## **NIBB CORE RESEARCH FACILITIES**



*Head* YOSHIDA, Shosei

The NIBB Core Research Facilities were launched in 2010 to support basic biological research at NIBB. They consist of three facilities that develop and provide state-of-theart technologies aimed at increasing the understanding of biological functions through the application of functional genomics, bioimaging, and bioinformatics. The NIBB Core Research Facilities also act as an intellectual hub to promote collaboration among NIBB researchers and other academic institutions.





Professor SHIGENOBU, Shuji

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The Functional Genomics Facility is a division of the NIBB Core Research Facilities organized jointly by NIBB and NIPS for the promotion of DNA and protein studies. The facility maintains a wide array of core research equipment, ranging from standard machinery (*e.g.* ultracentrifuges) to cutting edge tools (*e.g.* next generation DNA sequencers), which amount to 90 instruments in total. The facility is dedicated to fostering collaborations with researchers both at NIBB and other academic institutions worldwide through the provision of these tools as well as expertise. Our current focus is functional genomics. We also act as a bridge between experimental biology and bioinformatics through close consultation and training.

We recently renovated the facility building, and as part of this, the Visitors Lab and the Visitors Office were redesigned so that visiting scientists can work more effectively during their stay. In 2019, approximately 100 researchers came to use our facility and developed active collaborations, which consequently resulted in 21 co-authored papers published.

# **Representative Instruments** *Genomics*

The advent of next-generation sequencing (NGS) technologies is transforming modern biology thanks to ultra-highthroughput DNA sequencing. Utilizing HiSeq, NextSeq and MiSeq (Illumina), Sequel (PacificBio Sciences), and MinION and GridION (Oxford Nanopore Technologies), the Functional Genomics Facility is committed to joint research aimed at exploring new yet otherwise inaccessible fields in basic biology.

During 2019, we carried out 57 NGS projects in collaboration with researchers from academic institutions throughout the world. These projects cover a wide range of species (bacteria, animals, plants, and fungi) including both model and non-model organisms, and various other applications such as genomic re-sequencing, RNA-seq and ChIP-seq.



Figure 1. Next-generation sequencer

#### **Proteomics**

Two types of mass spectrometer and two protein sequencers, as listed below, are used for proteome studies in our facility. In 2019, we analyzed approximately 1000 samples with mass spectrometers and protein sequencers.

- LC-MS (AB SCIEX TripleTOF 5600 system)

- LC-MS (Thermo Fisher SCIENTIFIC Orbtrap Elite) Protein sequencer (ABI Procise 494 HT; ABI Procise 492 cLC)



Figure 2. Triple TOF LC/MS/MS System

### **Other analytical instruments** (excerpts)

- Cell sorter (SONY SH800)
- Bioimaging analyzer (Fujifilm LAS 3000 mini; GE FLA9000)
- Laser capture microdissection system (Thermo Fisher

Scientific Arcturus XT)

- Real-time PCR machine (Thermo Fisher Scientific ABI 7500)
- Ultracentrifuge (Beckman XL-80XP etc.)
- Microplate reader (PerkinElmer Nivo; Hitachi SH-9000Lab)
- Single-cell analysis system (Fluidigm C1)

# **Research activity by S. Shigenobu**

Professor Shuji Shigenobu is the principal investigator of the Laboratory of Evolutionary Genomics. Refer to the laboratory page for details.

#### **Publication List on Cooperation:**

[Original papers]

- Bessho-Uehara, M., Yamamoto, N., Shigenobu, S., Mori, H., Kuwata, K., and Oba, Y. (2020). Kleptoprotein bioluminescence: Parapriacanthus fish obtain luciferase from ostracod prey. Sci. Adv. 6, eaax4942. doi: 10.1126/sciadv.aax4942
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[Original paper (E-publication ahead of print)]

Shikanai, Y., Yoshida, R., Hirano, T., Enomoto, Y., Li, B., Asada, M., Yamagami, M., Yamaguchi, K., Shigenobu, S., Tabata, R., Sawa, S., Okada, H., Ohya, Y., Kamiya, T., and Fujiwara, T. Callose synthesis suppresses cell death induced by low-calcium conditions in leaves. Plant Physiol. 2020 Feb 5 doi: 10.1104/pp.19.00784

### SPECTROGRAPHY AND BIOIMAGING FACILITY



Specially Appointed Associate Professor KAMEI, Yasuhiro

Technical Staff:

Technical Assistant:

KONDO, Maki TANIGUCHI-SAIDA, Misako ICHIKAWA, Chiaki ISHIKAWA, Azusa NAKAGAWA, Mami

The Spectrography and Bioimaging Facility assists both The Spectrography and Bioimaging Facility assists both collaborative and core research by managing and maintaining research tools that use Light. The facility, under the guidance of Dr. Kamei, also provides technical support through the management of technical staff assisting in the advancement of collaborative and core research projects, as well as academic support to researchers (please refer to the Collaborative Research Group Research Enhancement Strategy Office section for more information). Among the equipment available are advanced biological microscopes, and the Okazaki Large Spectrograph for photobiology. The Okazaki Large Spectrograph is the world's largest wide spectrum exposure mechanism, and is capable of producing a range of wavelengths from 250 nm (ultraviolet) to 1,000 nm (infrared) along its 10 meter focal curve, thus allowing exposure to strong monochromatic light. The facility's microscopes, which include cutting edge devices such as confocal and multi-photon excitation microscopes, are an indispensable part of core and collaborative projects conducted by both internal and external researchers.

# Standard Instruments: Okazaki Large Spectrograph (OLS)

The spectrograph runs on a 30 kW Xenon arc lamp and projects a wavelength spectrum ranging 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* 



Figure 1. An example of an experiment using the Large Spectrograph. In this photo, various color rays (monochromatic light from right side and reflected by mirrors) are irradiated simultaneously to samples stored in cooling chambers.

*al.*, Photochem. Photobiol. *36*, 491-498, 1982). The spectrograph is dedicated to action spectroscopical studies of various light-controlled biological processes.

In addition to the other action spectroscopical studies concerning various regulatory and damaging effects of light on living organisms, research involving biological molecules and artificial organic molecules have been conducted since it was set up. 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 members of NIBB.

### Microscopes

This facility also provides bioimaging machinery, such as wide-field microscopes (Olympus IX-81 and BX-63), confocal microscopes (Leica TCS-SP8, Nikon A1R, Nikon A1Rsi and Yokogawa CSU-X1 with EM-CCD/ CMOS cameras), multi-photon microscopes (Olympus FV1000-MP, FV1200-MPs, Leica TCS-SP8 MPs) and other advanced laser microscopes boasting specialized, cutting edge technology (Light-sheet Microscope and Infrared Laser-Evoked Gene Operator microscope: IR-LEGO), which can be utilized by researchers within NIBB, as well as collaborative guest researchers. Starting from 2016, we commenced two new types of Collaborative Research Programs. One is a new category within the NIBB Collaborative Research for Integrative Bioimaging program using machinery and bioimage processing/analysis techniques, and the other is the Advanced Bioimaging Support Program (ABiS) which operates under the framework of the Grant-in-aid for Scientific Research on Innovative Areas.

The light-sheet microscope 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 tissues by illuminating specimens from the side with a light sheet (more information is given in the report submitted by Dr. Shigenori Nonaka's Laboratory for Spatiotemporal Regulations ). Dr. Nonaka conducted and supported about 10 Collaborative Research Program projects for Integrative Bioimaging. The IR-LEGO, developed by Drs. Shunsuke Yuba and Yasuhiro Kamei at the National Institute of Advanced Industrial Science and Technology



Figure 2. Microscope images of green algae, *Codium fragile*. Sample was stained by hoechst33342. (A) Bright and blue fluorescent marge image. (B) Blue fluorescent and red fluorescent marge image. Images were taken by visitor of cooperation program from Osaka City University (Seki, Soichiro). *C. fragile* (KU-0654) was provided by KU-MACC, Kobe University.

(AIST), can induce a target gene of interest by heating a single target cell *in vivo* with a high efficiency irradiating infrared laser (details are provided in the next section). The IR-LEGO was also used for about 10 Collaborative Research projects, including applications aimed at animals and plants.

### Workshop, Symposium and Training course

In 2019, we held the 7<sup>th</sup> biological image processing training course in cooperation with Drs. Kagayaki Kato, Shigenori Nonaka, Takashi Murata and Hiroshi Koyama. We also have been holding a "Bioimaging Forum" every year, which discusses bioimaging from various technical perspectives such as microscopy, new photo-technology, and computer science. This year we planned on staging the 14<sup>th</sup> NIBB Bioimaging Forum focused on micro CT technology in February, 2020. However, this forum was postponed until next year due to the global COVID-19 pandemic.

### **Research activity by Y. Kamei**

Specially Appointed Associate Professor Yasuhiro Kamei is the principal investigator of Laboratory for Biothermology. For details, please refer to the laboratory page.

### **Publication List on Cooperation**

[Original papers]

- Aoyama, S., Asahi, C., Sano, K., Kimura, S., Suzuki, T., Hatano, T. and Arimoto-Kobayashi, A. (2019). Isolation and identification of photoproducts from UVA-irradiated mixture of N-nitrosoproline with 2'-deoxyadenosine. J. Photochem. Photobiol A: Chem. 377, 159-166. doi: 10.1016/j.jphotochem.2019.03.016
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- Ikehata, H., Mori, T., Kamei, Y., Douki, T., Cadet, J., and Yamamoto, M. (2020). Wavelength- and tissue-dependent variations in the mutagenicity of cyclobutane pyrimidine dimers in mouse skin. Photochem. Photobiol. 96, 94-104. doi: 10.1111/php.13159
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- Nakane, Y., Shinomiya, A., Ota, W., Ikegami, K., Shimmura, T., Higashi, S., Kamei, Y., and Yoshimura, T. (2019). Action spectrum for photoperiodic control of thyroid-stimulating hormone in Japanese quail (*Coturnix japonica*). PLoS One 14, e022106. doi: 10.1371/journal. pone.0222106
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## **DATA INTEGRATION AND ANALYSIS FACILITY**

Assistant Professor: Technical Staff:

Technical Assistant:

UCHIYAMA, Ikuo NISHIDE, Hiroyo NAKAMURA, Takanori SUGIURA, Hiroki OKA, Naomi

The Data Integration and Analysis Facility supports research activities based on large-scale biological data analysis, such as genomic sequence, expression data, and imaging data analysis. To achieve this, the facility maintains high-performance computers with large-capacity storage systems. It accordingly supports the development of data analysis pipelines and database construction based on these systems, and also sets up websites to distribute data worldwide as well as providing basic technical support. In addition to computational analysis, the Data Integration and Analysis Facility supports NIBB's information infrastructure, the maintenance of the institute's network systems and provides 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 high-performance cluster system (HPE Apollo r2800, 20 nodes/800 cores, 192 GB memory/node), a shared memory parallel computer (HPE ProLiant DL560, 72 cores, 3TB memory; HP ProLiant DL980 G7, 80 cores, 4TB memory), a high-throughput storage system (DDN SFA7700X, 1.52PB+880TB), and a large capacity storage system (DELL PowerEdge R620, 720TB). All subsystems are connected via a high-speed InfiniBand network, so that large amounts of data can be efficiently processed. Some personal computers and color printers are also available for use. 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 and collaborative researchers. We have provided support in the construction and maintenance of published databases of various model and non-model organisms in particular. These include XDB (Xenopus laevis), PHYSCObase (Physcomitrella patens), iNewt (Pleurodales waltl), The Plant Organelles Database, MBGD (microbial genomes), and DB-HABs (harmful algal blooms).

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 ORION network connecting the three research institutes in Okazaki. Many local services, including sequence analysis, file sharing, 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/en).



Figure 1. Biological Information Analysis System

# Research activity by I. Uchiyama

Assistant Professor Ikuo Uchiyama is the principal investigator of the Laboratory of Genome Informatics. For more details, please refer to the laboratory page.