NIBB Core Research Facilities

Head
KOBAYASHI, Satoru

The NIBB Core Research Facilities were launched in 2010 to support basic biology research in NIBB. They consist of three facilities that are developing and providing state-of-the-art technologies to understand biological functions through functional genomics, bioimaging and bioinformatics.

The NIBB Core Research Facilities also act as an intellectual hub to promote collaboration among the researchers of NIBB and other academic institutions.

Functional Genomics Facility

Specially Appointed Associate Professor
SHIGENOBU, Shuji

Technical Staff:	*MORI, Tomoko*
	MAKINO, Yumiko
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Technical Assistant:	*ASAO, Hisayo*
	WAKAZUKI, Sachiko
	MATSUMOTO, Miwako
	FUJITA, Miyako
Secretary:	*ICHIKAWA, Mariko*

The Functional Genomics Facility is a division of the NIBB Core Research Facilities and organized jointly by NIBB and NIPS for promoting DNA and protein studies. The facility maintains a wide array of core research equipment, from standard machinery like ultracentrifuges to cutting edge tools such as next generation DNA sequencers, which amount to 60 different kinds of instrument. The facility is dedicated to fostering collaborations with researchers both of NIBB and other academic institutions worldwide by providing these tools as well as expertise. Our current focus is supporting functional genomics works that utilize mass spectrometers and DNA sequencers. We also act as a bridge between experimental biology and bioinformatics.

Representative Instruments

Genomics

The advent of next-generation sequencing (NGS) technologies is transforming today's biology by ultra-high-throughput DNA sequencing. Utilizing the SOLiD5500xl (Applied Biosystems), HiSeq2500, HiSeq1500 (Illumina), and MiSeq (Illumina) the Functional Genomics Facility is committed to joint research aiming to explore otherwise inaccessible new fields in basic biology.

During 2013 we carried out 41 NGS projects in collaboration with NIBB laboratories as well as the researchers of other academic institutions. These projects cover a wide range of species (bacteria, animals, plants, and humans) including both model and non-model organisms, and various applications such as genomic re-sequencing, RNA-seq and ChIP-seq.

Figure 1. Next-generation sequencer

Proteomics

Three different types of mass spectrometer and two protein sequencers, as listed below, are used for proteome studies in our facility. In 2013, we analyzed approximately 300 samples with mass spectrometers and 50 samples with protein sequencers.

- GC-Mass Spectrometer (JEOL DX-300)
- MALDI-TOF-MS (Bruker Daltonics REFLEX III)
- LC-Q-TOF MS (Waters Q-TOF Premier)
- Protein sequencer (ABI Procise 494 HT; ABI Procise 492 cLC)

Other analytical instruments

- Cell sorter (SONY SH800)
- Bioimaging Analyzer (Fujifilm LAS 3000 mini; GE FLA9000)
- Laser Capture Microdissection System (Arcturus XT)
- DNA Sequencer (ABI PRISM 310; ABI 3130xl)
- Real Time PCR (ABI 7500)
- Ultra Centrifuge (Beckman XL-80XP etc.)

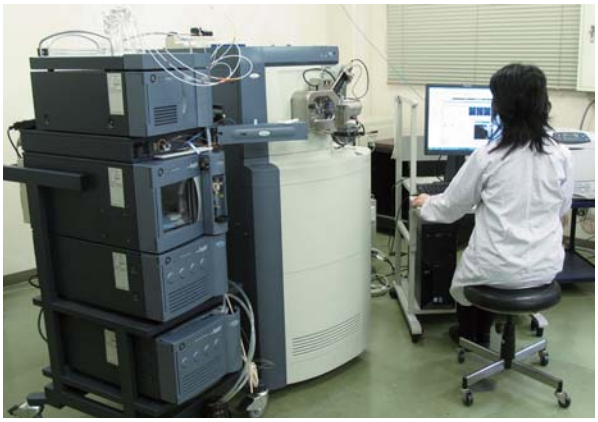

Figure 2. LC-Q-TOF mass spectrometer

Genome Informatics Training Course

We organize NIBB Genome Informatics Training Courses every year. In 2013, we provided two two-day training courses on next-generation sequence data analyses and transcriptome analysis. These courses are designed to introduce the basic knowledge and skills of bioinformatics analysis to biologists who are not familiar with bioinformatics.

Figure 3. NIBB Genome Informatics Training Course

Publication List on Cooperation

〔Original papers〕

- Arimura, T., Onoue, K., Takahashi-Tanaka, Y., Ishikawa, T., Kuwahara, M., Setou, M., Shigenobu, S., Yamaguchi, K., Bertrand, A.T., Machida, N., *et al*. (2013). Nuclear accumulation of androgen receptor in gender difference of dilated cardiomyopathy due to lamin A/C mutations. Cardiovasc. Res. *99*, 382–394.
- Ishikawa, T., Okada, T., Ishikawa-Fujiwara, T., Todo, T., Kamei, Y., Shigenobu, S., Tanaka, M., Saito, T.L., Yoshimura, J., Morishita, S., *et al*. (2013). ATF6α/β-mediated adjustment of ER chaperone levels is essential for development of the notochord in medaka fish. Mol. Biol. Cell *24*, 1387–1395.
- Okamoto, S., Shinohara, H., Mori, T., Matsubayashi, Y., and Kawaguchi, M. (2013). Root-derived CLE glycopeptides control nodulation by direct binding to HAR1 receptor kinase. Nat. Commun. *4*, 2191.
- Tabata, R., Kamiya, T., Shigenobu, S., Yamaguchi, K., Yamada, M., Hasebe, M., Fujiwara, T., and Sawa, S. (2013). Identification of an EMS-induced causal mutation in a gene required for boron-mediated root development by low-coverage genome re-sequencing in Arabidopsis. Plant Signal. Behav. *8*, e22534.
- Takahara, M., Magori, S., Soyano, T., Okamoto, S., Yoshida, C., Yano, K., Sato, S., Tabata, S., Yamaguchi, K., Shigenobu, S., *et al*. (2013). TOO MUCH LOVE, a novel kelch repeat-containing F-box protein, functions in the long-distance regulation of the Legume-Rhizobium symbiosis. Plant Cell Physiol. *54*, 433–447.
- Tokuda, G., Elbourne, L.D.H., Kinjo, Y., Saitoh, S., Sabree, Z., Hojo, M., Yamada, A., Hayashi, Y., Shigenobu, S., Bandi, C., *et al*. (2013). Maintenance of essential amino acid synthesis pathways in the *Blattabacterium cuenoti* symbiont of a wood-feeding cockroach. Biol. Lett. *9*, 20121153.
- Wang, Z., Pascual-Anaya, J., Zadissa, A., Li, W., Niimura, Y., Huang, Z., Li, C., White, S., Xiong, Z., Fang, D., *et al*. (2013). The draft genomes of soft-shell turtle and green sea turtle yield insights into the development and evolution of the turtle-specific body plan. Nat. Genet. *45*, 701–706.

〔Original paper (E-publication ahead of print)〕

- Uehara, M., Wang, S., Kamiya, T., Shigenobu, S., Yamaguchi, K., Fujiwara, T., Naito, S., and Takano, J. (2014). Identification and characterization of an Arabidopsis mutant with altered localization of NIP5;1, a plasma membrane boric acid channel, reveals the requirement for D-galactose in endomembrane organization. Plant Cell Physiol. 2013 Dec. 15.

● *Research activity by S. Shigenobu*

Specially Appointed Associate Professor: *SHIGENOBU, Shuji*
NIBB Research Fellow: *MAEDA, Taro*
Technical Assistant: *SUZUKI, Miyuzu*
Visiting Graduate Student: *OGAWA, Kota*

Symbiosis Genomics

"Nothing, it seems, exists except as part of a network of interactions." (Gilbert & Epel, 2008)

Every creature on the earth exists among a network of various biological interactions. For example, many multicellular organisms, including humans, harbor symbiotic bacteria in their bodies: some of them provide their hosts with essential nutrients deficient in the host's diet and others digest foods indigestible by the host alone. In spite of numerous examples of symbioses and its intriguing outcomes, the genetic and molecular basis underlying these interactions remains elusive. The goal of our group is to establish a new interdisciplinary science "Symbiosis Genomics", where we aim to understand the network of biological interactions at the molecular and genetic level. To this end, we take advantage of state-of-the-art genomics such as next-generation sequencing technologies.

I. Genomic revelations of a mutualism: the pea aphid and its obligate bacterial symbiont

Aphid species bear intracellular symbiotic bacteria in the cytoplasm of bacteriocytes, specialized cells for harboring the bacteria. The mutualism is so obligate that neither can reproduce independently. The 464 Mb draft genome sequence of the pea aphid, *Acyrthosiphon pisum*, in consort with that of bacterial symbiont *Buchnera aphidicola* illustrates the remarkable interdependency between the two organisms. Genetic capacities of the pea aphid and the symbiont for amino acid biosynthesis are complementary. The genome analysis revealed that the pea aphid has undergone characteristic gene losses and duplications. The IMB antibacterial immune pathway is missing several critical genes, which might account for the evolutionary success of aphids to obtain beneficial symbionts. Lineage-specific gene duplications have occurred in genes in a broad range of functional categories, which include signaling pathways, miRNA machinery, chromatin modification and mitosis. The importance of these duplications for symbiosis remains to be determined. We found several instances of lateral gene transfer from bacteria to the pea aphid genome. Some of them are highly expressed in bacteriocytes.

Aphid research is entering the post-genome era. We analyzed the transcriptome of aphid bacteriocytes using RNA-seq technology featuring a next-generation DNA sequencer. We found thousands of genes over-represented in

the symbiotic organ in comparison with the whole body. Many genes for amino acid metabolism are found to be over-represented as expected: the plant sap-eating insect depends on the bacterial symbionts to supply essential amino acids. In addition, many kinds of novel secretion proteins that are found only in aphid species are extremely enriched in the bacteriocytes. We also found that bacteriocytes express Distal-less (Dll), a homeodomain-containing transcription factor throughout the life cycle. Future study should focus on dissecting the genetic network of these components, which should allow us to understand the genetic basis on which symbiosis generates evolutionary novelty.

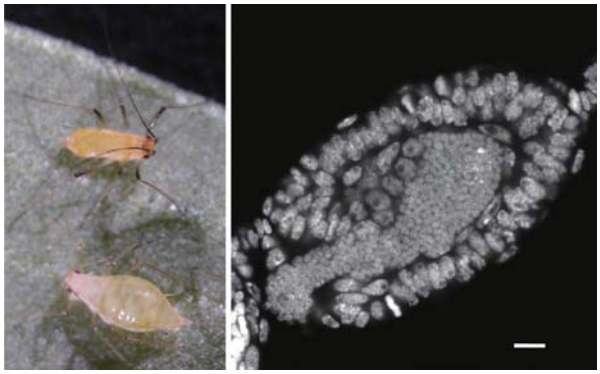

Figure 1. Pea aphids and the bacterial symbiont, *Buchnera*. Adult aphids (Left). A developing viviparous embryo which symbionts are infecting (Right). Scale bar = 20um.

Publication List

〔Original papers〕

- Chang, C.-C., Hsiao, Y.-M., Huang, T.Y., Cook, C.E., Shigenobu, S., and Chang, T.-H. (2013). Noncanonical expression of caudal during early embryogenesis in the pea aphid *Acyrthosiphon pisum*: maternal cad-driven posterior development is not conserved. Insect Mol. Biol. *22*, 442–455.
- Hayashi, Y., Shigenobu, S., Watanabe, D., Toga, K., Saiki, R., Shimada, K., Bourguignon, T., Lo, N., Hojo, M., Maekawa, K., *et al*. (2013). Construction and characterization of normalized cDNA libraries by 454 pyrosequencing and estimation of DNA methylation levels in three distantly related termite species. PLoS ONE *8*, e76678.
- Shibata, T.F., Maeda, T., Nikoh, N., Yamaguchi, K., Oshima, K., Hattori, M., Nishiyama, T., Hasebe, M., Fukatsu, T., Kikuchi, Y., *et al*. (2013). Complete genome sequence of *Burkholderia* sp. strain RPE64, bacterial symbiont of the bean bug *Riptortus pedestris*. Genome Announc. *1*, e00441–13.
- Shigenobu, S., and Stern, D.L. (2013). Aphids evolved novel secreted proteins for symbiosis with bacterial endosymbiont. Proc. Royal Soc. B Biol. Sci. *280*, 20121952.
- Suzuki, M.M., Yoshinari, A., Obara, M., Takuno, S., Shigenobu, S., Sasakura, Y., Kerr, A.R., Webb, S., Bird, A., and Nakayama, A. (2013). Identical sets of methylated and nonmethylated genes in *Ciona intestinalis* sperm and muscle cells. Epigenetics Chromatin *6*, 38.

Spectrography and Bioimaging Facility

Specially Appointed Associate Professor
KAMEI, Yasuhiro

Technical Staff: *HIGASHI, Sho-ichi*
TANIGUCHI-SAIDA, Misako
UCHIKAWA, Tamaki
Technical Assistant: *ICHIKAWA, Chiaki*
Secretary: *ISHIKAWA, Azusa*

The Spectrography and Bioimaging Facility assists both collaborative and core research by managing and maintaining research tools that use “Light”. The facility also provides technical support through management of technical staff assisting in the advancement of collaborative and core research projects, as well as academic support to researchers. Among its tools are advanced microscopes for biology and the Okazaki Large Spectrograph for photobiology. The Okazaki Large Spectrograph is the world’s largest wide spectrum exposure mechanism, capable of producing a range of wavelengths from 250 nm (ultraviolet) to 1,000 nm (infrared) along its 10 meter focal curve; allowing exposure to strong monochromatic light. The facility’s microscopes, which are cutting edge devices such as confocal and multi-photon excitation microscopes, are used by both internal and external researchers as vital equipment for core and collaborative research projects.

Representative Instruments:

Okazaki Large Spectrograph (OLS)

The spectrograph runs on a 30 kW Xenon arc lamp and projects a wavelength spectrum from 250 nm (ultraviolet) to 1,000 nm (infrared) onto its 10 m focal curve with an intensity of monochromatic light at each wavelength more than twice as much as that of the corresponding monochromatic component of tropical sunlight at noon (Watanabe *et al*., Photochem. Photobiol. *36*, 491-498, 1982).

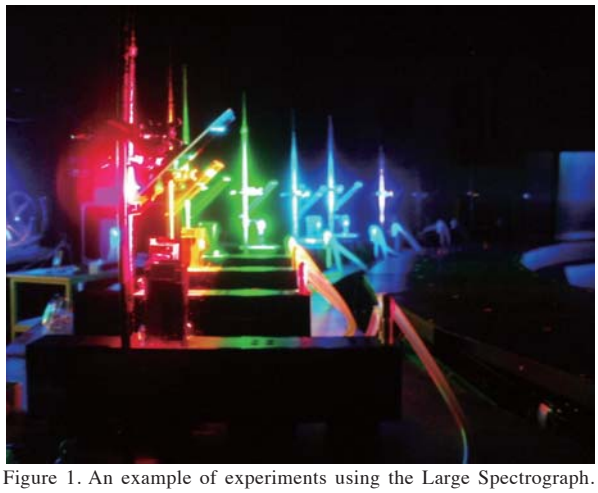

Figure 1. An example of experiments using the Large Spectrograph. Various color rays (monochromatic light from right side and reflected by mirrors) were irradiated simultaneously to samples in cooling chambers.

The spectrograph is dedicated to action spectroscopical studies of various light-controlled biological processes.

The NIBB Collaborative Research Program for the Use of the OLS supports about 10 projects every year conducted by both visiting scientists, including foreign researchers, as well as those in NIBB.

Action spectroscopical studies for various regulatory and damaging effects of light on living organisms, biological molecules, and artificial organic molecules have been conducted.

Microscopes

This facility also has Bioimaging machines such as widefield microscopes (Olympus IX-81, BX-63 and KEYENCE BZ-8000), confocal microscopes (Olympus FV1000, Nikon A1R, Nikon A1Rsi, Carl Zeiss Duo 5 and Yokogawa CSU-X1), multi-photon microscopes (Olympus FV1000-MP, Leica SP8 MPs) and other advanced custom-made laser microscopes with special aims (Digital Scanned Light-sheet Microscope: DSLM and Infrared Laser-Evoked Gene Operator microscope: IR-LEGO) for users in NIBB and collaborative guest researchers. We began Collaborative Research Programs using these machines in 2010.

The DSLM was developed by Dr. Ernst Stelzer's group at the European Molecular Biology Laboratory (EMBL). This microscope can realize high-speed z-axis scanning in deeper tissue by illuminating a specimen from the side with a light sheet (more information is given in Dr. Nonaka's section: Lab. for Spatiotemporal Regulations). Dr. Nonaka conducted and supported 7 projects of the Collaborative Research Program for the Use of the DSLM. The IR-LEGO was developed by Drs. Shunsuke Yuba and Yasuhiro Kamei at the National Institute of Advanced Industrial Science and Technology (AIST). This microscope can induce a target gene of interest by heating a single target cell *in vivo* with a high efficiency irradiating infrared laser (Kamei *et al*. Nat. Methods, 2009). Details are described in the next section. The IR-LEGO was also used for 10 Individual Collaborative Research projects, including applications for animals and higher plants.

Workshop and Symposium

In 2013, we held workshops (training courses) on IR-LEGO for vertebrates (frog and fish) and biological image processing. We also have been holding a "Bioimaging Forum" every year which discusses Bioimaging from various directions such as microscopy, new photo-technology, and computer science.

Publication List on Cooperation

〔**Original papers (Selected)**〕

- Allorent, G., Tokutsu, R., Roach, T., Peers, G., Cardol, P., Girard-Bascou, J., Seigneurin-Berny, D., Petroutsos, D., Kuntz, M., Breyton, C., Franck, F., Wollman, F.-A., Niyogi, K.K., Krieger-Liszkay, A., Minagawa, J. and Finazzi, G. (2013). A dual strategy to cope with high light in *Chlamydomonas reinhardtii*. Plant Cell. *25*, 545-557.
- Ikehata, H., Higashi, S., Nakamura, S., Daigaku, Y., Furusawa, Y., Kamei, Y., Watanabe, M., Yamamoto, K., Hieda, K., Munakata, N., and Ono, T. (2013). Action spectrum analysis of UVR genotoxicity for skin: the border wavelengths between UVA and UVB can bring serious mutation loads to skin. J. Invest. Dermatol. *133*, 1850-1856.
- Shikata, T., Matsunaga, S., Iseki, M., Nishide, H., Higashi, S., Kamei, Y., Yamaguchi, M., Jenkinson, I.R., and Watanabe, M. (2013). Blue light regulates the rhythm of diurnal vertical migration in the raphidophyte red-tide alga *Chattonella antiqua*. J. Plankton Res. *35*, 542-552.
- Okuyama, T., Isoe, Y., Hoki, M., Suehiro, Y., Yamagishi, G., Naruse, K., Kinoshita, M., Kamei, Y., Shimizu, A., Kubo, T., and Takeuchi, H. (2013). Controlled cre/loxP site-specific recombination in the developing brain in medaka fish, *Oryzias latipes*. PLoS ONE. *8*, e66597.
- Murata, T., Sano, T., Sasabe, M., Nonaka, S., Higashiyama, T., Hasezawa, S., Machida, Y., and Hasebe, M. (2013). Mechanism of microtubule array expansion in the cytokinetic phragmoplast. Nat. Commun. *4*, 1967.
- Sato-Numata, K., Numata, T., Okada, T., and Okada, Y. (2013). Acid-sensitive outwardly rectifying (ASOR) anion channels in human epithelial cells are highly sensitive to temperature and independent of CIC-3. Pflugers Arch-Eur. J. Physiol. *465*, 1535-1543.
- Suzaki, T., Ito, M., and Kawaguchi, M. (2013). Induction of localized auxin response during spontaneous nodule development in *Lotus japonicus*. Plant Signal Behav. *8*, e23359.
- Takahara, M., Magori, S., Soyano, T., Okamoto, S., Yoshida, C., Yano, K., Sato, S., Tabata, S., Yamaguchi, K., Shigenobu, S., Takeda, N., Suzaki, T., and Kawaguchi, M. (2013). Too much love, a novel Kelch repeat-containing F-box protein, functions in the long-distance regulation of the legume-Rhizobium symbiosis. Plant Cell Physiol. *54*, 433-447.
- Yamagata, Y., Kaneko, K., Kase, D., Ishihara, H., Nairn, A.C., Obata, K., and Imoto, K. (2013). Regulation of ERK1/2 mitogen-activated protein kinase by NMDA-receptor- induced seizure activity in cortical slices. Brain Res. *24*, 1-10.
- Kimura, E., Deguchi, T., Kamei, Y., Shoji, W., Yuba, S., and Hitomi, J. (2013). Application of infrared laser to the zebrafish vascular system: gene induction, tracing, and ablation of single endothelal cells. Arterioscler. Thromb. Vasc. Biol. *33*, 1264-1270.
- Hira, R., Ohkubo, F., Tanaka, Y.R., Masamizu, Y., Augustine, J.G., Kasai, H., and Matsuzaki, M. (2013). In vivo optogenetic tracing of functional corticocortical connections between motor forelimb areas. Front. Neural Circuits. *7*, 55.
- Shimada, A., Kawanishi, T., Kaneko, T., Yoshihara, H., Yano, T., Inohaya, K., Kinoshita, M., Kamei, Y., Tamura, K., and Takeda, H. (2013). Trunk exoskeleton in teleosts is mesodermal in origin. Nat. Commun. *4*, 1639.
- Kobayashi, K., Kamei, Y., Kinoshita, M., Czerny, T., and Tanaka, M. (2013). A heat-inducible Cre/LoxP gene induction system in medaka. Genesis. *51*, 59-67.
- Moritoh, S., Komatsu, Y., Yamamori, T., and Koizumi, A. (2013). Diversity of retinal ganglion cells identified by transient GFP transfection in organotypic tissue culture of adult marmoset monkey retina. PLoS ONE. *8*, e54667.
- Suzaki, T., Kim, C.S., Takeda, N., Szczyglowski, K., and Kawaguchi, M. (2013). TRICOT encodes an AMP1-related carboxypeptidase that regulates root nodule development and shoot apical meristem maintenance in *Lotus japonicus*. Development *140*, 353-361.

● *Research activity by Y. Kamei*

Specially Appointed Associate Professor: *KAMEI, Yasuhiro*

NIBB Research Fellow: *HATTORI, Masayuki*

My research group promotes two advanced microscope projects; "observation" and "manipulation" using optical and biological technologies. The aim of our "observation project" is deep-seeing in living organisms using adaptive optics (AO) which were well-developed in the field of astronomy as

a key technology of large telescopes such as the Subaru telescope in Hawaii. Although observation of telescopes on the earth may be disturbed by fluctuation in the atmosphere, AO technology can cancel this disturbance. On the other hand, living materials have particular refractive indexes, therefore, some organelles act as a disturbance of the ideal optical path for microscope observation just like the atmosphere does for telescopes. AO technology also can recover this disturbance by sensing and correcting wave fronts using a wave front sensor and deformable mirror. Hence, we developed a custom-made wide-field microscope equipped with an AO system for observation of living organisms as a collaboration with Dr. Tamada in NIBB and Dr. Hayano in the National Astronomical Observatory of Japan (NAOJ) and got high-resolution bright field and fluorescent images of living cells. Our result indicated that improvement of optical resolution was restricted in a small

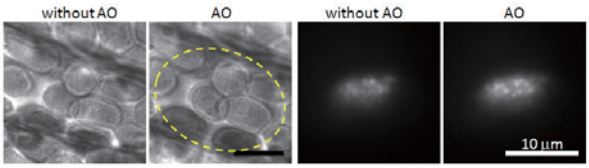

Figure 1. Effects of adaptive optics (AO) to the wide-field microscope images (bright field and fluorescence of plant cells).

area which is called the "isoplanatic patch" (Figure 1).

Second, the aim of our "manipulation project" is to control gene expression *in vivo*. Gene function analysis must be evaluated at the cell level *in vivo*. To achieve spatiotemporal-controlled gene expression we employed one of the stress responses, the heat shock response. The heat shock promoter is the transcription regulation region of heat shock proteins and all organisms have this mechanism. Positioning the target gene downstream of the promoter, we can induce the target gene expression by local heating.

Infrared (IR) beams can heat water molecules, which are the main constituent of cells, hence, we can heat a single cell by irradiating IR to a target cell using a microscope. We have developed a microscope, IR laser evoked gene operator (IR-LEGO), specialized for this purpose (Figure 2). The IR-LEGO microscope can irradiate an IR laser to a single cell *in vivo* such as *C. elegans*, medaka, zebrafish, *Xenopus* and *Arabidopsis*, to induce the heat shock response at a desired timing.

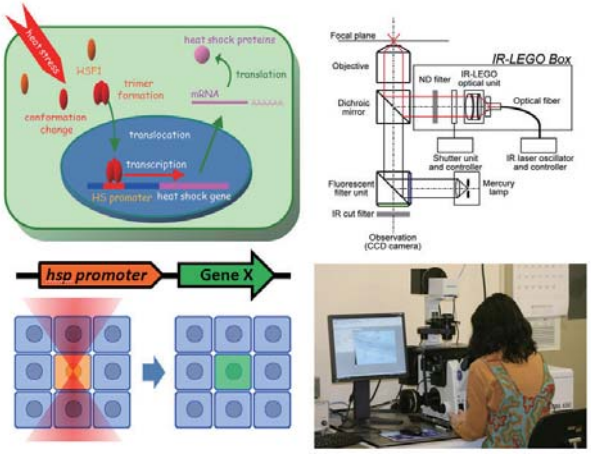

Figure 2. Schematic illustration of local gene induction system and an infrared laser-evoked gene operator (IR-LEGO) microscope system in NIBB.

Optimal heating induces the heat shock response and subsequent gene expression, while an excess results in cell death. Hence, we must precisely control laser heating. We evaluated time course and spatial heating profiles, and the results presented that temperature of the target area rose rapidly and kept a constant level dependant on IR laser power, additionally, the heated area was adequately as small as a typical cell size.

With this in mind, we tried to induce gene expression in various species. At first, we reported an IR-LEGO experiment in living *C. elegans*. Target gene expression in a target cell could be induced with only 1 s-IR irradiation. Whereas the optimal power range which can induce gene induction without cell damage was limited. Excess laser power resulted in cell death or cessation of cell division. We confirmed that an optimal irradiation, e.g. 11 mW for 1 s, induced physiological gene expression in the target cell and subsequent cell division or morphogenesis underwent normal development. Next, we tried the experiment in other animals, medaka, zebrafish and *Xenopus*, and the higher plant, *Arabidopsis*, since all organisms have a heat shock response system. We succeeded in local gene induction in the species as expected.

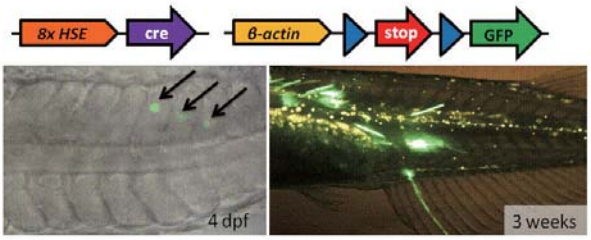

Figure 3. Cre-loxP mediated long-term GFP marking in a living medaka individual for linage tracing.

Studies of cell fates, cell-cell interaction, or analysis of non-cell autonomous phenomena require a fine control system of gene expression in experiments. IR-LEGO will be a powerful tool for these studies in combination with molecular biological techniques, such as the cre-loxP system. By Applying IR-LEGO to a mutant and its rescue transgenic strain; using hsp-cre with a rescue gene which is sandwiched by loxP sequences, we will achieve single-cell knockout experiments in living organisms, and reveal fine interaction between the cells. We are now testing this system using medaka. We have already constructed a medaka TILLING library and a screening system for reverse genetic mutant screening, furthermore we have confirmed a system operation of a cre-loxP system in medaka using IR-LEGO (Figure 3).

Publication List

〔Original papers〕

- Ikehata, H., Higashi, S., Nakamura, S., Daigaku, Y., Furusawa, Y., Kamei, Y., Watanabe, M., Yamamoto, K., Hieda, K., Munakata, N., and Ono, T. (2013). Action spectrum analysis of UVR genotoxicity for skin: the border wavelengths between UVA and UVB can bring serious mutation loads to skin. J. Invest. Dermatol. *133*, 1850-1856.
- Ishikawa, T., Okada, T., Ishikawa-Fujiwara, T., Todo, T., Kamei, Y., Shigenobu, S., Tanaka, M., Saito, T.L., Yoshimura, J., Morishita, S., Toyoda, A., Sakaki, Y., Taniguchi, Y., Takeda, S., and Mori, K. (2013). ATF6a/b-dediated adjustment of ER chaperone levels is essential for development of the notochord in medaka fish. Mol. Biol. Cell *24*, 1387-1395.
- Kimura, E., Deguchi, T., Kamei, Y., Shoji, W., Yuba, S., and Hitomi, J. (2013). Application of infrared laser to the zebrafish vascular system: gene induction, tracing, and ablation of single endothelal cells. Arterioscler. Thromb. Vasc. Biol. *33*, 1264-1270.
- Kobayashi, K., Kamei, Y., Kinoshita, M., Czerny, T., and Tanaka, M. (2013). A heat-inducible Cre/LoxP gene induction system in medaka. Genesis. *51*, 59-67.
- Okuyama, T., Isoe, Y., Hoki, M., Suehiro, Y., Yamagishi, G., Naruse, K., Kinoshita, M., Kamei, Y., Shimizu, A., Kubo, T., and Takeuchi H. (2013). Controlled Cre/loxP site-specific recombination in the developing brain in medaka fish, *Oryzias latipes*. PLoS ONE *8*, e66597.
- Shikata, T., Matsunaga, S., Iseki, M., Nishide, H., Higashi, S-I., Kamei, Y., Yamaguchi, M., Jenkinson, I.R., and Watanabe, M. (2013). Blue light regulates the rhythm of diurnal vertical migration in the raphidophyte red-tide alga *Chattonella antiqua*. J. Plankton Res. *35*, 542-552.
- Shimada, A., Kawanishi, T., Kaneko, T., Yoshihara, H., Yano, T., Inohaya, K., Kinoshita, M., Kamei, Y., Tamura, K., and Takeda, H. (2013). Trunk exoskeleton in teleosts is mesodermal in origin. Nature Commun. *4*, 1639.

Data Integration and Analysis Facility

Assistant Professor:	*UCHIYAMA, Ikuo*
Technical Staff:	*MIWA, Tomoki*
	NISHIDE, Hiroyo
	NAKAMURA, Takanori
Technical Assistant:	*OKA, Naomi*

The Data Integration and Analysis Facility supports research activities based on large-scale biological data analysis, such as genomic sequence analysis, expression data analysis, and imaging data analysis. For this purpose, the facility maintains high-performance computers with large-capacity storage systems. On the basis of this system, the facility supports development of data analysis pipelines, database construction and setting up websites to distribute the data worldwide. In addition to computational analysis, the Data Integration and Analysis Facility supports NIBB's information infrastructure, the maintenance of the network system in the institute and computer/network consultation for institute members.

Representative Instruments

Our main computer system is the Biological Information Analysis System (BIAS) (Figure 1), which consists of a shared memory parallel computer (DELL PowerEdge R905; 4 nodes/16 cores, 256GB memory), a high-performance cluster system (DELL PowerEdge M1000e+M610; 32 nodes/256 cores, 768GB memory) and a large-capacity storage system (DELL Equallogic; 35TB SAS, 26TB SATA, 750GB SSD). All subsystems are connected via a high-speed InfiniBand network so that large amounts of data can be processed efficiently. Some personal computers and color/monochrome printers are also available. On this system, we provide various biological databases and data retrieval/analysis programs, and support large-scale data analysis and database construction for institute members. Especially, we have supported the construction and maintenance of published databases of various model organisms including XDB (*Xenopus laevis*), PHYSCObase (*Physcomitrella patens*), DaphniaBASE (*Daphnia magna*), The Plant Organelles Database, and MBGD (microbial genomes).

Figure 1. Biological Information Analysis System

The facility also provides network communication services. Most of the PCs in each laboratory, as well as all of the above-mentioned service machines, are connected by a local area network, which is linked to the high performance backbone network ORION connecting the three research institutes in Okazaki. Many local services, including sequence analysis services, file sharing services, and printer services, are provided through this network. We also maintain a public World Wide Web server that hosts the NIBB home page (http://www.nibb.ac.jp/).

Research activity by I. Uchiyama

Assistant professor I. Uchiyama is the principal investigator of the Laboratory of Genome Informatics, which currently focuses on microbial comparative genomics studies. For details, please refer to the laboratory page (p. ##).