Nakano, H., *et al.* (2017). A new species of *Xenoturbella* from the western Pacific Ocean and the evolution of *Xenoturbella*. BMC Evolutionary Biology *17*, 245.
4. Nakano, H. (2014). Survey of the Japanese coast reveals abundant placozoan populations in the northern Pacific Ocean. Scientific Reports *4*, 5356.
5. Nakano, H., *et al.* (2013). *Xenoturbella bocki* exhibits direct development with similarities to Acoelomorpha. Nature Communications *4*, 1537.

Kentaro Nakano

Molecular Dynamics and Cellular Function of Cytoskeletons and membranes

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Keywords: **actin, cytokinesis, fission yeast, phagocytosis, *Tetrahymena***

My goal is to understand the molecular mechanisms that control cell behavior, such as cell division, cell morphogenesis, and intracellular trafficking, from the perspective of the cytoskeletons and membranes. These processes are fundamental to life. In my lab, unicellular organisms, including fission yeast and ciliate *Tetrahymena*, are used as models for this purpose. We try to achieve the goal by combining several methodologies, including genetics, cell biology, and biochemical approaches.

Selected publications

1. Morita, R., K. Nakano, Y. Shigeta, & R. Harada. 2020. Molecular Mechanism for the Actin-Binding Domain of α-Actinin Ain1 Elucidated by Molecular Dynamics Simulations and Mutagenesis Experiments. *J. Phys. Chem. B* 124, 8495–8503.
2. Morita, R., M. Takaine, O. Numata, & K. Nakano. 2017. Molecular dissection of the actin-binding ability of the fission yeast α-actinin, Ain1, *in vitro* and *in vivo*. *J. Biochem.* 162, 93-102.
3. Yasuda, T., M. Takaine, O. Numata, & K. Nakano. 2016. Anillin-related protein Mid1 regulates timely formation of the contractile ring in the fission yeast *Schizosaccharomyces japonicus*. *Genes Cells* 21, 594-607.
4. Shiozaki, N.,Nakano, K., Kushida, Y., Noguchi, T.Q., Uyeda, T.Q., Wloga, D., Dave,D., Vasudevan, K.K., Gaertig, J. & Numata, O. (2013) ADF/cofilin is not essential but critically important for actin activities during phagocytosis in *Tetrahymena thermophila*. *Eukaryot. Cell.*, 12, 1080-1086.
5. Nakano, K., M. Toya, A. Yoneda, Y. Asami, A. Yamashita, N. Kamasaki, M. Osumi, & M. Yamamoto. 2011. Pob1 ensures cylindrical cell shape by coupling two distinct Rho signaling events during secretory vesicle targeting. *Traffic* 12, 726-739.

Takuro Nakayama

Molecular Evolution of Unicellular Organisms

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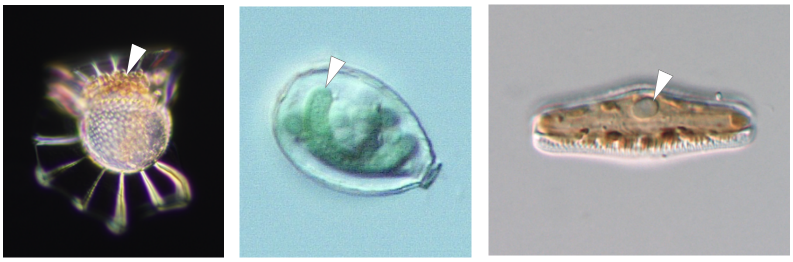
Keywords: **evolution, symbiosis, genome, cyanobacteria, protists**

Symbiogenesis and Diversity of Unicellular Organisms

Looking over the diversity of life, with only some exceptions of a few lineages (animals and plants), most organisms are unicellular. We are researching on the evolution and diversity of unicellular organisms, as an essential factor for a better understanding of life on Earth. Particularly, we focus on symbiotic phenomena among unicellular organisms, and aim to elucidate the evolution of intracellular symbiosis and its ecological role through various nucleic acid sequence analysis methods.



Protists with symbiotic cyanobacteria (arrowheads)

Selected publications

1. Kawachi M, Nakayama T, Kayama M, Nomura M, Miyashita H, et al. (2021) Rappemonads are haptophyte phytoplankton. *Curr Biol* 31: 2395-2403.
2. Sarai C, Tanifuji G, Nakayama T, Kamikawa R, Takahashi K, et al. (2020) Dinoflagellates with relic endosymbiont nuclei as models for elucidating organellogenesis. *Proc Natl Acad Sci USA* 117: 5364–5375.
3. Nakayama T, Nomura M, Takano Y, Tanifuji G, Shiba K, et al. (2019) Single-cell genomics unveiled a cryptic cyanobacterial lineage with a worldwide distribution hidden by a dinoflagellate host. *Proc Natl Acad Sci* 116: 15973–15978.
4. Nakayama T, Kamikawa R, Tanifuji G, Kashiyama Y, Ohkouchi N, et al. (2014) Complete genome of a nonphotosynthetic cyanobacterium in a diatom reveals recent adaptations to an intracellular lifestyle. *Proc Natl Acad Sci* 111: 11407–11412.
5. Nakayama T, Ishida K (2009) Another acquisition of a primary photosynthetic organelle is underway in Paulinella chromatophora. *Curr Biol* 19: R284–R285.

Ryusuke Niwa

Molecular and Physiological Genetics of Insects

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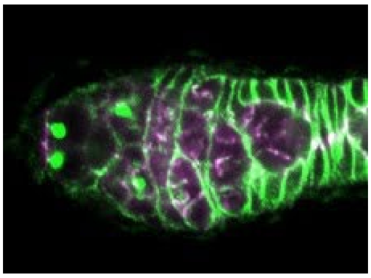
Keywords: **interorgan communication, stem cell, homeostasis, developmental timing, *Drosophila melanogaster***

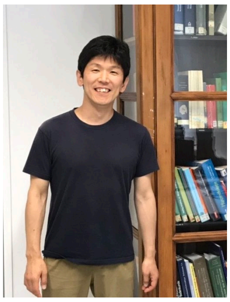


My research interests are in the areas of developmental biology, cell biology, neuroendocrinology, and molecular genetics in insects, particularly the fruit fly *Drosophila melanogaster*. Currently I am interested in understanding how interorgan communication is adaptively involved in regulations of nutrient-dependent developmental plasticity, mating-induced female germline stem cell proliferation, reproductive dormancy, and the host-parasitoid wasp interactions.

Selected Publications

1. Yoshinari Y, Kosakamoto H, Kamiyama T, Hoshino R, Matsuoka R, Kondo S, Tanimoto H, Nakamura A, Obata F, **Niwa R** (2021) The sugar-responsive enteroendocrine neuropeptide F regulates lipid metabolism through glucagon-like and insulin-like hormones in *Drosophila melanogaster*. ***Nature Communications*** 12: 4818.
2. Yoshinari Y, Ameku T, Kondo S, Tanimoto H, Kuraishi T, Shimada-Niwa Y, **Niwa R** (2020) Neuronal octopamine signaling regulates mating-induced germline stem cell increase in female *Drosophila melanogaster*. ***eLife*** 9: e57101.
3. Imura E, Shimada-Niwa Y, Nishimura T, Hückesfeld S, Schlegel P, Ohhara Y, Kondo S, Tanimoto H, Cardona A, Pankratz MJ, **Niwa R** (2020) The Corazonin-PTTH neuronal axis controls systemic body growth by regulating basal ecdysteroid biosynthesis in *Drosophila melanogaster*. ***Current Biology*** 30: 1–10.
4. Koiwai K, Inaba K, Morohashi K, Enya S, Arai R, Kojima H, Okabe T, Fujikawa Y, Inoue H, Yoshino R, Hirokawa T, Kato K, Fukuzawa K, Shimada-Niwa Y, Nakamura A, Yumoto F, Senda T, **Niwa R** (2020) An integrated approach unravels a crucial structural property required for the function of the insect steroidogenic Halloween protein Noppera-bo. ***Journal of Biological Chemistry*** 295: 7154-7167.
5. Ameku T, Yoshinari Y, Texada MJ, Kondo S, Amezawa K, Yoshizaki G, Shimada-Niwa Y, **Niwa R** (2018) Midgut-derived neuropeptide F controls germline stem cell proliferation in a mating-dependent manner. ***PLOS Biology*** 16: e2005004.
6. Komura-Kawa K, Hirota K, Shimada-Niwa Y, Yamauchi R, Shimell M, Shinoda T, Fukamizu A, O'Connor MB, **Niwa R** (2015) The *Drosophila* zinc finger transcription factor Ouija board controls ecdysteroid biosynthesis through specific regulation of *spookier*. ***PLOS Genetics*** 11: e1005712.
7. Shimada-Niwa Y, **Niwa R** (2014) Serotonergic neurons respond to nutrients and regulate the timing of steroid hormone biosynthesis in *Drosophila*. ***Nature Communications*** 5: 5778

Kazuharu Ohashi



Pollinator-mediated evolution of flowers

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Keywords: **floral ecology, foraging, plant-animal interactions, pollination**

Research in our lab covers a wide range of topics, with the common theme that they all involve plant-animal interactions. We use field, indoor experimental, and computational approaches to elucidate how plants have evolved various floral traits and combinations to maximize fitness, mediated through interactions with diverse organisms. We often focus on how flower visitors such as bumble bees and other insects respond to variation in a set of floral traits at different spatial scales, based on foraging economics that has been neglected in the past studies of floral evolution. We have learned from our research that one could effectively predict and test what behavioral responses floral traits have evolved to elicit from animals by incorporating knowledge from behavioral ecology, animal physiology, and animal psychology. To promote such interdisciplinary research in evolutionary ecology, we have collaborated with researchers from diverse fields, such as behavioral ecologists and animal physiologists/psycologists.

Selected publications

1. Ohashi, K., A. Jürgens, and J. D. Thomson (2021) Trade-off mitigation: a conceptual framework for understanding floral adaptation in multispecies interactions. Biological Reviews 96(5): 2258-2280.
2. Ohashi, K. and A. Jürgens (2021) Three options are better than two: compensatory nature of different pollination modes in *Salix caprea* L. Journal of Pollination Ecology (SCAPE Special Issue) 28(2021): 75-90.
3. Ohashi, K., T. T. Makino, and K. Arikawa (2015) Floral colour change in the eyes of pollinators: testing possible constraints and correlated evolution. Functional Ecology 29(9): 1144-1155.
4. Ohashi, K. and J. D. Thomson (2009) Trapline foraging by pollinators: its ontogeny, economics and possible consequences for plants. Annals of Botany 103(9): 1365-1378.
5. Ohashi, K. and T. Yahara (2002) Visit larger displays but probe proportionally fewer flowers: counterintuitive behaviour of nectar-collecting bumble bees achieves an ideal free distribution. Functional Ecology 16(4): 492-503.

Naoki Okamoto

Neuroendocrine mechanisms regulating development and behavior in insects

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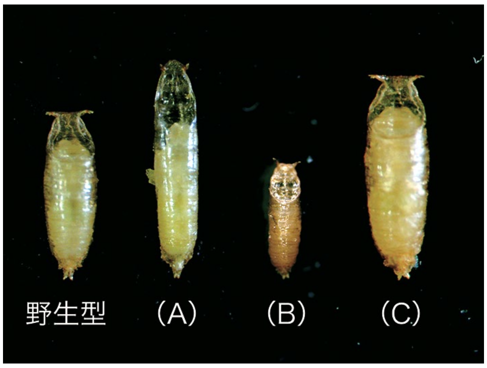
Keywords: **Comparative endocrinology, Insect physiology, Developmental biology, Hormones, Neuropeptides, *Drosophila melanogaster***

We are interested in understanding neuroendocrine mechanisms that control important biological phenomena such as growth, metamorphosis, and behavior during insect development. Mainly by using powerful fruit fly genetic tools, we aim to understand what kind of hormones and receptors are involved in these regulatory mechanisms and how they function at the molecular level.



Genetic regulation of the function of hormones in the fruit fly *Drosophila melanogaster* induces changes in the body size and shape of individuals during development.
(A) Suppression of the neuropeptide that controls body contraction during puparium formation results in elongated pupae.
(B) Suppression of the function of insulin-like peptides significantly suppresses systemic body growth and results in small pupae.
(C) Inhibition of steroid hormone production delays pupation and results in large pupae.

Selected publications

1. **Okamoto, N.** and Yamanaka, N. (2020). Steroid hormone entry into the brain requires a membrane transporter in *Drosophila*. ***Curr. Biol.*** 30:359-366.
2. **Okamoto, N.** et al. (2018). A membrane transporter is required for steroid hormone uptake in *Drosophila*. ***Dev. Cell*** 47: 294-305.
3. **Okamoto, N.** and Nishimura, T. (2015). Signaling from glia and cholinergic neurons controls nutrient-dependent production of an insulin-like peptide for *Drosophila* body growth. ***Dev. Cell*** 35: 295-310.
4. **Okamoto, N.** et al. (2013). A secreted decoy of InR antagonizes insulin/IGF signaling to restrict body growth in *Drosophila*. ***Genes Dev.*** 27: 87-97.
5. **Okamoto, N.** et al. (2012). Conserved role for the Dachshund protein with *Drosophila* Pax6 homolog Eyeless in insulin expression. ***PNAS*** 109: 2406-2411.
6. **Okamoto, N.** et al. (2009). A fat body-derived IGF-like peptide regulates post-feeding growth in *Drosophila*. ***Dev. Cell*** 17: 885-891.

Michiyuki Ono

Plant Developmental Physiology

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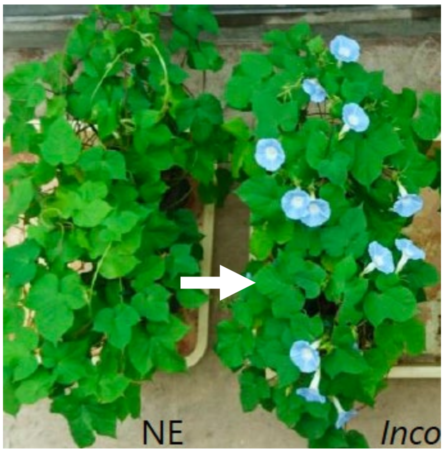
Keywords: **photoperiodism, flowering, making new flower, edible vaccine**

Japanese morning glory (*Ipomoea nil, formally Pharbitis nil*) is one of the plants selected for the national bio-resource project (NBRP) of MEXT Japan. *I. nil* has long been studied as the model plant of the short-day induction of flowering and the garden plant with significant variation. Using CRISPRed mutant lines and wild strains, we are uncovering the mechanisms in photoperiodic regulation of flower-induction and flower-opening.

We are developing a new self-illuminating system for plant that allows the non-invasive detection of changes in gene expression for observing circadian rhythm *etc*. This system also can be applied to make self-illuminating plants that may facilitate understanding GM crop through "Science Arts", like as our GM Yellow flower *etc*.

We have been also collaborating with medical researchers on the developing edible vaccine against to viruses and food poisonings.



CRISPRed Early Flowering

CRISPRed White

GM Yellow

Selected publications

1. Watanaba, K., Oda-Yamamizo, C., Sage-Ono, K., Ohmiya, A. and Ono, M. (2018) Alteration of flower colour in *Ipomoea nil* through CRISPR/Cas9-mediated mutagenesis of carotenoid cleavage dioxygenese 4. Transgenic Research 27: 25-38.
2. Watanabe, K., Kobayashi, A., Endo, M., Sage-Ono, K., Toki, S. and Ono, M. (2017) CRISPR/Cas9-mediated mutagenesis of the *dihydroflavonol-4-reductase-B* (*DFR-B*) locus in the Japanese mornig glory *Ipomoea (Pharbitis) nil.* Scientific Reports 7: 10028.
3. Watanabe, K., Oda-Yamamizo, C., Sage-Ono, K., Ohmiya, A. and Ono, M. (2017) Overexpression of carotenogenic genes in the Japanese morning glory *Ipomoea* (*Pharbitis*) nil. Plant Biotechnology 34: 177-185.
4. Ono, M., Kataoka, M., Yokoyama, M., Ifuku, O., Ohta, M., Arai, S., Kamada, H. and Sage-Ono, K. (2013) Effects of 9,10-ketol-octadecadienoic acid (KODA) application on single and marginal short-day induction of flowering in *Pharbitis nil* cv. Violet. Plant Biotechnology 30: 1-8.

Kazuichi Sakamoto

Molecular Biology of Health and Nutrition

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We have developed a new bioassay system to find and evaluate natural bioactive compounds (e.g. phytochemicals, plant extracts, fermented foods, and animal tissues) that influence health and aging; this novel bioassay system uses nematodes to characterize the bioactivity of natural substances. Because of its biological characteristics (easy culture, short lifespan, and availability of mutants), the nematode is a suitable and well-characterized model for investigating the physiology and mechanisms of human aging and disease. We are using this animal to screen for biomaterials with potential benefits for human health.

To promote health (prevention and amelioration of lifestyle-related diseases) and youth (anti-aging and vitality), we are searching for natural bioactive compounds. We are scientifically evaluating the bioactivity of these substances and developing novel bioactive materials. We are also conducting applied studies to develop functional foods, functional feeds, cosmetics, and medicines.

Phytochemicals such as catechin from tea, resveratrol from red grapes, and hydroxytyrosol from olives are famous bioactive compounds that can act against aging and help protect against lifestyle-related diseases. We are using these materials in functional foods, cosmetics, medicines, and other materials to promote health and slow aging.

Select Publications

1) Drira, R., Chen, S., and Sakamoto, K. (2011). Oleuropein and hydroxytyrosol inhibited adipocyte differentiation in 3T3-L1 cells. Life Sciences, *89*, 708-716.
2) Kim, H., and Sakamoto, K. (2011). (-)-Epigallocatechin gallate suppresses adipocyte differentiation through the MEK/ERK and PI3K/AKT pathways. Cell Biology International, *36,* 147-153.
3) Shintani, H., Furuhashi, T., Hano, H., Matsunaga, M., Usumi, K., Shudo, N., and Sakamoto, K. (2011). Physiological Effects of Salmon Milt Nucleoprotein on Movement, Stress Tolerance and Lifespan of *C. elegans.* Food and Nutrition Sciences, *3*, 48-54.
4) Nomura, T., Horikawa, M., Shimamura, S., Hashimoto, T., and Sakamoto, K. (2010). Fat accumulation in *Caenorhabditis elegans* is mediated by SREBP homolog SBP-1. Genes and Nutrition, *5*, 17-27.
5) Kamon, M., Zhao, R., and Sakamoto, K. (2010). Green tea polyphenol (-)-epigallocatechin gallate suppressed the differentiation of murine osteoblast MC3T3-E1. Cell Biology International, *34*, 109-116.

Keisuke Sakurai

Neurophysiology

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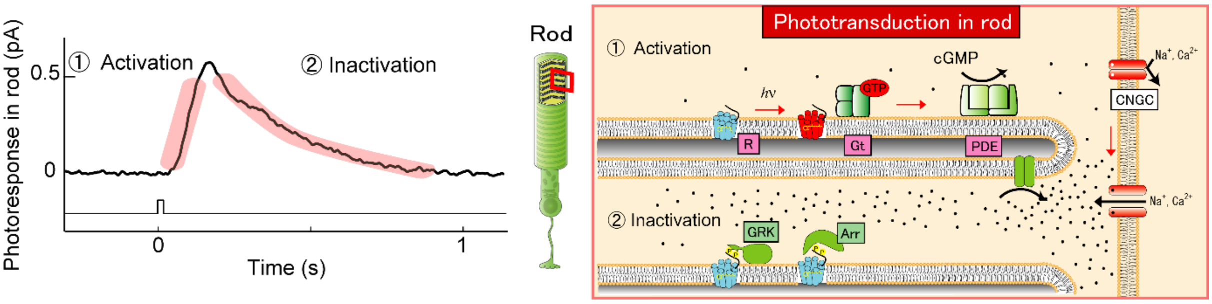
Keywords: **photoreceptor, retina, mouse, electrophysiology, opsin**

In vertebrate species, most ambient information is derived through photoreceptors where light is absorbed and signaled to the nervous system. Visual perception initiates with light absorption by rod and cone photoreceptors in the retina, which mediate dim light vision and bright light vision, respectively. In addition to the vision, light reception by inner retinal neurons or extraocular photoreceptors is thought to be of great importance to animal behaviors such as circadian phase shift and body colour change. Our research aims to elucidate the underlying light perception mechanism by which absorbed photons are converted into an electrical response and signaled to the brain. To achieve this goal, we primarily use electrophysiological techniques in combination with genetically manipulated animals, which is powerful to elucidate molecular mechanisms in neurons.



Rod and cone photoreceptors employ homologous or sometimes even identical proteins in their phototransduction cascades, indicating that the same principles of phototransduction are likely to exist. Despite these similarities, rods and cones exhibit important functional differences, with still largely unknown origins.

Selected publications

1. Sakurai, K. : Physiological characteristics of photoreceptors in the lamprey, *Lethenteron Japonicum*" *Zoological Science*, 34(4), 326~330, 2017
2. Kojima, K., Y. Matsutani , T. Yamashita , M. Yanagawa , Y. Imamoto , Y. Yamano , A. Wada , O. Hisatomi , K. Nishikawa , K. Sakurai , & Y. Shichida: Adaptation of cone pigments found in green rods for scotopic vision through a single amino acid mutation. *Proceedings of the National Academy of Sciences*,114(21), 5437~5442, 2017
3. Sakurai, K., F. Vinberg, T. Wang, J. Chen, & V. J. Kefalov:The Na(+)/Ca(2+), K(+) exchanger 2 modulates mammalian cone phototransduction.*Scientific Reports.* 6:32521, 2016
4. Sakurai, K., Chen, J., Khani, S. C., & V. J. Kefalov: Regulation of mammalian cone phototransduction by recoverin and rhodopsin kinase.*Journal of Biological Chemistry,* 290(14), 9239~9250, 2015

Yasunori Sasakura

Developmental Genetics

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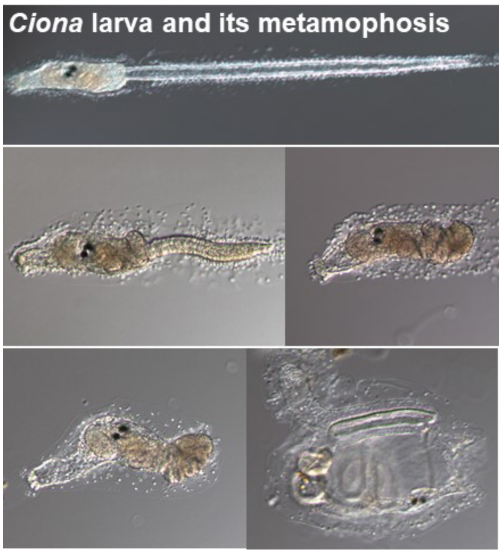
Keywords: **chordate, *Ciona*, metamorphosis, neuron, evolution**



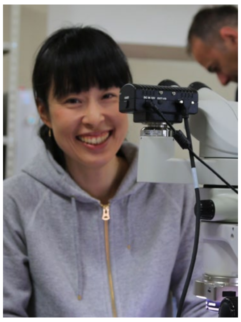
Our group is interested in developmental mechanisms of the marine invertebrate chordate *Ciona intestinalis*. *Ciona* is the model species of tunicate ascidians. Among invertebrates, tunicate is the closest living relative of vertebrate. Studies of tunicates are thus necessary for elucidating evolution of vertebrates. In *Ciona*, tools for investigating molecular mechanisms have been established, such as well-annotated genome sequence and embryological techniques. We have established the methods for manipulating genomes and genes in *Ciona*, as exemplified by transposon-based transgenesis and genome editing. Using these techniques, we are addressing mechanisms underlying development of *Ciona*.

We currently focus on metamorphosis. Swimming tadpole larvae of *Ciona* complete metamorphosis within a few days, and they start sessile adult life. *Ciona* larvae possess only 177 neurons. The simple nervous system regulates complicated metamorphic processes. We are interested in the molecular and cellular mechanisms underlying metamorphosis; how signaling molecules and neurotransmitters regulate destruction of larval organs and construction of adult organs to complete this event. By comparing mechanisms of metamorphosis between animals, we aim to understand the evolution of metamorphic events among animals.

Selected publications

1. Yamaji, S. et al. (2020). Orchestration of the distinct morphogenetic movements in different tissues drives tail regression during ascidian metamorphosis. *Developmental Biology* 465:66-78.
2. Hozumi, A. et al. (2020). GABA-Induced GnRH Release Triggers Chordate Metamorphosis. *Current Biology* 30:1555-1561.
3. Yoshida, K. et al. (2017). Hox-mediated endodermal identity patterns pharyngeal muscle formation in the chordate pharynx. *Development* 144:1629-1634.
4. Matsunobu, S. and Sasakura, Y. (2015). Time course for tail regression during metamorphosis of the ascidian Ciona intestinalis. *Developmental Biology* 405:71-81.
5. Treen, N. et al. (2014). Tissue-specific and ubiquitous gene knockouts by TALEN electroporation provide new approaches to investigating gene function in *Ciona*. *Development* 141:481-487.

Yukie Sato



Behavioural & Evolutionary Ecology

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Keywords: **sexual selection, social behaviour, speciation, conservation biology, biological control, Acarology**

The general aim of my research is to reveal the mechanisms of ecological diversification at the level of species and populations, as well as speciation mechanisms. Furthermore, I deal with behavioral variations in different individuals of the same population. In particular, I focus on social behavior and mating behavior in spider mites. Spider mites are small arthropod herbivores less than 1 mm in length. They are good model organisms because they complete their development (egg to adult) in a short period (ca. 5 - 20 days under optimal conditions) and they can be mass-reared in small spaces. These advantages allow investigation of the following projects:

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- Alternative reproductive tactics in spider mite males
- Speciation in haplodiploid spider mites
- Kin selection and lethal male fights
- Reproductive interference between invasive and native spider mites
- Biological control for invasive bamboo mites in Europe

Selected publications

1. Sato, Y., Fujiwara, S., Egas, M., Matsuda, T. and Gotoh, T. (2021). Patterns of reproductive isolation in a haplodiploid mite, *Amphitetranychus viennensis*: prezygotic isolation, hybrid inviability and hybrid sterility. *BMC Ecology and Evolution* 21: 177.
2. Sato, Y., Tsuda, Y., Sakamoto, H., Egas, M., Gotoh, T., Saito, Y., Zhang, Y.-X., Lin, J.-Z., Chao, J.-T. and Mochizuki, A. (2019). Phylogeography of lethal male fighting in a social spider mite. *Ecology and Evolution* 9: 1590-1602.
3. Sato, Y., Sakamoto, H., Gotoh, T., H., Saito, Y., Chao, J.-T., Egas, M. and Mochizuki, A. (2018). Patterns of reproductive isolation in a haplodiploid – strong post-mating, prezygotic barriers among three forms of a social spider mite. *Journal of Evolutionary Biology* 31: 866-881.
4. Sato, Y., Sabelis, M.W. and Egas, M. (2014). Alternative male mating behaviour in the two-spotted spider mite: dependence on age and density. *Animal Behaviour* 92: 125-131.
5. Sato, Y., Egas, M., Sabelis, M.W., and Mochizuki, A. (2013) Male-male aggression peaks at intermediate relatedness in a social spider mite. Ecology and Evolution 3: 2661-2669.

Kyoichi Sawamura

Mechanisms of Speciation in Drosophila

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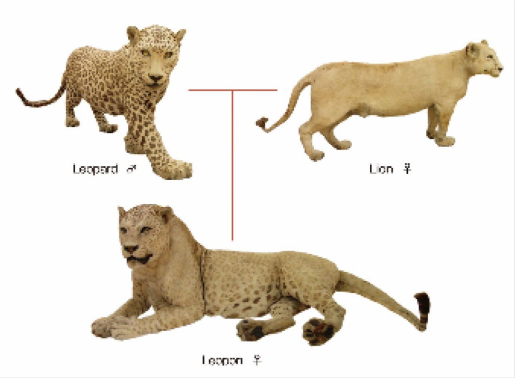
Keywords: **reproductive isolation, hybrid incompatibility, interspecific introgression, natural population, courtship/copulatory behavior**

Do you know what an interspecific hybrid is? Mules from mares and donkeys, leopons from lionesses and leopards… Interspecific hybrids are rare in nature; most of them are sterile and therefore cannot produce descendants. If these hybrids were not rare, then biological species would become fused and lost from the world. In other words, species exist because of reproductive isolation: the origin of new species is completed by acquiring reproductive isolation between populations. Therefore, speciation is a major driving force of evolution. The purpose of our research is to elucidate the genetic mechanisms of speciation.



Male leopons are sterile.
Specimen: National Museum of Nature and Science, Tokyo
Photo: K. Maehara & T. Murata; Courtesy of S. Kawada

Our model organism is Drosophila. Genomic sequencing has been completed in ~50 Drosophila species. The biodiversity of this genus is spectacular: 3950 extant species (and 12 fossil species) have been described in the Drosophilidae (Brake & Bächli, 2008). Furthermore, Drosophila has many crossable sibling species pairs and can be used to provide useful experimental systems for investigating the genetic mechanisms of speciation.

Selected publications

1. Onuma, M. *et al*. (2021) Genital coupling and copulatory wounding in the *Drosophila auraria* species copmlex (Diptera: Drosophilidae). *Biol J Linnean Soc* in press
2. Hama, Y. *et al*. (2020) Long-term coexistence of a hybridization-derived population of *Drosophila parapallidosa* with closely related *Drosophila ananassae* (Diptera: Drosophilidae). *Entomol Sci* 23: 405-415.
3. Hirai, K. *et al*. (2018) Genetic analysis of *Elys* mutations in *Drosophila* show maternal-effect lethality and interactions with *Nucleoporin* genes. *G3* 8: 2421-2431.
4. Shirata, M. *et al*. (2014) Allelic asymmetry of the *Lethal hybrid rescue* (*Lhr*) gene expression in the hybrid between *Drosophila melanogaster* and *D. simulans*: confirmation by using genetic variations of *D. melanogaster*. *Genetica* 142: 43-48.
5. Maehara, K. *et al*. (2012) Genetic dissection of *Nucleoporin 160* (*Nup160*), a gene involved in multiple phenotypes of reproductive isolation in *Drosophila*. *Jpn J Genet* 87: 99-106.

Kogiku Shiba

Cell Biology

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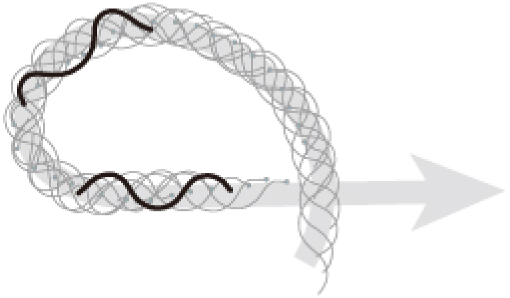
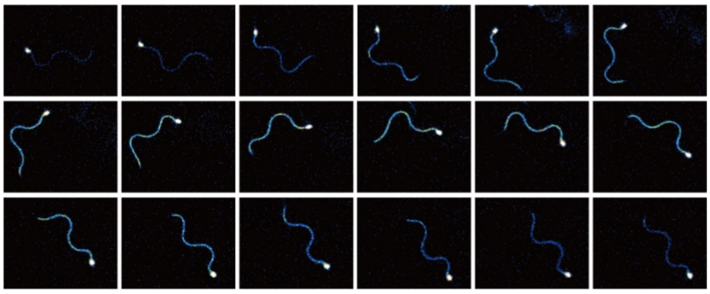
Keywords: **sperm, flagella, cilia, fertilization, cell motility**

The structures of cilia and flagella have been highly conserved through evolution and play important roles in sperm motility, embryonic locomotion, current generation in epidermal tissues such as the oviduct and trachea, and cell signal reception. We are using the embryos or sperm of marine invertebrates such as tunicates, sea urchins, fishes and snails to study the regulatory mechanism of ciliary and flagellar movement. Research topics are a signaling pathway in sperm motility activation and chemotaxis to egg, and a regulatory mechanism of flagellar and ciliary waveforms. To analyze motility and waveforms in cilia and flagella we are using a high-speed camera, a stroboscopic lighting system, auto-tracking software, and a Ca^{2+}-imaging system.





Selected publications

1. Sasaki K†, Shiba K†, Nakamura A†, Kawano N, Satouh Y, Yamaguchi H, Morikawa M, Shibata D, Yanase R, Jokura K, Nomura M, Miyado M, Takada S, Ueno H, Nonaka S, Baba T, Ikawa M, Kikkawa M, Miyado K, Inaba K. Calaxin is required for cilia-driven determination of vertebrate laterality. ***Commun Biol*** 2:226. (2019) †equal contribution.
2. Shiba K, Inaba K. Inverse relationship of Ca^{2+}-dependent flagellar response between animal sperm and prasinophyte algae. ***J Plant Res*** 130(3):465-473. (2017)
3. Miyata H, Satouh Y, Mashiko D, Muto M, Nozawa K, Shiba K, Fujihara Y, Isotani A, Inaba K, Ikawa M. Sperm calcineurin inhibition prevents mouse fertility with implications for male contraceptive. ***Science***, 350(6259):442-5. (2015)
4. Shiba K, Inaba K. Distinct roles of soluble and transmembrane adenylyl cyclases in the regulation of flagellar motility in *Ciona* sperm. ***Int J Mol Sci*** 15(8):13192-208. (2014)
5. Shiba K, Shibata D, Inaba K. Autonomous changes in the swimming direction of sperm in the gastropod *Strombus luhuanus*. ***J Exp Biol*** 217(Pt 6):986-96. (2014)

Yasuteru Shigeta

Theoretical biophysics

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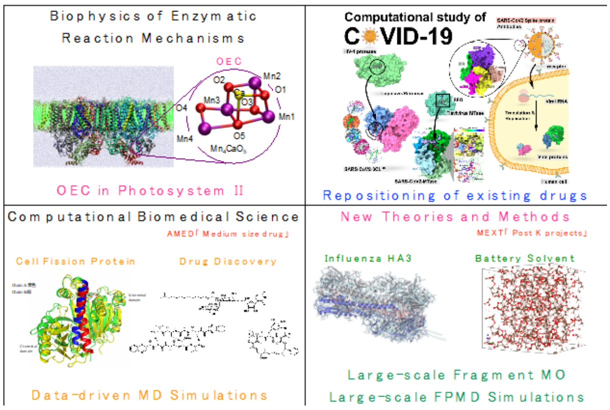
Keywords: **Theoretical calculations, Drug Discovery, Bioenergetics**

Phenomena expressing in life are dominated by a series of chemical reactions driven by macromolecules such as proteins, nucleic acids, lipids, and sugars. To understand the life, the fundamental molecular mechanisms of biological phenomena should be clarified by investigating the electronic structure changes and the spatial rearrangements of atoms accompanied by the chemical reactions. In our group, dynamic structure-function correlations of biomolecules are explored by using theoretical calculations such as quantum chemical and classical molecular dynamics simulations.

Using these methods, we have investigated catalytic chemical reaction mechanisms in bioenergy conversion processes such as electron transport chain, photosystems, and hydrogenase at microscopic level. In particular, the stability of X-ray and/or neutron crystallographic structures was examined by using quantum chemical calculations, and then electron transport pathways in a given protein were estimated to specify the detailed mechanism. We have also conducted the drug discovery researches on antiviral candidates towards Dengi, Zika, and SARS-Cov-2 viruses. The use of supercomputers enables us to examine protein-drug interaction more precisely and screen the potential drugs from many candidates.



Selected publications

1. A. Kimura, H. Kitoh-Nishioka, Y. Shigeta, S. Ito, (2021) Comparison of Light Harvesting Mechanisms of Photosynthetic Type-I Reaction Centers of Heliobacteria with Photosystem I. Pigments Site Energy Distribution and Exciton States", *J. Phys. Chem. B*, 125(15), 3727-3738.
2. T. Murakawa, K. Kurihara, M. Shoji, C. Shibazaki, T. Sunami, T. Tamada, N. Yano, T. Yamada, K. Kusaka, M. Suzuki, Y. Shigeta, R. Kuroki, H. Hayashi, T. Yano, K. Tanizawa, M. Adachi, T. Okajima (2020), Neutron crystallography of copper amine oxidase reveals a keto form cofactor and proton sharing, *Proc. Nat. Acad. Sci. U.S.A.* 117, 10818-10824.
3. B. Nutho, P. Mahalapbutr, K. Hengphasatporn, N.C. Pattaranggoon, N. Simanon, Y. Shigeta, S. Hannongbua, T. Rungrotmongkol (2020) Why are lopinavir and ritonavir effective against the newly emerged Coronavirus 2019?: Atomistic insights into the inhibitory mechanisms, *Biochemistry*, 59(18), 1769-1779.

Yuko Shimada

Developmental Biology and Genetics

詳しい研究内容と業績はHPへGO

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https://researchmap.jp/yukoshimada
Keywords: Drosophila melanogaster, ecdysteroid biosynthesis, neuroendocrine system, steroid hormone

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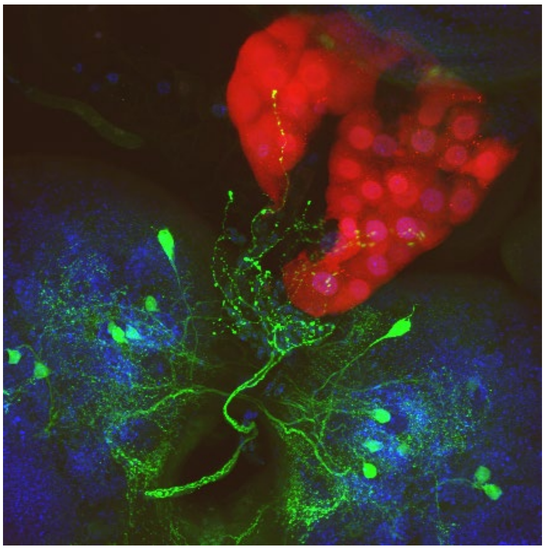
Nutrient-Neuro-endocrine Mechanisms of Maturation in *Drosophila melanogaster*

How do the organisms know their appropriate timing of maturation from the juvenile to the adult? One of the key regulatory mechanisms is steroid hormone biosynthesis in response to various environmental conditions. We have been studying the neuronal regulatory mechanism of steroid hormone biosynthesis in the fruit fly *Drosophila melanogaster*. By using molecular genetics, cell biological analysis, and live-imaging system, we are trying to understand how the genetic program of organisms is flexibly coordinated to accomplish the development from eggs to individuals. Anyone and everyone are welcome to share our scientific interests in the lab!



Selected publications:

1. **The Drosophila Individual Activity Monitoring and Detection System (DIAMonDS)**
   Seong KH, Matsumura T, **Shimada-Niwa Y**, Niwa R, Kang Siu.
   eLife 9:e58630, Nov, 2020

2. **The Corazonin-PTTH Neuronal Axis Controls Systemic Body Growth by Regulating Basal Ecdysteroid Biosynthesis in *Drosophila melanogaster*.**
   Imura E, **Shimada-Niwa Y**, Nishimura T, Hückesfeld S, Schlegel P, Ohhara Y, Kondo S, Tanimoto H, Cardona A, Pankratz MJ, Niwa R.
   Current biology 30(11) 2156-2165, Jun 8, 2020

3. **Protocols for Visualizing Steroidogenic Organs and Their Interactive Organs with Immunostaining in the Fruit Fly *Drosophila melanogaster*.**
   Imura E, Yoshinari Y, **Shimada-Niwa Y**, Niwa R.
   Journal of visualized experiments 122, e55519, Apr, 2017

Takashi Shiratori

Phylogeny and evolution of microbes

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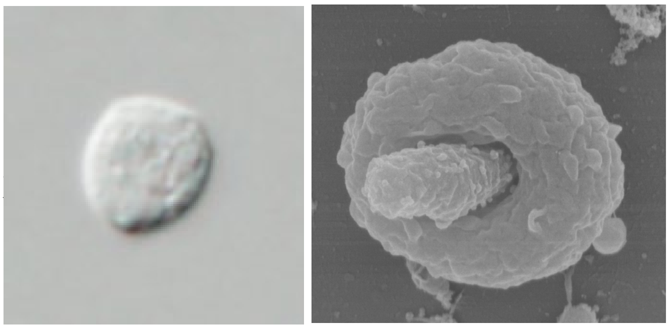
Keywords: **protist, molecular phylogeny, evolution, prokaryote, microbiology**

Most of the phylogenetic diversity is dominated by prokaryotes and unicellular eukaryotes. However, most of them have not been adequately studied due to the lack of culture strains. To clarify the whole picture of the tree of life and the process of the evolution, it is necessary to discover unknown microorganisms from the environment and study them.

We screen novel unicellular organisms from various environments, isolate and cultivate them, and analyze their fine structures using electron and fluorescence microscopy and genome and transcriptome data to clarify the early evolution, diversity, and phylogenetic relationships of life on the earth.



Light and electron micrographs of *Candidatus* Uab amorphum. We discovered this bacterium in the Republic of Palau in 2015 and showed it performs cell uptake like a eukaryote. Because of this unusual feature, this bacterium is important for revealing the early evolution of eukaryotes.

Selected publications

1. Shiratori, T. Yabuki, A. Ishida, K. (2020) Morphology, Ultrastructure, and Phylogeny of Two Novel Species of *Ventrifissura* (*V. oblonga* n. sp. and *V. velata* n. sp., Thecofilosea, Cercozoa). *Protist*, 171:125731.
2. Shiratori, T. Shigekatsu, S. Kakizawa, Y. Ishida, K (2019) Phagocytosis-like cell engulfment by a novel planctomycete bacterium. *Nature Communicarions*, 10:5529.
3. Shiratori, T. Fujita, S. Shimizu, T. Nakayama, T. Ishida, K. (2017) *Viridiuvalis adhaerens* gen. et sp. nov., a novel colony-forming chlorarachniophyte. *Journal of Plant Research*, 130:999-1012.
4. Shiratori, T. Thakur, R. Ishida, K. (2017) *Pseudophyllomitus vesiculosus* (Larsen and Patterson 1990) Lee, 2002, a poorly studied phagotrophic biflagellate is the first characterized member of stramenopile environmental clade MAST-6. Protist, 168:439-451.
5. Shiratori, T. Ishida, K. (2016) A new heterotrophic cryptomonad: *Hemiarma marina* n. g., n. sp. The Journal of Eukaryotic Microbiology, 63:804-812.

Hiroshi Shitara

Molecular Genetics of Mitochondrial DNA in Mammals

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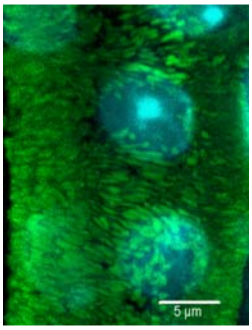
Mitochondria play important roles in cell functions such as ATP production and apoptosis. Mammalian mitochondria contain multiple copies of approximately 16-kbp double-stranded DNA with a closed circular conformation. Two genetic characteristics that are major specific phenomena observed during the inheritance of mitochondrial DNA (mtDNA) are maternal inheritance and rapid segregation. We have been investigating the mode of mtDNA transmission in a mouse model.

Our particular focus is the genetic machinery of rapid segregation. Usually, 1000 to 10,000 copies of mtDNA molecules exist in a single somatic cell, and the mutation rate of mtDNA is higher than that of nuclear DNA. Thus, mtDNA is thought to show heteroplasmy: in other words, more than one type of mtDNA exists in a cell. However, rapid shifts in mtDNA variants between generations have been observed in several species, and mtDNA homoplasmy is maintained in most individuals. Our group previously proposed models for the mitochondrial bottleneck effect, which is a concept for the genetic machinery of rapid segregation. We are currently investigating mtDNA and mitochondrial segregation by using transgenic mouse strains.



Confocal image of mitochondria in kidney from mtGFP-Tg mice. Mitochondria were visualized by using green fluorescent protein. Nuclei are counterstained with DAPI (blue).

Select Publications

1. Yamaguchi, J., Nishiyama, S., Shimanuki, M., Ono, T., Sato, A., Nakada, K., Hayashi, J., Yonekawa, H., and Shitara, H. (2012). Comprehensive application of an mtDsRed2-Tg mouse strain for mitochondrial imaging. Transgenic Res *21*, 439-447.
2. Nishiyama, S., Shitara, H., Nakada, K., Ono, T., Sato, A., Suzuki, H., Ogawa, T., Masaki, H., Hayashi, J., and Yonekawa, H. (2010). Over-expression of Tfam improves the mitochondrial disease phenotypes in a mouse model system. Biochem Biophys Res Commun *401*, 26-31.
3. Cao, L., Shitara, H., Sugimoto, M., Hayashi, J., Abe, K., and Yonekawa, H. (2009). New evidence confirms that the mitochondrial bottleneck is generated without reduction of mitochondrial DNA content in early primordial germ cells of mice. PLoS Genet *5*, e1000756.
4. Cao, L., Shitara, H., Horii, T., Nagao, Y., Imai, H., Abe, K., Hara, T., Hayashi, J., and Yonekawa, H. (2007). The mitochondrial bottleneck occurs without reduction of mtDNA content in female mouse germ cells. Nat Genet *39*, 386-390.

Akiko Shoji

Behavioural Ecology

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Keywords: **life-history, foraging, migration, toxicology, biologging**

My research focuses on many facets of behavioural ecology, dealing with spatial ecology, life-history, individuality, ecotoxicology and population dynamics. I study the interactions between prey and predator as well as individuality and fitness mainly on top avian predators such as colonial seabirds and raptors, addressing a range of questions from understanding the consequences of migratory strategies on individual fitness and population dynamics, to investigating foraging strategies in sympatric species and incubation strategies from an ecophysiology point of view, the mechanism of carry-over effects in migratory species. I recently expanded my research interest to include understanding the mechanism of biotransport through behaviour and the extent of the consequences on trans-ecosystems. I am currently leading projects on seabirds and raptors breeding in the Pacific Ocean. I am collaborating with various researchers and NGOs which lead some of my research results to help making conservation policies in the Atlantic Ocean.

Tufted puffins breeding at Middleton Island, Alaska, USA where we are currently studying wintering movements and behaviour with bio-logging techniques. Through collaboration with Dr. Kyle Elliott at McGill University in Montréal, Dr. Stéphane Aris-Brosou at University of Ottawa in Canada, and Dr. Anntte Fayet at Oxford University, and many more cannot be listed all here, we are tagging several seabirds in the Pacific Ocean.

Selected publications

1. Shoji et al. (2021) Geolocators link marine mercury with levels in wild seabirds throughout their annual cycle: consequences for trans-ecosystem biotransport. Environmental Pollution 284: 117035
2. Shoji, A.et al.(2019) Biotransport of metallic trace elements from marine to terrestrial ecosystems by seabirds. Environmental Toxicology & Chemistry 38: 106-114.
3. Van-Tatenhove, A. et al. (2018) Streaked shearwater Calonectris leucomelas moonlight avoidance in response to low aerial predation and effects of wind speed and direction on colony attendance. Marine Ornithology 46: 177-185
4. Shoji, A.et al.(2016) Physiological constraints scale with body mass during dives in auks: a comparative analysis. Comparative Biochemistry and Physiology 196:54-60
5. Shoji, A.et al.(2015) Breeding phenology and winter activity predict subsequent breeding success in a trans-global migratory seabird. Biology Letters 11: 20150671

Takuya Suzaki

Plant Molecular Biology, Plant-microbe symbiosis

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Keywords: root nodule symbiosis, legume, environmental response, transcription factor, organ-to-organ communication

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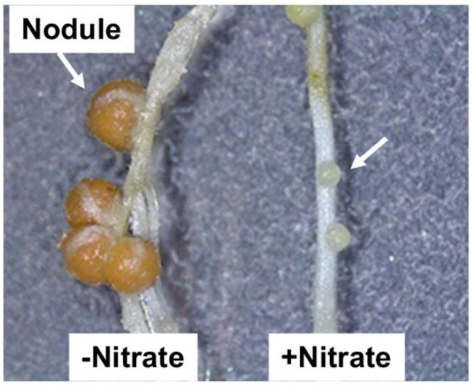

Using genetic and molecular biological approaches, we are trying to elucidate molecular mechanisms underlying plant-microbe symbiosis with a model legume *Lotus japonicus* and nitrogen-fixing bacteria called rhizobia. We are particularly interested in to reveal the molecular mechanisms by which plants control root nodule symbiosis in response to the change of environmental factors. Examples of research projects: "Studies on transcription factors that regulate root nodule symbiosis", "Organ-to-organ communication to regulate root nodule symbiosis", "Control of root nodule symbiosis in response to nutritional environment",etc.

Selected publications

1. Nishida, H., Nosaki, S., Suzuki, T., Ito, M., Miyakawa, T., Nomoto, M., Tada, Y., Miura, K., Tanokura, M., Kawaguchi, M. and *Suzaki, T. (2021) Different DNA-binding specificities of NLP and NIN transcription factors underlie nitrate-induced control of root nodulation. ***Plant Cell*** 33:2340-2359.
2. *Suzaki, T., Takeda, N., Nishida, H., Hoshino, M., Ito, M., Misawa, F., Handa, Y., Miura, K. and Kawaguchi, M. (2019) *LACK OF SYMBIONT ACCOMODATION* controls intracellular symbiont accommodation in root nodule and arbuscular mycorrhizal symbiosis in *Lotus japonicus*. ***PLOS Genet.*** 15:e1007865.
3. Nishida, H., Tanaka, S., Handa, Y., Ito, M., Sakamoto, Y., Matsunaga, S., Betsuyaku, S., Miura, K., Soyano, T., Kawaguchi, M. and *Suzaki, T. (2018) A NIN-LIKE PROTEIN mediates nitrate-induced control of root nodule symbiosis in *Lotus japonicus*. ***Nat. Commun.*** 9:499.
4. *Suzaki, T., Ito, M., Yoro, E., Sato, S., Hirakawa, H. Takeda, N. and Kawaguchi, M. (2014) Endoreduplication-mediated initiation of symbiotic organ development in *Lotus japonicus*. ***Development*** 141:2441-2445.
5. *Suzaki, T., Yano, K., Ito, M., Umehara, Y., Suganuma, N. and Kawaguchi, M. (2012) Positive and negative regulation of cortical cell division during root nodule development in *Lotus japonicus* is accompanied by auxin response. ***Development*** 139:3997-4006.

Daichi G. Suzuki

Evolutionary Behavioral Neurobiology

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https://researchmap.jp/suz_dg?lang=en

Keywords: **cyclostomes, hagfish, lamprey, brain, evolution**

Evolution of neural circuits, behavior, and mind of basal vertebrates

Cyclostomes (lampreys and hagfish) are the only surviving jawless fishes, the earliest vertebrates. As being basal-most group of vertebrates, they provide crucial information for understanding early evolution of the vertebrates. To elucidate the evolutionary origin of vertebrate brain, behavior, and mind, we take an integrative approach combining molecular biology, neuroscience, bioinformatics, and so on.

Although lampreys and hagfish form a monophyletic group, they show different lifestyles and lineage-specific adaptations. As lampreys transform from riverbed-burrowing larvae to actively swimming adults, their visual system shows stepwise development from immature photoreception to matured image-forming vision. In contrast, hagfish live in the deep sea and thus show a degenerate visual system. Instead, they have a sophisticated olfactory system and an enlarged pallium, the brain region homologous to the mammalian cortex. We focus on these peculiarities to reconstruct ancestral conditions.

Selected publications

1. Suzuki, D. G., Wada, H., and Higashijima, S. (2021). Generation of knock-in lampreys by CRISPR-Cas9-mediated genome engineering. *Scientific Reports* 11:19836.
2. Suzuki, D. G. (2021). Consciousness in jawless fishes. *Frontiers in Systems Neuroscience* 15:751876.
3. Suzuki, D. G., Pérez-Fernández, J., Wibble, T., Kardamakis, A. A., and Grillner, S. (2019). The role of the optic tectum for visually evoked orientating and evasive movements. *Proc. Natl. Acad. Sci. USA* 116(30):15272–15281.
4. Suzuki, D. G. and Grillner, S. (2018). The stepwise development of the lamprey visual system and its evolutionary implications. *Biological Reviews* 93:1461–1477.
5. Suzuki, D. G., Murakami, Y., Escriva, H., and Wada, H. (2015). A comparative examination of neural circuit and brain patterning between the lamprey and amphioxus reveals the evolutionary origin of the vertebrate visual center. *Journal of Comparative Neurology* 523(2):251–261.

Iwane Suzuki

Mechanisms of signal perception by sensory kinases in photosynthetic organisms

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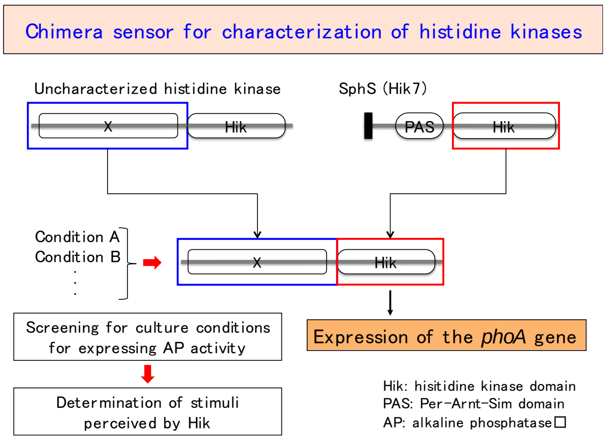
Living organisms recognize changes in their environmental conditions and regulate their gene expression to acclimate to such changes. However, the molecular mechanisms of signal perception by cellular sensors are not yet well characterized. We developed a way to construct chimeric sensors, which contain a signal-recognition domain from an unknown sensory kinase and a kinase domain from the well-studied phosphate-deficient sensor, SphS, from the cyanobacterium *Synechocystis* sp. PCC 6803. This system is a powerful tool for studying the functions of sensory kinases and the molecular mechanisms of signal perception, as well as for developing artificial switches to regulate gene expression in systems biology.



Construction of a chimeric sensory kinase in *Synechocystis*. A phosphate sensor, SphS, regulates expression of the *phoA* gene encoding alkaline phosphatase (AP). The chimeric sensory kinase containing the signal-recognition domain of an uncharacterized kinase and the kinase domain of SphS regulate the expression of the *phoA* gene under the conditions perceived by the uncharacterized sensory kinase.

Select Publications

1. Y. Shimura, Y. Shiraiwa, I. Suzuki (2012) Characterization of the subdomains in the amino-terminal region of histidine kinase Hik33 in the cyanobacterium *Synechocystis* sp. PCC 6803, *Plant Cell Physiol.*, **53**, 1255–1266
2. J.G. Rowland, X. Pang, I. Suzuki, N. Murata, W.J. Simon, A.R. Slabas (2010) Identification of components associated with thermal acclimation of photosystem II in *Synechocystis* sp. PCC6803, *PLoS One* **5**, e10511
3. S. Kimura, Y. Shiraiwa, I. Suzuki (2009) Function of the N-terminal region of the phosphatesensing histidine kinase, SphS, in *Synechocystis* sp. PCC 6803, *Microbiol.* **155**, 2256-2264
4. T. Sakayori, Y. Shiraiwa, I. Suzuki (2009) A *Synechocystis* homolog of SipA protein, Ssl3451, enhances the activity of the histidine kinase Hik33, *Plant Cell Physiol.* **50**, 1439-1448
5. Y. Kanesaki, H. Yamamoto, K. Paithoonrangsarid, M. Shoumskaya, I. Suzuki, H. Hayashi, N. Murata (2007) Histidine kinases play important roles in the perception and signal transduction of H_2O_2 in the cyanobacterium, *Synechocystis*. *Plant J.* **49**, 313-324

Kenta Tanaka

Evolutionary & Conservation Ecology

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Keywords: **plant, plants-related interaction, mountain, grassland, forest**

How has biodiversity in front of us evolved and how could it be conserved? To answer this question, we conduct evolutionary & conservation ecology of plants and interacting organisms at the genetic- to community- levels in mountains, grasslands and forests.

In various model organisms, more than half of genes have no known function, and interest has focused on the role of those genes in field ecosystems. *Arabidopsis kamchatica*, closely related to the plant model *A. thaliana*, adapts to an elevation of 0 ~ 3000 m, and its life span evolved to vary greatly depending on elevation. We are identifying the "life span gene" and related environmental adaptation.

Grasslands that have been for > 300 years remain in ski resorts, reservoirs and mountain castles. Their legacy effects maintain high biodiversity in plants, butterflies, moths, beetles and fungi. In the Sugadaira grasslands, genetic resources over ¥ 10,000,000,000 are being lost, unknown and unused. The results of this research are being used to conserve biodiversity through regional cooperation.

Selected publications

1. Inoue, T., Yaida, Y. A., …., Ushimaru, A. & Kenta, T. (2021). The effects of temporal continuities of grasslands on the diversity and species composition of plants. Ecological Research, 36:24-31.
2. Toju, H., Kurokawa, H., & Kenta, T. (2019). Factors influencing leaf-and root-associated communities of bacteria and fungi across 33 plant orders in a grassland. Frontiers in Microbiology 10:241
3. Timothy Paape, …., Kenta Tanaka, Tomoaki Nishiyama, Renat Sabirov, Jun Sese, Kentaro K. Shimizu (2018) Patterns of polymorphism and selection in the subgenomes of the allopolyploid Arabidopsis kamchatica. Nature communication 9(1): 3909
4. T. Kenta, A. Yamada & Y. Onda. 2011. Clinal variation in flowering time and vernalisation requirement across a 3000-m altitudinal range in perennial *Arabidopsis kamchatica* ssp. *kamchatica* and annual lowland subspecies *kawasakiana*. Journal of Ecosystem and Ecography S6:1-10. doi:10.4172/2157-7625.S6-001
5. T. Kenta, N. Inari, T. Nagamitsu, K. Goka, & T. Hiura. 2007. Commercialized European bumblebee can cause pollination disturbance: an experiment on seven native plant species in Japan. Biological Conservation 134:298-309

Yukihiko Toquenaga

Population Biology

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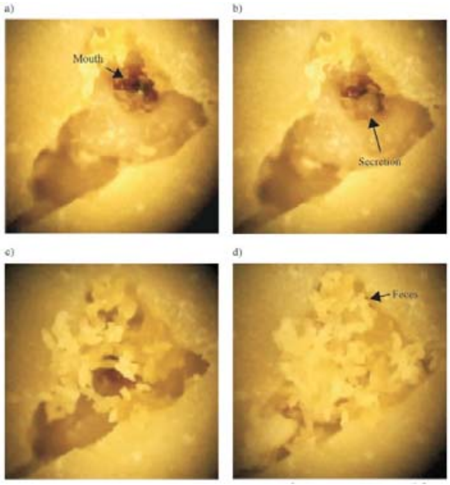
I am an associate professor in the Doctoral Program in Biological Sciences at the University of Tsukuba, where I teach ecology, theoretical biology, biometry, and computer programming. I specialize in population biology using a wide range of materials, including natural communities of egrets and herons in the eastern region of the Kanto Plain; laboratory populations of bean weevils collected from all over the world; natural populations of bumble bees in urban and rural regions, and the *in silico* digital bugs that occupy gigabytes on the hard disks attached to my computers. I am using these materials to question, in an evolutionary sense, why some organisms live in groups but others tend to live solitarily. My speciation philosophy was converted to Wrightian from Fisherian when I studied evolution and ecology under Prof. Michael Wade in 1995–1996. I believe that Wright's shifting balance scheme is realistic. I'm often described as a theoretician, but I consider myself primarily to be an ecological field worker. Somehow I have become good at capturing wild egrets and herons by hand!



The photographs (clockwise from the top left panel) show a larva of *Callosobruchus maculatus*, a notorious bean-weevil pest of legume seeds, constructing a rough wall inside a bean when it happened to break into the cavity of another larva. The larva has used feces and a secreted substance to form the wall. The *C. maculatus* larvae are of the scramble type, so multiple adults can emerge from a bean, but if the wall structure is artificially removed the larva will fight with the other larva in the cavity and one or both of them will die as a result. The rough wall acts as a kind of language that prevents fights between inherently quarrelsome larvae.

Select Publications

1. Mashiko, M., Fujioka, M., Moriya, K., Hagimoto, T., Yamaguchi, M., and Toquenaga, Y. (2012). Natural hybridization between a Little Egret (*Egretta garzetta*) and a Chinese Pond Heron (*Ardeola bacchus*) in Japan. Waterbirds *35*, 160-163.
2. Kondo, N., Tuda, M., Toquenaga, Y., Lan, Y-C., Buranapanichpan, S., Horng, S-B., Shimada, M., and Fukatsu, T. (2011). *Wolbachia* infections in world populations of bean beetles (Coleoptera: Chrysomelidae: Bruchinae) infesting cultivated and wild legumes. Zool Sci *14*, 166-172.
3. Suzuki-Ohno, Y., Kawaguchi, L., Munidasa, D., and Toquenaga, Y. (2010). Do bumble bee queens choose nest sites to maximize foraging rate? -Testing models of nest site selection- Behav. Ecol Sociol *63*, 1353-1362.
4. Toquenaga, Y., and Kokuvo, N. (2010). Full-sib reconstruction in haplodiploid populations. Appl Entomol Zool *45*, 59-64.
5. Otsuka, Y. , and Toquenaga, Y. (2009). The Patch Distribute Producer-Scrounger Game, J Theor Biol, *260*, 261-266.
6. Mano, H., and Toquenaga, Y. (2008). Wall-making Behavior in *Callosobruchus maculatus* (Coleoptera: Bruchidae). Ann Entomol Soc Am *101*, 449-455.

Fuminori Tsuruta

Molecular and cellular neurobiology

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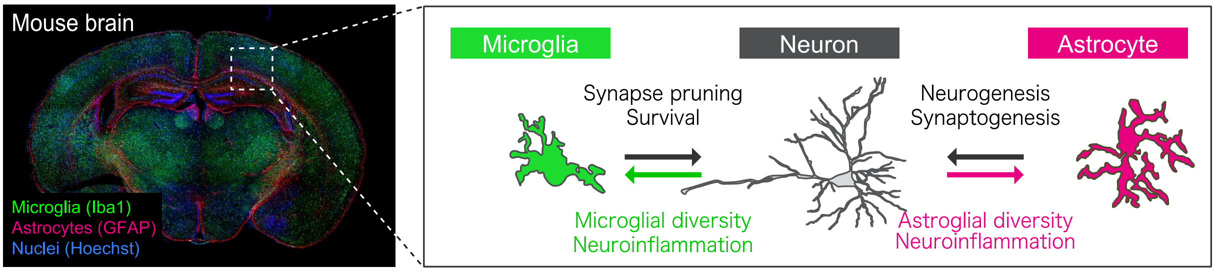
Keywords: **microglia, astrocytes, neurons, neuroinflammation, neurogenesis, synaptogenesis, developmental disorders, neurodegeneration**

Our laboratory is interested in understanding the mechanisms of how glial cells contribute to neurogenesis, synaptogenesis, and neural circuits formations. Also, we have been investigating mechanisms by which glial dysfunctions cause an increased risk of neuronal disorders. Currently, we implement several projects, such as (1) microglial diversity regulated by extracellular micronuclei, (2) microglial maturation and purine metabolism, (3) atypical secretory pathway in neurons and astrocytes, (4) hypothermia control mediated by neuron-astrocyte interaction. Moreover, we have been developing tools and screening systems to elucidate abnormal post-translational modifications that induce neuroinflammation. We aim to clarify some of the principles of neuron-glia interactions in the developing brain through these challenging projects. We welcome highly motivated students interested in molecular neuroscience to investigate the mechanisms underlying glial functions.



➡ Approach to understanding the glial functions and neuronal disorders

Selected publications

Yano S, Akiyama K, Tsuchiya R, Kubotani H, Chiba T, Nagata T, Tsuruta F
A MATLAB-based program for three-dimensional quantitative analysis of micronuclei reveals that neuroinflammation induces micronuclei formation in the brain
Sci Rep 11, 18360 (2021)

Okajima T, Tsuruta F
Exploring genes that control microglial heterogeneity and transition.
Neural Regen Res. 16:2397-2398 (2021)

Okajima T, Gu Y, Teruya R, Yano S, Taketomi T, Sato B, Chiba T, Tsuruta F
Atypical cadherin FAT3 is a novel mediator for morphological changes of microglia
eNeuro. ENEURO.0056-20.2020 (2020)

Kim J, Nakamura J, Hamada C, Taketomi T, Yano S, Okajima T, Kashiwabara SI, Baba T, Sato B, Chiba T, Tsuruta F
USP15 deubiquitinates TUT1 associated with RNA metabolism and maintains cerebellar homeostasis
Mol. Cell Biol. 40:e00098-20 (2020)

Hiroshi Wada

Evolutionary Developmental Biology

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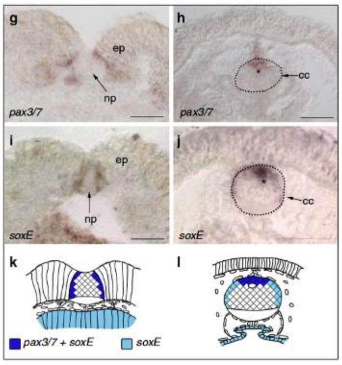
Our interest is in the evolutionary processes of various animal body plans. We are especially interested in the following issues.

1) Establishment and evolution of the chordate body plan. Chordates acquired several novel characters such as notochord, dorsal central nervous system, vertebrae, and pharyngeal arches. We explore how these novel organs evolved by comparing developmental genetics in amphioxus and lampreys.

2) Evolution of echinoderm larval morphology. Echinoderms show two types of larvae, pluteus and auricularia. We asked how these discrete larval morphologies evolved by comparing developmental genetics in sea urchins and starfish.

3) Evolution of bivalve shell plate in bivalve mollusks. Bivalve mollusks acquired bilaterally separated shell plates, and this unique morphology is visible as early as the gastrula stage, showing that the separated shell plates are established by modifying their early embryogenesis.

4) Establishment of the unique body plan of caprellids. The unique body plan of the caprellids was established from a gammarid-like body plan through the loss of some thoracic limbs and abdominal segments. We are seeking the genetic modification response for this loss. We are interested in this phenomenon because some caprellid species re-acquired the limbs.



Expression of *pax3/7* and *soxE*, whose homologues are involved in the differentiation of the dorsal neural tube in vertebrates, mark dorsal part of the acorn worm nerve cord, showing that acorn worms possess similar DV patterning mechanism in their nerve cord. (Miyamoto and Wada, Nature Comm. (2013).

Publications

1. Suzuki, D. G., Murakami, Y., Escriva, H. and Wada. H. (2015) A comparative examination of neural circuit and brain patterning between the lamprey and amphioxus reveals the evolutionary origin of the vertebrate visual center. J. Comp. Neurol. 523, 251-261.
2. Miyamoto, N. and Wada. H. (2013) Hemichordate neurulation and the origin of the neural tube. Nat. Comm. 4, 2713
3. Morino, Y., Koga, H., Tachibana, K., Shoguchi, E., Kiyomoto, M. and Wada. H. (2012). Heterochronic Activation of VEGF Signaling and the Evolution of the Skeleton in Echinoderm Pluteus Larvae. Evol. Dev. 14, 428-436.

Shigeki Wada

Biological Oceanography

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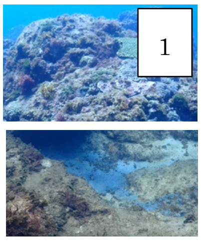
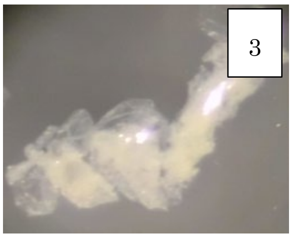
Keywords: **biogeochemistry, carbon sequestration, ocean acidification**

Marine ecosystems have face serious threat from environmental change. To mitigate and adapt against those issues, we have to understand the mechanisms of ecosystems and thereby predict the response to environmental stressors. Our laboratory has mainly focused on three topics; 1) Ecosystem response to ocean acidification, 2) Estimation of Blue Carbon, and 3) Mechanisms of marine snow formation.

1) Ecosystem response to ocean acidification: Ocean acidification is caused by anthropogenic CO$_2$ emission. A part of CO$_2$ released by human activity is absorbed to surface ocean, and disturbance of carbonate chemistry leads serious effects on marine organisms. Using natural analogues of ocean acidification; volcanic CO$_2$ seeps, we have assessed the response of marine ecosystems to ocean acidification.
2) Blue Carbon: Coastal vegetation such as macroalgae and seagrass has been recently focused as carbon sink termed as Blue Carbon, because a part of organic carbon derived from their photosynthetic products is sequestrated into sediment and deep sea. We trace the fate of photosynthetic products to understand their contribution to Blue Carbon
3) Marine snow, particles settling to deep sea, has a role as a carrier of organic carbon, and its contribution to carbon sequestration buffers climate change. Combination of biological and physical process would be important in the mechanism of marine snow formation, but it has been largely unknown. We have assessed the effect of physical disturbance to dynamics of marine snow to understand the mechanisms of carbon sequestration in pelagic ecosystems.





1) Normal (upper) and high CO$_2$ (lower) sites,
2) Survey in marine forest of macroalgae
3) Marine snow formed by physical disturbance

Selected publications

1. Wada, S. et al. (2021). Ocean acidification increases phytobenthic carbon fixation and export in a warm-temperate system. *Estuarine, Coastal and Shelf Science* 250:107113.
2. Wada, S. et al. (2020). Seasonal dynamics of seawater CO2 system at a coastal site near the southern tip of Izu Peninsula, Japan. *Journal of Oceanography* 76:227-242.
3. Wada, S. et al. (2020). Aggregation of marine organic matter by bubbling. *Journal of Oceanography* 76:317-326.
4. Wada, S. & Hama, T. (2013). Conttribution of macroalgae to coastal dissolved organic matter pool. *Estuarine, Coastal and Shelf Science* 129:77-85.

Matthew Wood

Science Communication

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Carefully considered public communication of science and related issues is vital for a healthy relationship between science and the society that both depends on and supports it. It is becoming increasingly apparent that this communication is multifaceted, highly complex, and must be better understood to face the challenges of our progressively science-reliant society.

I have broad academic interests in the areas of public perceptions of science and scientists; the portrayal of science in news and the media; risk perception; and the use of visual media to communicate science concepts and issues in informal education settings.

I develop and conduct undergraduate and postgraduate courses in communication skills and introductory science communication. These courses are designed to equip students to effectively communicate their future research. In a previous life I trained in marine biology and environmental chemistry, and worked on projects searching for potential new drugs from marine invertebrates.

Shunsuke Yaguchi

Developmental Biology
(Shimoda Marine Research Center)

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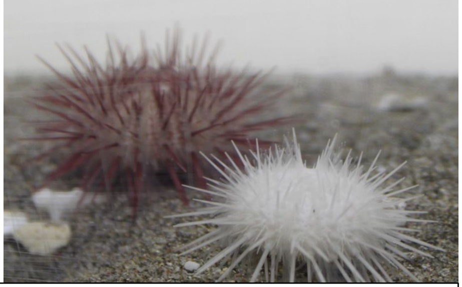
Keywords: **sea urchin, nervous system, neural function, axis specification**

The primary research goal of our lab is to understand the molecular mechanisms of embryonic axis specification and formation in the sea urchin. It has been suggested that this embryo has two independent, maternally specified axes, primary (anterior-posterior) and secondary (dorsal-ventral). My previous work showed that specification of these two axes is linked by a single transcription factor, FoxQ2, during early embryogenesis. My goal is to try to understand how FoxQ2 is related to, or interacts with, signaling pathways like the Wnt/ß-catenin, Nodal, and BMP2/4, which are responsible for axis specification and formation.

Another research goal is to understand the molecular mechanisms of neurogenesis and neural functions, including the specification and patterning of the neurogenic ectoderm that develops at the anterior end of the sea urchin embryo.



Recently we have succeeded to make genetically modified sea urchins like albino by applying CRISPR/Cas9.

Selected publications

1. Yaguchi J, Yaguchi S. Sea urchin larvae utilize light for regulating the pyloric opening. **BMC Biology.** 2021; 19:64
2. Yaguchi S, Yaguchi J, Suzuki H, Kinjo S, Kiyomoto M, Ikeo K, Yamamoto T. Establishment of homozygous knock-out sea urchins. **Current Biology**. 2020; 30:R427-429.
3. Yaguchi J, Yaguchi S. Evolution of nitric oxide regulation of gut function. **Proc Natl Acad Sci USA (PNAS).** 2019; 116:5607-5612. DOI: 10.1073/pnas.1816973116
4. Yaguchi J, Yamazaki A, Yaguchi S. Meis transcription factor maintains the neurogenic ectoderm and regulates the anterior-posteriot patterning in embryos of a sea urchin, Hemicentrotus pulcherrimus. **Dev** . **Biol.** 2018;444:1-8.
5. Suzuki H, Yaguchi S. Transforming growth factor-ß signal regulates gut bending in the sea urchin embryo. **Dev Growth Differ**. 2018;60:216-225.

Kensuke Yahata

Arthropod phylogeny and systematics

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Keywords: **Arthropoda, comparative morphology, phylogeny, systematics**

The Phylum Arthropoda is known to have a huge species diversity. And there is also great diversity in the morphology of various organs and tissues. Although morphological features of many organs and tissues have been investigated in the past centuries, there will be many structures that we do not know well yet. Some of these unknown structures may have important phylogenetic significance. In my laboratory, we are clarifying the phylogenetic significance of the characteristics newly discovered in the arthropods from the viewpoint of comparative morphology. The following are two examples of our research.

In one project, we identified distinctive structure in ovaries of myriapods. Although the Myriapoda has been known to have few new traits that characterize the taxon, this ovarian structure is considered to have important phylogenetic significance as an undoubted synapomorphy of the Myriapoda. In another project, we newly found some structures for appendage autotomy in centipedes. And we clearly suggested that the difference in the degree of development of the autotomic structures is related to the frequency of their autotomic behaviors and that the difference also corresponds to their order level phylogeny. Our researches will not only add new insights to arthropod morphology but also contribute to a better understanding of arthropod phylogeny and evolution.

Selected publications

1. Chikami, Y. and K. Yahata (2019) Comparative morphology of ovarian follicle in two polydesmid millipedes: evolutionary implication on folded structure of follicle epithelium in Polydesmida (Myriapoda: Diplopoda). *Proc. Arthropod. Embryol. Soc. Jpn.*, 52, 1–9.
2. Yahata, K., E. Umetani and Y. Chikami (2018) Morphological study of the ovary in *Hanseniella caldaria* (Myriapoda; Symphyla): The position of oocyte-growth and evolution of ovarian structure in Arthropoda. *Arthropod Structure and Development*, 47, 655–661.
3. Niikura, M., M. Honda and K. Yahata (2015) Phylogeography of Semiterrestrial Isopod, *Tylos granuliferus*, on East Asian Coasts. *Zool. Sci.*, 32, 105–113.
4. Suguro, T. and K. Yahata (2014) Taxonomic notes on Japanese species of the genera *Pseudicius* and *Tasa* (Araneae: Salticidae). *Acta Arachnol.*, 63, 87–97.
5. Miyachi, Y. and K. Yahata (2012) Morphological study of ovarian structures in scolopendromorph centipedes (Myriapoda: Chilopoda) with special reference to the position of oocyte growth. *Proc. Arthropod. Embryol. Soc. Jpn.*, 47, 21–28.
6. Matsui, A. and K. Yahata (2012) Study of autotomic structure in centipedes (Arthropoda: Chilopoda). *Proc. Arthropod. Embryol. Soc. Jpn.*, 47, 11–19.