NATIONAL UNIVERSITY CORPORATION
OKAYAMA UNIVERSITY

Institute of Plant Science and Resources

IPSR
SINCE 1914





CONTENTS

Atmospheric Stress Unit

Soil Stress Unit

Biotic Stress Unit

Genetic Resources Unit

Applied Genomics Unit

I History

The Institute was founded in 1914 as the "Oohara Institute for Agricultural Research" by Magosaburo Oohara, a leading citizen of Kurashiki City, with the purpose of advancing agricultural sciences.

After the Second World War, the Institute became affiliated with the School of Agricultural Science of Okayama University founded in 1951, and became the"Institute for Agricultural Biology"under the direct supervision of the University in 1953. Initially, five research divisions were organized; Applied Entomology, Biochemistry, Plant Genetics, Plant Pathology and Plant Physiology. Later new divisions were added, Micrometeorology in 1960, Biological Water Quality in 1966 (the name of this division was changed to Water Quality in 1975), Weed Science in 1970 and the Barley Germplasm Center in 1979.

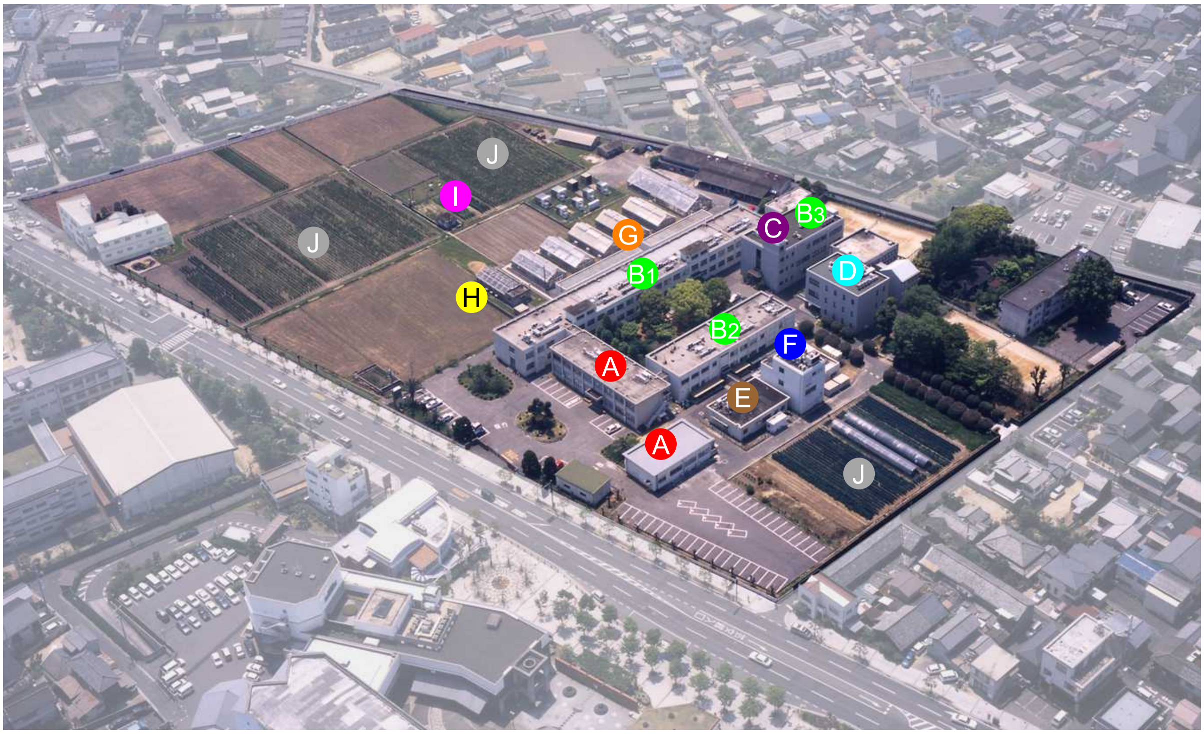
The Institute has carried out research on bioresources from an array of viewpoints for 70 years. The English name of the Institute was officially changed to the "Institute for Agricultural and Biological Sciences, Okayama University" in 1970.

In order to meet the new scientific and social demands, the Institute was reorganized and renamed" The Research Institute for Bioresources, Okayama University" in 1988. The new Institute was composed of three divisions including nine laboratories, a division for a Foreign Visiting Professor and the Barley Germplasm Center. The last division and the center were unified to establish the Barley and Wild Plant Resource Center in 1997. Again this institute was reorganized in 2003. The new organization is composed of the Division of Functional Biology and Genetics, the Division of Environmental Response Analysis, and the Barley and Wild Plant Resource Center.

In 2004, Okayama University along with a number of other universities were restructured and realigned under the National University Corporation system. Since the institute was approved in June, 2009 as a center-of-excellence in the fields of “plant genetic resources and plant stress science” by the Ministry of Education, Culture, Sports, Science and Technology, Japan, it was reorganized as the “Institute of Plant Science and Resources (IPSR)” on April 1, 2010, as a joint usage and research center for scientists in Japan, particularly addressing plant stress studies using genetic resources of barley and wild plant species.

This institute also contributes to the education of students in the Graduate School of Natural Science and Technology and Graduate School of Environmental Science (Master’s and Doctor’s Degree Course) at Okayama University

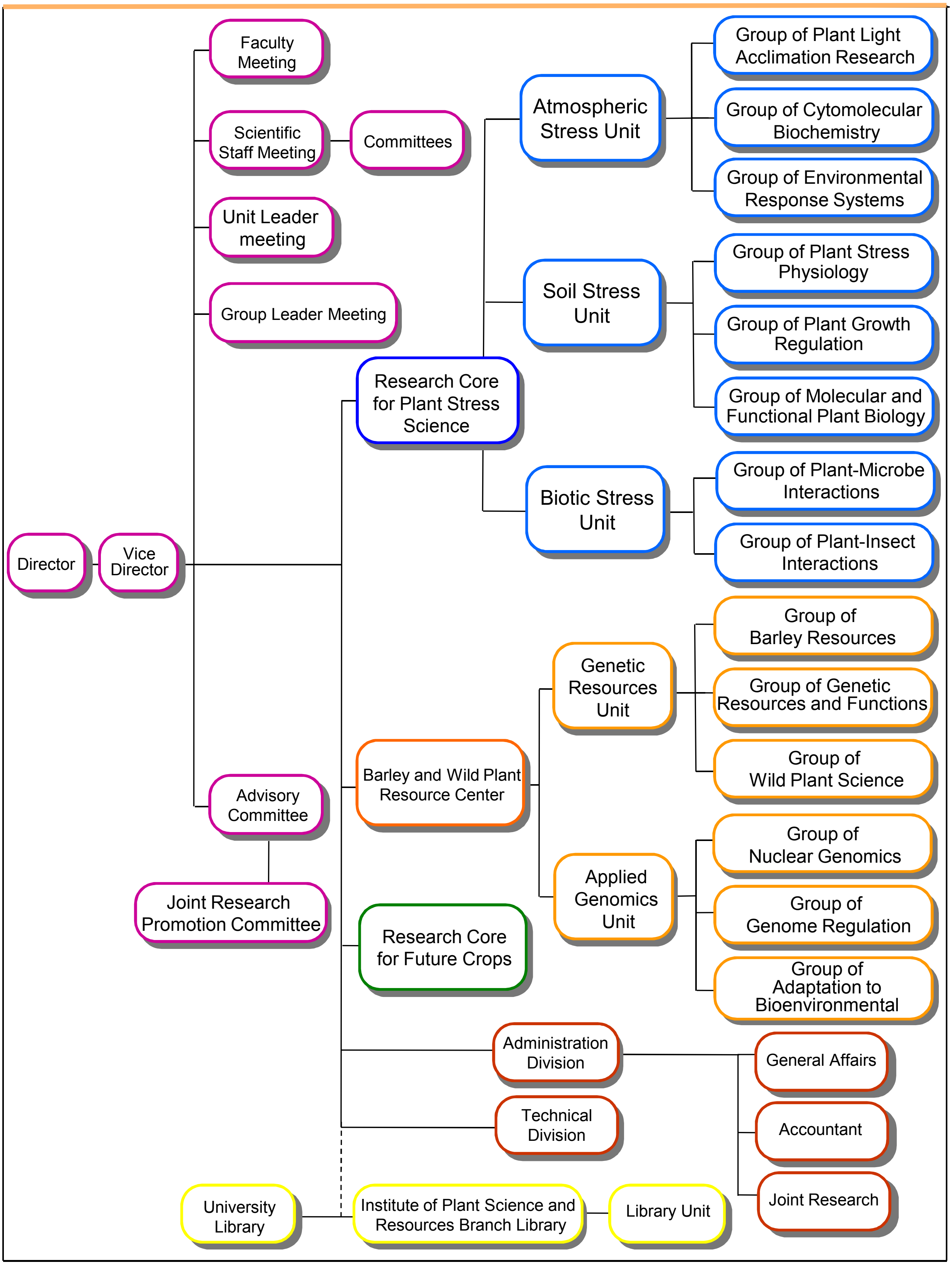
II Building



A	Administration	F	Gene Research Building
B1 ~ B3	Laboratory	G	Greenhouses
C	Barley and Wild Plant Resource Center	H	Isolation Greenhouse
D	Library	I	Climate Station
E	RI Laboratory	J	Research Fields

Total area	38,007 m^2
Building area	9,144 m^2

III Organization



IV Number of Staff

Full-time Staff

Professors	Associate Professors	Assistant Professors	Research Associate	Technical Officials	Administration Officials	Total
10	8	13	1	9	5[1]	46[1]

[ ] Librarian of Institute of Plant Science and Resources Branch Library

Part-time Staff

Part-Time Technical Assistants	Part-Time Researchers	Part-Time Workers	Tota1
11(1)	8	26	45(1)

( ) Woman Tenure-Track

Advisory Committee

Members outside the Univ.	Takashi Endo	Dean, Graduate School of Agriculture, Kyoto Univ.
	Kazuo Shinozaki	Director, Plant Science Center, RIKEN
	Naoko Nishizawa	Prof., Research Institute for Bioresources and Biotechnology, Ishikawa Pref. Univ.
Members at the Univ.	Yuichiro Takahashi	Prof., Graduate School of Natural Science and Technology, Okayama Univ.
	Tomonori Shiraishi	Prof., Graduate School of Natural Science and Technology, Okayama Univ.

Joint Research Promotion Committee

Members outside the Univ.	Motoyuki Ashikari	Prof., Bioscience and Biotechnology Center, Nagoya Univ.
	Toru Fujiwara	Prof., Biotechnology Research Center, Tokyo Univ.

V Education at Graduate School of Natural Science and Technology

Master's course

Graduate School	Division	Department
Natural Science and Technology	Science for Bioresources	Plant Stress Science

Doctor's course

Graduate School	Division	Department
Natural Science and Technology	Bioscience	Plant Stress Science

Number of students		2009	2010	2011
Master's course	New students (from outside the Okayama Univ.)	9 (9)	8 (8)	4 (3)
	Total students	17	18	13
	Persons that received a degree	6	9	–
Doctor's course	New students (entered at Oct.)	3 (+3)	1 (+3)	2
	Total students	11	13	12
	Persons that received a degree (by submitting a thesis)	3	3	–
Total	Total students	30	30	25

VI Library and Publications

Institute of Plant Science and Resources Branch Library, Okayama University

The Institute library was established in 1921, and is recognized as one of the best agricultural and biological libraries in Japan, with an extensive selection of scientific periodicals as well as rare and valuable books.

These materials have been available to the public since its establishment, and have been consulted by researchers from all over Japan. Some of special collections are exhibited on the occasion of permanent or special exhibition.

Library materials

Total number of books	184,015 (92,871 Japanese and 91,144 foreign)
Total number of periodicals	12,085 (7,457 Japanese and 4,628 foreign)

Special collections

Pfeffer's collection	11,730 volumes relating to botany collected by Dr. W. Pfeffer(1845-1920), professor of Leipzig University. Pflanzenphysiologie (Pfeffer, W.) etc.
Oohara's collection of Chinese books	4,720 volumes relating to early Chinese agriculture
Oohara's collection of Japanese agricultural books	2,576 volumes relating to Japanese agriculture and wild plants, issued during the Edo and Meiji era.

Pflanzenphysiologie (Pfeffer, W.)

The Konyo-manroku (An essay relating to Japanese agriculture written by Konyo Aoki)

Publications

Bulletin of the Institute of Plant Science and Resources, Okayama University, issued once or twice a year since 1992.

VII Public offering of joint research and major equipment

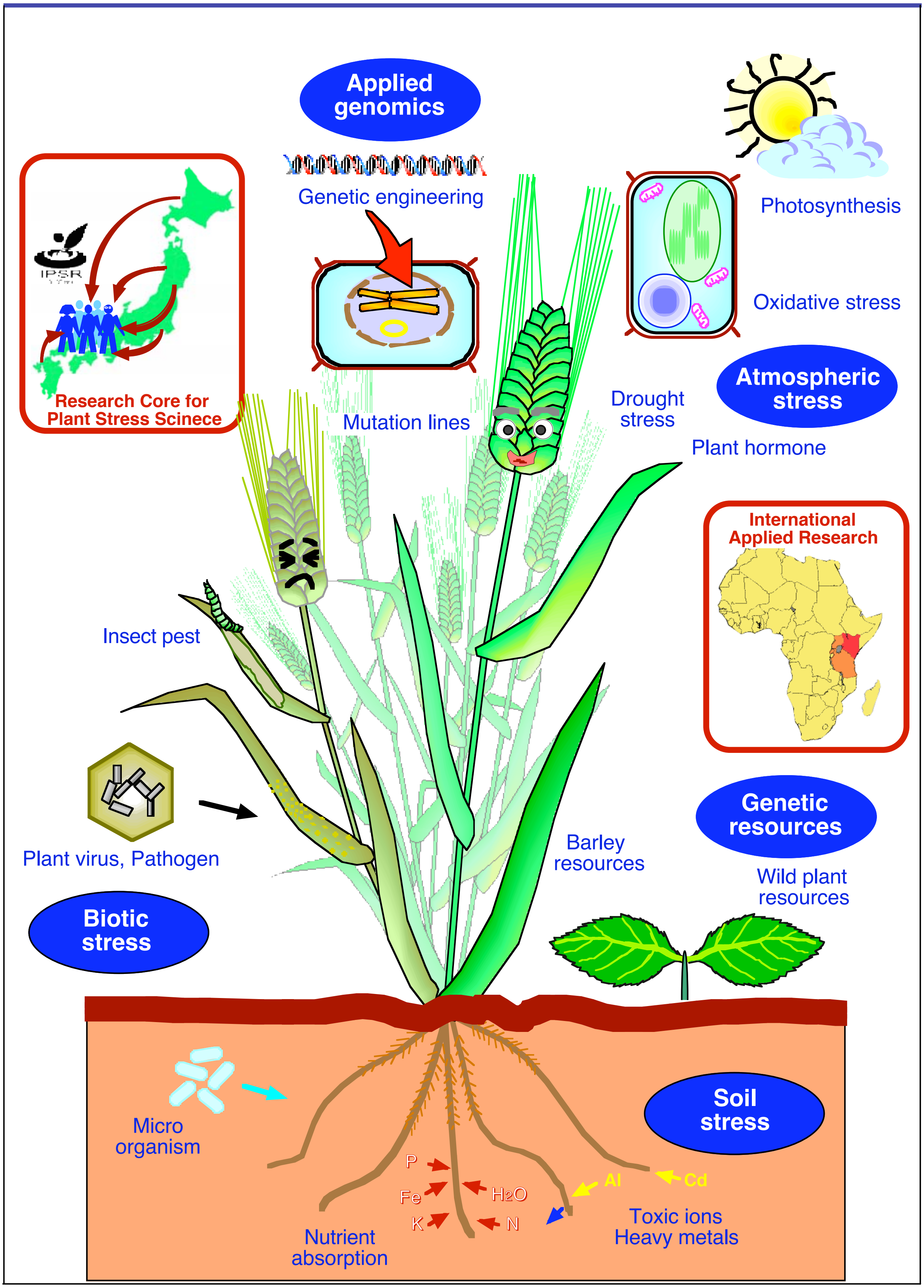
Public offering of collaborative research

Institute of Plant Science and Resources (IPSR) publicly offers opportunities for joint research with outside researchers. After evaluation by the Joint Research Promotion Committee and the Steering Committee, researchers with selected proposals can perform joint research at the institute. All studies are conducted in conformity with the rules of the institute and under a collaboration agreement. A public offering of collaborative research is made every year. The deadline is the end of February. For more details, please check our homepage http://www.rib.okayama-u.ac.jp/index-j.html

Major equipment

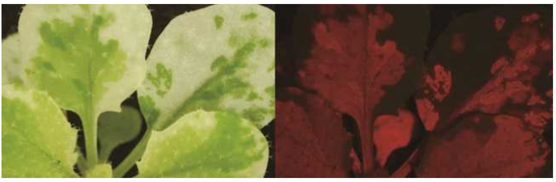
The institute offers research facilities and equipment for collaborators of selected proposals. Major equipment is as listed below.

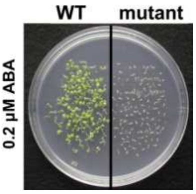
- Energy-saving growth system for transgenic plants
- TEM
- SEM
- DNA sequencer
- DNA microarray scanner
- ICP－MS
- MALDI－TOF/MS/MS


Applied genomics
Genetic engineering
Photosynthesis
Oxidative stress
Research Core for Plant Stress Scinece
IPSR
Mutation lines
Drought stress
Atmospheric stress
Plant hormone
International Applied Research
Insect pest
Plant virus, Pathogen
Biotic stress
Barley resources
Genetic resources
Wild plant resources
Micro organism
Soil stress
P
Fe
K
H2O
N
Al
Cd
Nutrient absorption
Toxic ions
Heavy metals

VIII Research Core for Plant Stress Science

Plant stresses are classified into three major factors as described below. Research units corresponding to respective stress factors carry out collaborative studies. In each unit, plant stress responses and plant interactions with other organisms are studied using various approaches of physiology, biochemistry, pathology, and genetics. Barley and wild plant germplasm collected at the institute will be used effectively to develop stress-tolerant crop plants.





Atmospheric Stress Unit

Under atmospheric environments, fluctuations of light intensity, temperature, or humidity can significantly reduce plant growth and ultimately affect the crop yield. To acclimate to such atmospheric stresses, plants have evolved various ways by which growth defects can be minimized. The atmospheric Stress Research Unit specifically examines light stress on photosynthetic apparatus in chloroplasts, response to oxidative stress caused by reactive oxygen species, and roles of a phytohormone—abscisic acid—during drought, and aim at understanding the mechanism(s) that enable plants to tolerate atmospheric stresses at the molecular level. Combined with the use of available genetic resources, our research will facilitate engineering of crops that are acclimated to the atmospheric stresses.

Soil Stress Unit

Problem soils including acid, alkaline, salt and heavy-metal contaminated soils comprise approximately 70% of world’s arable soils. Because of deficiency and/or excess of minerals, the productivity and quality of crops on these soils are low. Drought (shortage of soil water) is also a major limiting factor for crop production. It is a key to enhancing crop productivity and to improving crop product safety on problem soils to solve future shortage problems related to foods and fuels. In this unit, we specifically examine the response and tolerance mechanisms of plants to problem soil stresses such as drought, salt, aluminum toxicity, iron deficiency, heavy metals, etc. Our goal is to breed crops with increased productivity and safety on problem soils.

Biotic Stress Unit

Plants are exposed to various biotic stresses in the environment. They are exemplified by infectious pathogens such as viruses, bacteria and fungi, and destructive insects. By contrast, numerous microorganisms support the healthy growth of plants, e.g., those infecting plant pathogens to attenuate their virulence, soil-borne organisms that are mutualistic to plants, and beneficial microorganisms residing on the aerial parts of plants. The ultimate goal of this unit is to achieve “Healthy Plant Growth.” To attain this goal, we study plant responses to organisms that are influential to plant growth; we also study the molecular mechanisms of their effects, which enhances a better understanding of the dynamic interactions that occur among organisms affecting plants and those that occur between plants and organisms.

Group of Plant Light Acclimation Research

Professor Wataru Sakamoto
Assistant Professor Ryo Matsushima

Our group studies plant adaptation to light environment. To this end, we specifically examine chloroplasts. Photosynthetic apparatuses in chloroplasts are constantly damaged by excess light energy. Therefore, it is important to understand mechanisms(s) for plants to acclimate to strong light. Chloroplast development is a complex process that occurs during plant growth. We employ various approaches to investigate and engineer important factors affecting chloroplast development.

1. Damage and repair of photosynthetic complexes

Photosynthetic protein complexes in thylakoid membranes of chloroplasts are prone to receive oxidative damage. Therefore, they develop a sophisticated repair system by which photodamage is targeted to Photosystem II. We study critical factors such as proteases involved in this repair system.

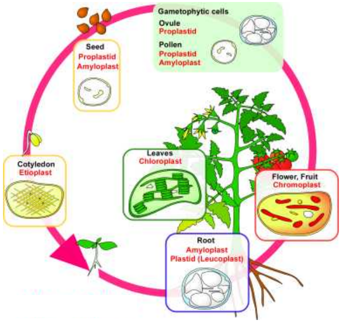
2. Studies of signals/factors controlling plastid development and multi-function

Proplastid (precursor of plastids) can differentiate into plastids of various types such as chloroplasts and amyloplasts. Our molecular genetic studies attempt to identify signals/factors that control plastid development.

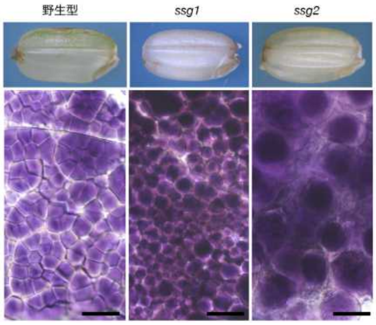
3. Continuity and genetic engineering of plastid genome

Plastids originate from cyanobacterial endosymbiosis and carry their own genome. Our studies specifically examine the inheritance mode of plastid DNAs (maternal inheritance) and on genetically engineering plastid genomes, which can provide a useful strategy for foreign gene expression in plants.

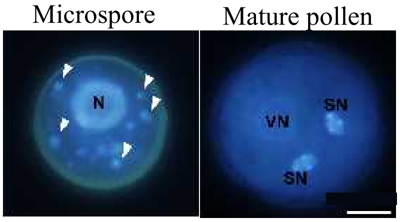
Measurement of photosynthetic activity



Life cycle of plastids



Amyloplast-related rice mutants



Organellar DNA degradation
during pollen development

Group of Cytomolecular Biochemistry

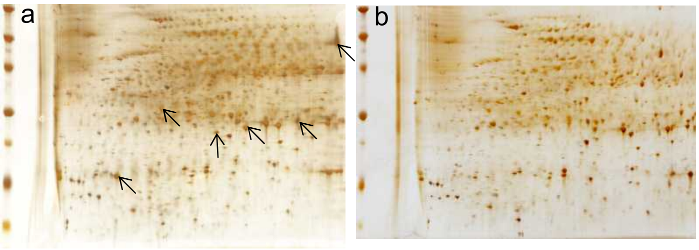
Associate Professor Haruyoshi Konno
Associate Professor Manabu Sugimoto

Plants are sensitive to various environmental stimuli. They respond to physical, chemical, and biological stress factors. Consequently, plants can undergo changes in their development, morphology, and physiology during their life cycle.

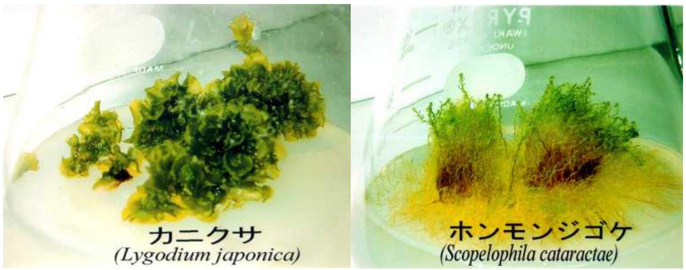
We have elucidated the physiological function and stress tolerance mechanisms of plant cells under stress conditions using biochemical techniques.

Current research includes

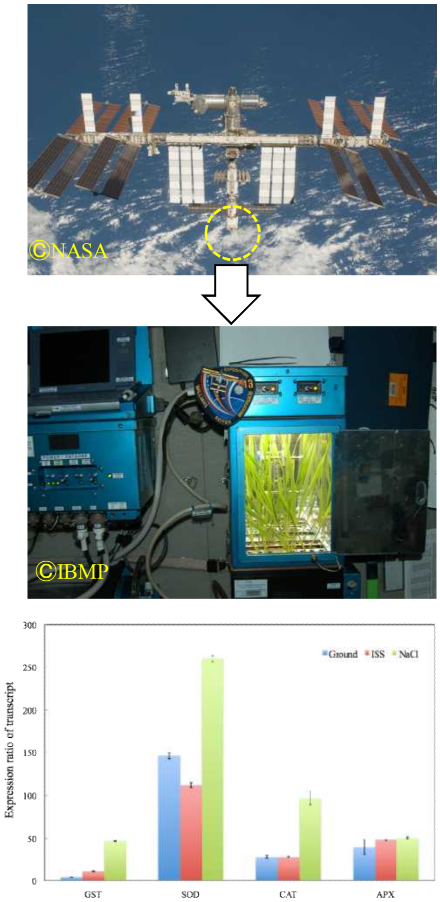
1) Functions of genes and proteins expressed in plants exposed to a space environment and oxidative stress, and their application to the development of stress-tolerant plants.
2) Mechanisms of metal tolerance in wild plants.
3) Characteristics of plant cell walls and their degrading enzymes.



Two-dimensional gel profiles of proteins extracted from roots of salt-tolerant barley (a) and salt-sensitive barley (b). Specific protein spots located in salt-tolerant barley (arrows).



Fern (L) and moss (R) grown in a copper-rich medium.



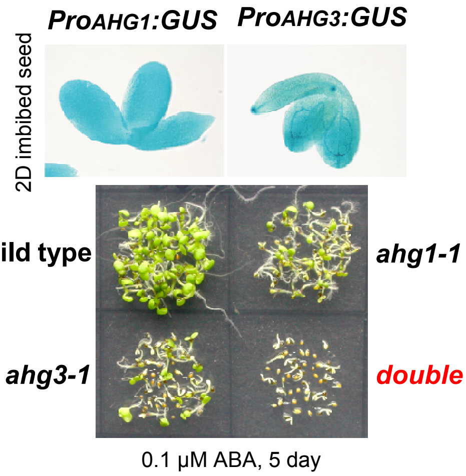
Gene expression of plants grown in the plant growth chamber onboard Russian segment of the International Space Station.

Group of Environmental Response Systems

Professor	Takashi Hirayama
Assistant professor	Izumi Mori

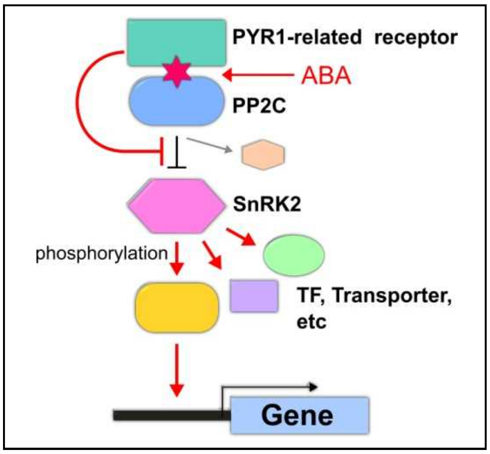
As sessile organism, plants cannot move. Therefore, plants must sense and adapt to environmental changes. They are presumed to have unique mechanisms that are used for environmental stress responses. Our group has been studying the mechanisms of responses to abiotic stresses such as drought stress and to phytohormones involved in these processes using molecular genetics, molecular biology, and cell physiology. Our goal is to understand the stress-sensing mechanisms and interactions between various hormonal responses.

A phytohormone, abscisic acid (ABA), is deeply involved in abiotic stress responses of plants. Several plants with abnormal responses to abscisic acid (ABA) have been isolated from the model plant Arabidopsis and then analyzed. Through molecular genetic analysis of these mutants and biochemical characterization of the gene products, we established a major ABA signaling pathway comprising PYR1 type ABA receptor, PP2C, and SnRK2. We are also studying interactions between ABA and other plant hormones.



PP2C mutants, *ahg1* & *ahg3*

Genetic impairment in two type 2C protein phosphatases (PP2C), AHG1 and AHG3, caused strong ABA hypersensitivity in germination. Upper panel, expression pattern in seeds; lower, ABA sensitivity in germination.

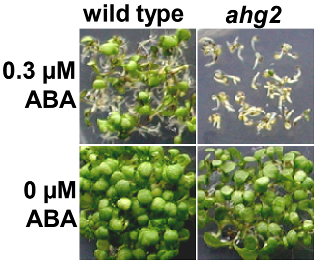


Model of the major ABA signaling pathway

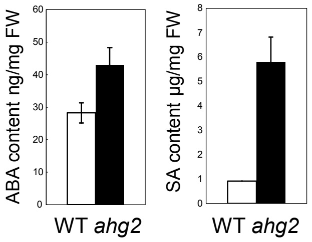
The PYR1-type ABA receptor binds to PP2Cs and inhibits their activity in the presence of ABA. It subsequently induces activation of SnRK2 protein kinases that activate a series of ABA responsive mechanisms, such as transcription factors and transporters.

Novel mutant, *ahg2-1*

ahg2-1 exhibits hypersensitivity to both ABA and salicylic acid (SA), which are believed to function in a mutually antagonistic fashion. Analyzing this mutant is expected to provide new clues to dissect the complex interaction between these two hormones. *AHG2* encodes enzymes involved in RNA degradation indicating RNA metabolisms somehow take part in the hormone responses and interactions.



ABA sensitivity at germination



Endogenous hormone levels

Group of Plant Stress Physiology

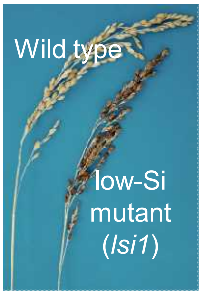
Professor Jian Feng Ma
Assistant Professor Naoki Yamaji

Crop production on 70% of the world's soil is limited by mineral stresses, which include deficiency of essential elements and/or excess of essential and other elements. To improve crop production on these problem soils, our group specifically examines the response of plants to mineral stresses, especially for understanding the tolerance mechanisms from the gene to the whole plant level.

Beneficial effects of silicon

In fact, Si is the only element which alleviates multiple plant stresses including diseases, pests, and lodging. Rice is a typical Si-accumulating plant. It requires great amount of Si for healthy growth.

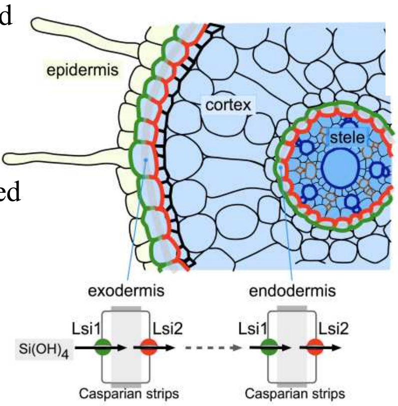
Suppression of leaf blast



Effect on grain discoloration

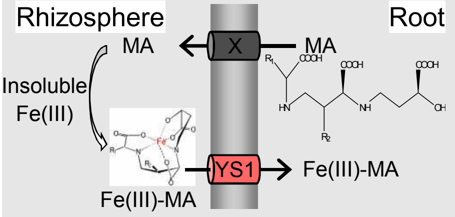
Molecular mechanism of rice Si uptake

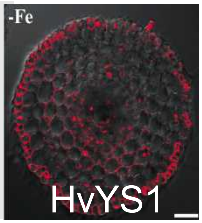
The Si influx and efflux transporters Lsi1 and Lsi2 are localized at opposite sides of the root exodermis and endodermis. The Si transported into the cells by Lsi1 is exported by Lsi2 to reach the stele.



Tolerance mechanism of Fe-deficiency stress

Gramineous plants acquire insoluble soil iron by secreting mugineic acids (MAs) as an iron chelator from the roots. Barley has a specific transporter, HvYS1, for Fe(III)-MA complex at the root epidermis.

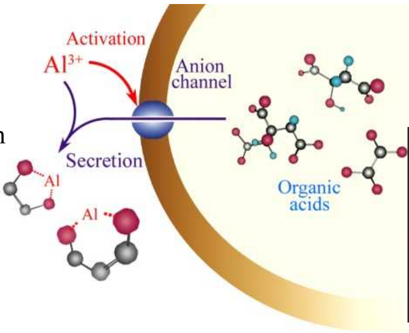


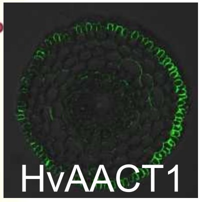


Tolerance mechanisms of Al-toxicity

In acidic soil, toxicity of aluminum ion (Al^{3+}) is the major factor limiting crop production. However, some species have evolved various strategies to detoxify Al.

The Al-tolerant cultivars of barley secrete citrate from the roots, which is mediated by an Al-activated citrate transporter HvAACT1.





Metal-accumulating plants

Plant growth is usually inhibited by metals at high concentrations. However, a few plant species are known to accumulate metals at high concentrations without exhibiting symptoms of toxicity. Hydrangea (left) and *Thlaspi caerulescens* (right) respectively represent two examples of Al-accumulators and Cd and Zn hyperaccumulators, respectively. They detoxify metals internally by forming non-phytotoxic complexes with ligands and/or sequestering of the metals to the vacuoles.

Group of Plant Growth Regulation

Professor Yoko Yamamoto
Assistant Professor Takayuki Sasaki

Aluminum (Al) ion is a major limiting factor of crop growth in acidic soils. We study both Al toxicity and tolerance mechanisms. Major toxic symptoms are cell elongation inhibition and cell death. The mechanisms of these symptoms are analyzed, particularly addressing sugar uptake and sugar metabolisms now. Furthermore, the effect of Al stress on photosynthesis in shoot parts is analyzed to elucidate how stress at root parts will be recognized and overcome on a whole plant level. On the other hand, we isolated wheat Al-tolerant gene (also acid-soil-tolerant gene), *ALMT1*, which encodes Al-activated malate transporter. Now, the expression and functional analyses (e.g. activation mechanism by Al) are studied using molecular-biological and electrophysiological techniques. Furthermore, because the *ALMT* gene family is specific to plants, the functional diversity of the *ALMT1* homologues is studied.

Fig. 1 Al symptom in acidic soil

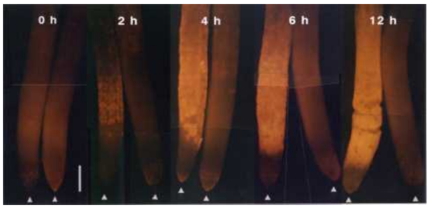


Fig. 2 Reactive oxygen species (ROS) induced by Al in pea roots

Al ion triggers ROS production at the root elongation zone (shown as orange by DHE staining; right, control root; left, Al-treated root). Yamamoto et al. (2002, 2003)

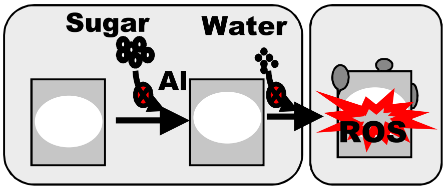


Fig. 3 Mechanism of cell elongation inhibition by Al

In tobacco cells, Al ion inhibits sugar uptake, which is apparently a direct cause of the inhibition of water uptake (namely, cell elongation inhibition). Then, ROS production is induced, which engenders cell death. Abdel-Basset et al. (2010) et al. (2010)

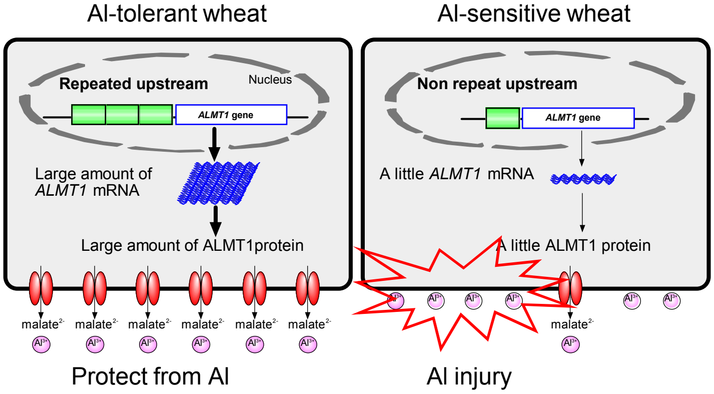


Fig. 4 Relationship between upstream sequence of *ALMT1* and Al tolerance in wheat

The number of repeats in the *ALMT1* upstream region is correlated positively with the levels of *ALMT1* expression and Al tolerance. This finding enabled the development of molecular markers based on the Al tolerance gene of wheat. Sasaki et al. (2006), Raman et al. (2008)

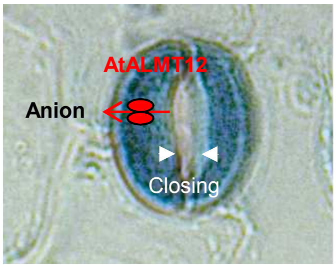


Fig. 5 Guard-cell AtALMT12

AtALMT12 anion transporter is required for stomatal closure in *Arabidopsis*. It is important to know the functional diversity of the plant specific ALMT-type transporter family. Sasaki, Mori, Furuichi et al. (2010)

Group of Molecular and Functional Plant Biology

Associate Professor Maki Katsuhara
Assistant Professor Mineo Shibasaka

In this laboratory, we study response mechanisms of plants against drought and salt stress environments, especially the molecular functions of plant cell and biomembranes. At present, the following research is underway:

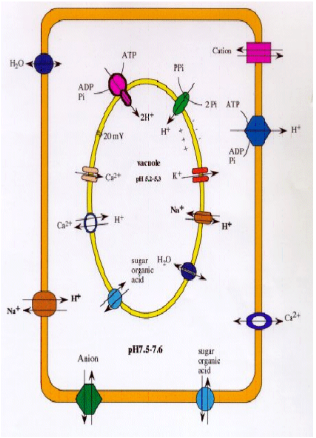
- ≫ Structure and function of water channels (aquaporins)
  - ●Regulatory mechanisms of water transport activity in aquaporins
  - ●Aquaporins permeating molecules other than water (CO_2 and H_2O_2)
- ≫ Plant molecular and cell physiological studies of the stress tolerance mechanism
  - ●Relation between stress response and controlling expression of aquaporins and water transport activities in roots
  - ●Functional analysis of membrane transport proteins against salt stress
  - ●Stress-induced programmed cell death
- ≫ New technology for roof-top greening with high drought-stress tolerance

Goals of our research are:

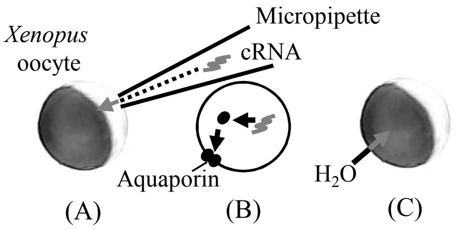
- ◆ Increase of crop production with plants growing well under stressful environments
- ◆ Promotion of environmental greening and controlling global water crisis

We use the following techniques and methods as well as general physiological and molecular biological methods:

Measurement of root functions (water permeability, ion transport)/ *Xenopus* oocyte expression system/ Electrophysiological measurements/Tracer experiments/ Complementary transgenic experiment with yeast mutants/Bioinformatics



Transport proteins in the plant cell.



Xenopus oocyte expression system. The cRNA synthesized with template cDNA is injected into a *Xenopus* oocyte (A). Protein is composed in the oocyte cell and membrane protein is incorporated in a plasma-membrane (B). With hypotonic conditions, water flows into the oocyte. The cell starts swelling if the expressed protein has a water transport activity (C).

Roof-top greening with a thin-layer/fixed soil system (top) and a wetland type (bottom)

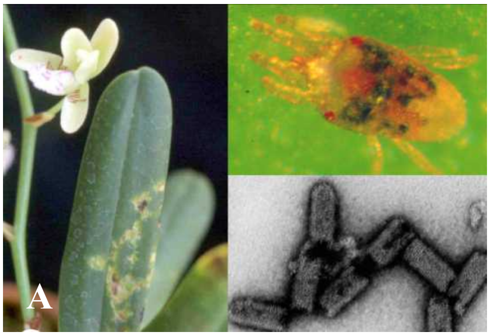
Group of Plant-Microbe Interactions

Professor	Nobuhiro Suzuki
Assistant Professor	Hideki Kondo
Assistant Professor	Akio Tani

Plant growth is influenced by various microorganisms including beneficial and harmful ones. Among them are plant-infecting viruses that severely damage crops, and mycoviruses infecting phytopathogenic fungi that serve as biocontrol (virocontrol) agents. In addition, an increasing number of plant-mutualistic bacteria and fungi that enhance plant growth and stress tolerance have been found. This group is mainly engaged in the three projects explained below.

1 plant/pathogenic virus/vector

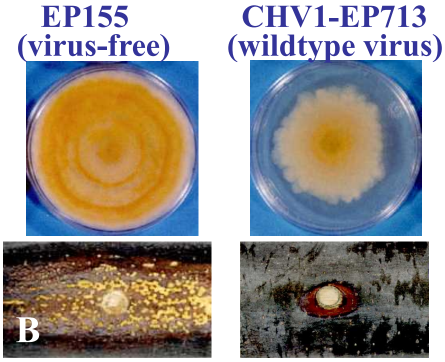
Three systems—orchids/viruses/*Brevipalpus californicus*, *Arabidopsis thaliana*/viruses, and *Triticeae*/viruses—are the subjects of exploration at the molecular, cellular, and individual levels of pathogenesis, replication, and vector transmissibility of plant viruses, and plant responses to virus infections. Plant virus-based vectors are also developed.



A. OFV: symptoms in an orchard, the vector *Brevipalpus californicus* and virus particles

2 plant/pathogenic fungus/virus

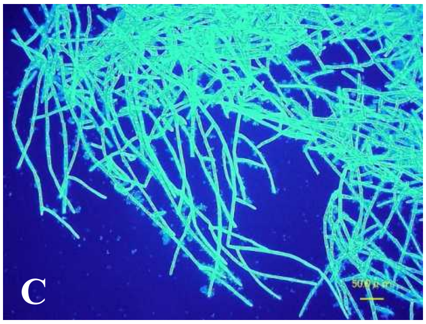
Using two combinations, chestnut/chestnut blight fungus/mycoviruses and fruit tree/root rot fungi/mycoviruses, viral replication and symptom expression were investigated at the molecular and cellular levels for use in virocontrol of the plant pathogenic fungi.



B. Chestnut blight fungus infected with a hypovirus

3 plant/mutualistic microorganism

The ecology of microorganisms interacting with plants in the phyllosphere is investigated. We seek and identify microorganisms that are capable of enhancing plant growth, and reveal its mechanism to apply microorganisms for crop improvement.



C. Interaction of bacteria and protonemata of *Racomitrium japonicum*, which is a moss that is used for roof greening

Group of Plant-Insect Interactions

Professor Ivan Galis

Plant defenses against insects evolved in a long term process of co-evolution of plants and herbivorous insects. In this process, plants developed enormous diversity in their chemical and mechanical defenses, and tuned regulation of defense mechanism to optimize the distribution of plant resources between defense and growth. Two main defense strategies of plants against insects involve direct and indirect defense mechanisms:

(1) Direct defenses are based on the production of toxic chemicals that directly inhibit feeding of herbivores

(2) During indirect defense, plants produce volatile compounds that attract natural enemies of herbivores that provide efficient protection to plants

<u>In the group, we focus on understanding of plant-herbivore interactions and induction of direct and indirect defenses in plants at following levels:</u>

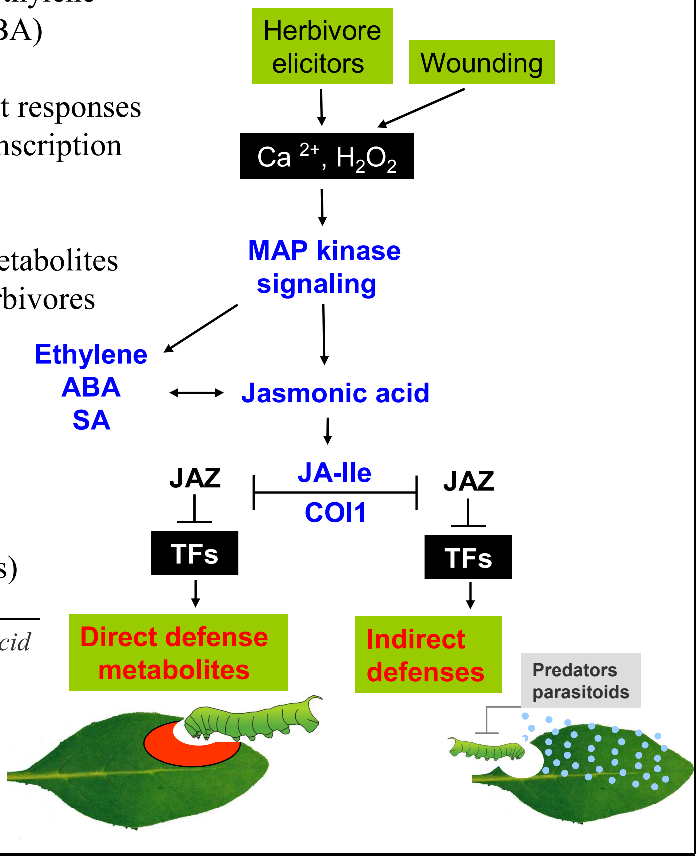
(A) Recognition of herbivore attack by plants and identification of herbivore-specific elicitors

(B) Role and cross-talk of plant stress hormones in signal transduction of herbivory-related signals: jasmonic acid (JA) * ethylene * salicylic acid (SA) * abscisic acid (ABA)

(C) Transcriptional regulation of plant responses to herbivore attack and the role of transcription factors (TFs) in defense

(D) Identification of novel defense metabolites that mediate plant defense against herbivores including:

- phenolic compounds
- terpenoids
- alkaloids
- proteinase inhibitors (PIs)
- green leaf volatiles (GLVs)
- volatile organic compounds (VOCs)



Herbivore attack induces burst of jasmonic acid which is converted to jasmonoyl-isoleucine (JA-Ile) that mediates COI1-dependent degradation of JAZ repressor proteins, transcriptional reprogramming and activation of defense responses in plants.

IX Barley and Wild Plant Resource Center

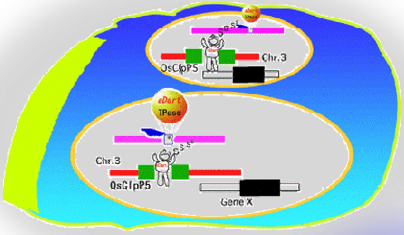
The Barley and Wild Plant Resource Center was established in 1997. Currently, the center consists of two research units, each of which comprises some research groups. The Genetic resources unit collects and preserves barley and wild plant species, providing users access to important resources to support future research and breeding activities. The Applied genomics unit develops new resources and techniques supporting the use of plant genetic resources in plant breeding. The center promotes collaborative research using the above-described internationally significant resources and techniques in plant science.

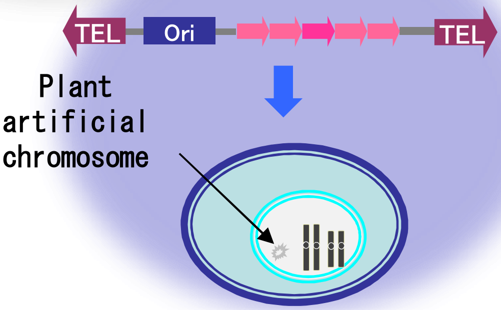
Genetic Resources Unit

The unit preserves massive collection and detailed genomic information in barley. Using these tools, we analyze the barley gene functions, such as high environmental adaptability and traits of agricultural importance. The unit maintains resources and information related to seed samples and genome analysis in barley and wild plants to support comparative studies with other plant species, especially cereal crops. In wild plant collection, evaluation of stress tolerance and agriculturally important traits are to be conducted as future research efforts.

Applied Genomics Unit

This unit is intended to report analysis and identification of useful genes conferring resistance to environmental stresses in transposon-tagged and other mutants and also in wild plant species. Additionally, we develop advanced transformation and order-made gene-modification techniques for generating plants that are tolerant to various environmental stresses.





Group of Barley Resources

Professor	Kazuhiro Sato
Assistant Professor	Hideya Yoshida
Assistant Professor	Daisuke Saisho

The barley germplasm collection in Okayama University includes about 14,000 accessions and has a high reputation as a representative genebank in the barley secondary diversity center of East Asia. The genebank was also nominated as one of the centers and as the secretary institution of the International Barley Core Collection. The main objectives of our group are (1) collection and preservation of barley germplasm, (2) evaluation of genetic diversity within the germplasm, (3) database documentation and worldwide sample distribution, (4) genetic analysis of significant traits in barley, and (5) development of genome resources including large scale cDNA sequences and clones, molecular markers and DNA libraries to accelerate genome-based barley diversity analysis.

Cultivars: **10,980**
(landraces & improved varieties)

Genetic stocks: **2,498**
Mutants
Trisomics series
Linkage testers
Isogenic lines

Wild relatives **628**
ssp. *spontaneum*
wild *Hordeum* species

Fig. 1. Number of barley accessions (left) and examples of barley genetic resources (right). A chlorophyl mutant (upper right) and plants of a species in wild *Hordeum* (lower right).

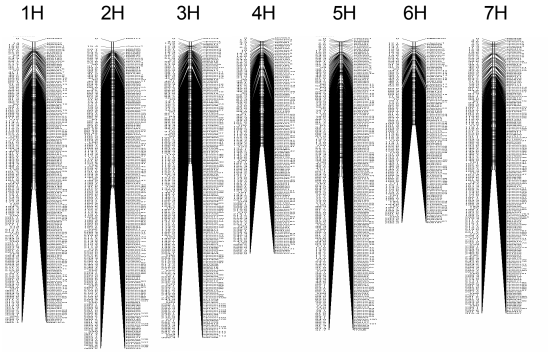


Fig. 3. Development of a high-density genetic map using EST markers in barley.

Fig. 2. Web accessible databases on genebank information
Barley germplasm database (left) and barley EST database (right), website: http://www.shigen.nig.ac.jp/barley/

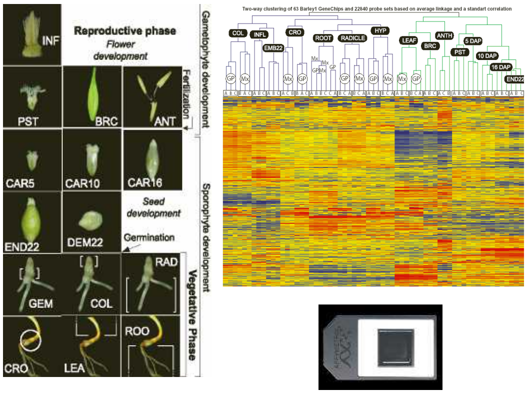


Fig. 4. Release of the GeneChip® barley genome array from Affymetrix and its base line experiments conducted through collaboration by the international barley research community. 15 barley tissues representing the key stages of plant development (left). Two-way clustering of signal expressions on 63 tissue samples vs. 22,840 probe sets (upper right). Photo of the GeneChip array (lower right).

Group of Genetic Resources and Functions

Professor Shin Taketa
Assistant Professor Naoki Shitsukawa

This group was formed 1) to isolate useful genes from genetic resources including barley and its allied species, and 2) to analyze the roles of these genes by various approaches. Barley is the world's fourth most important cereal crops, and the Center maintains a large barley collection from all over the world. Our main interest is genes controlling seed / flower morphology and quality-related characteristics.

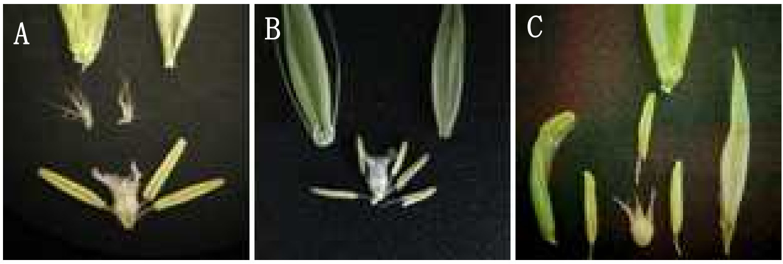
1) Genetics of the covered/naked caryopsis character in barley

Typical barley cultivars have caryopsis with adhering hulls at maturity, known as covered (hulled) barley. However, a few barley cultivars are of a freethreshing variant, called naked (hulless) barley. Covered barley is used as an animal feed and for brewing, although naked barley is well suited for use as human food. The covered/naked caryopsis is controlled by a single gene (*nud*) on chromosome arm 7HL. Using positional cloning, we found that an ethylene response factor (ERF) transcription family controls the trait. Functional analyses of *Nud/nud* gene are underway (Lower left panel).

2) Analyses of floral homeotic genes in barley

Despite the importance of barley as a crop and many unique mutant collections, only a few genes that function in inflorescence development have been identified. The floral organ formation of higher plants has been explained using the "ABCDE model". Basically, the ABCDE model can be applied also to monocot plants, but some unsolved problems exist for grass species. For example, the molecular entity of class A gene, which regulates specification of outer floral organs, and the mechanism of whorl-specific regulation are still under debate. To answer these questions, we are studying expression profiles of barley homeotic genes, and are attempting to identify new inflorescence genes by screening rich barley mutant collections (Lower right panel).

Barley caryopsis of covered (left) and naked (right) cultivars.



Floral organs of the WT barley (A). The *fan* mutant has additional stamens instead of lodicules (B). The KM2 mutant has split palea and lacks lodicules (C).

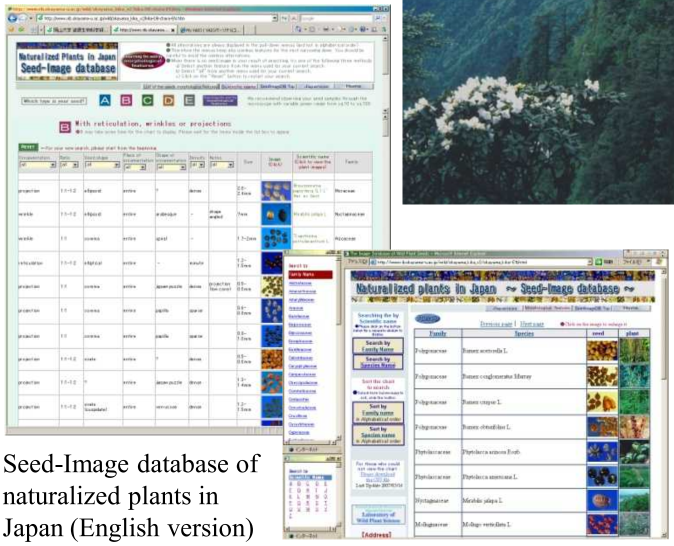
Group of Wild Plant Science

Associate Professor Takashi Enomoto
Associate Professor Shoji Sonoda
Assistant Professor Jun Yamashita

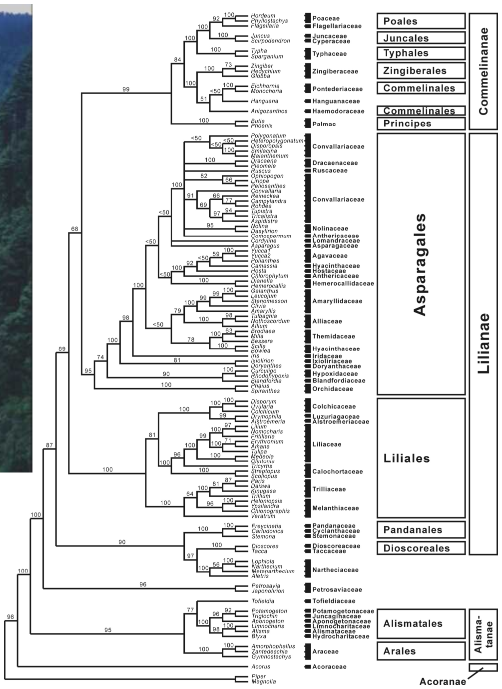
Since the foundation of our Institute, our laboratory has been collecting seeds of wild plants from all over Japan and Southeast Asia and preserving them with their voucher specimens. We have collected 29,792 seed accessions of 5,125 species of wild plants. Among them, 16,566 accessions of 3,782 species have been preserved in frozen storage. Our seed bank contains almost all the weed species of Japan, as well as many salt plants, water plants, and endangered plants. All data on the seed accessions and their vouchers have been deposited in the database with photographic files of the seeds. We hope to exchange the deposited seeds upon request for pursuit of joint studies. A seed-image database of naturalized alien plants in Japan is available on the WEB (http://www.rib.okayama-u.ac.jp/wild/okayama_kika_v2/ Seed-image-database.html). It is a leading world center among seed-image databases that enable users to search the seeds using morphological characters. We have also been studying molecular phylogeny of vascular plants—mainly monocotyledons. The voucher specimens of seed collections, DNA analyses, and geographic distributions of plants are preserved in our herbarium.

Intensive use of pesticides for pest control has engendered the worldwide emergence of resistant pests. Pesticide resistance is conferred by increased metabolic detoxification and decreased sensitivity of the target sites. A more efficient pest management system is also being developed through analyses of fundamental mechanisms of pesticide resistance.

Field surveys in Japan, Korea, China, Russia, Vietnam, India, Sri Lanka, Bangradesh, etc.



Seed-Image database of naturalized plants in Japan (English version)

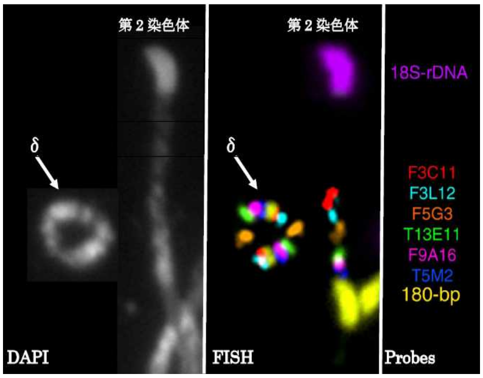


A molecular phylogenetic tree of monocotyledons based on DNA sequences from the plastid *matK* and *rbcL* genes (2004)

Group of Nuclear Genomics

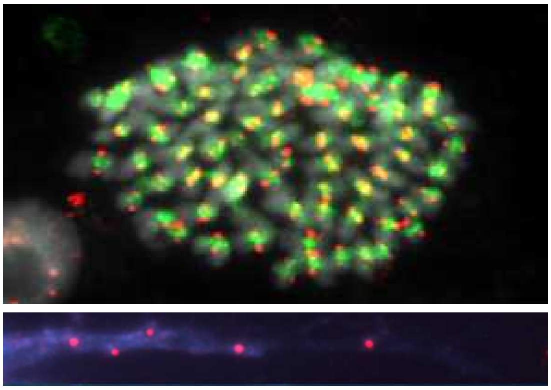
Professor	Minoru Murata
Associate Professor	Kiyotaka Nagaki
Research Associate	Yutaka Ogura

Nuclei which have very complex structures and various functions are the most important organelle in eukaryotic cells. Nuclear DNA is divided and packed into chromosomes, enabling accurate transmission of genetic information to daughter cells. Our research group is studying the molecular structures and functions of nuclei and chromosomes, mainly in plants. Our most recent goal is development of artificial plant chromosomes by analyzing chromosome functional elements: centromeres, telomeres, and replication origins. We are also interested in chromatin structure and gene expression.



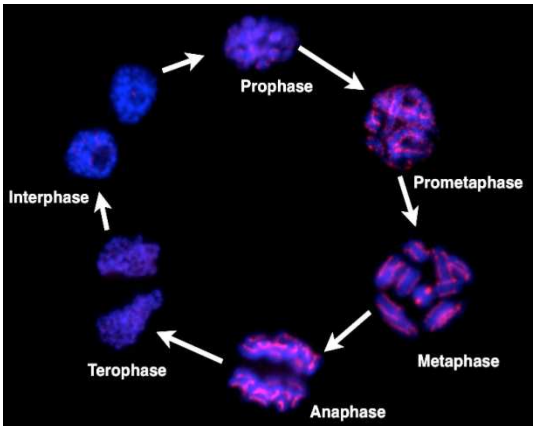
A stable ring minichromosome in *Arabidopsis thaliana*

Fluorescence *in situ* hybridization (FISH) probed BAC clones revealed that δ is a ring minichromosome originated from a short arm of chromosome 2, with size of 3.7 Mb.



Arabidopsis centromere-specific histone H3 (HTR12) visualized by immunostaining

Upper– metaphase chromosomes from a cultured cell; Lower– extended chromatin fibers from cultured cells. Red signals are from HTR12.



Analysis of holocentric chromosomes in *Luzula nivea*

In most eukaryotic species, only one centromere per chromosome is located at a primary constriction site. However, no primary constrictions are found in *Luzula nivea* chromosomes. Therefore, it is believed that an entire region of the chromosome acts as a centromere. The existence of such chromosomes, called "holocentric chromosomes", has been known for 60 years, but their actual structures have not been observed. For this study, we isolated a cDNA encoding a centromeric histone H3 variant from *L. nivea* (LnCENH3) and raised an anti-LnCENH3 peptide antibody based on the deduced amino-acid sequence. Immunostaining with the antibody clearly revealed the linear shape of the centromeres at prophase to telophase. It also revealed the dramatic decrease of LnCENH3 at interphase.

Group of Genome Regulation

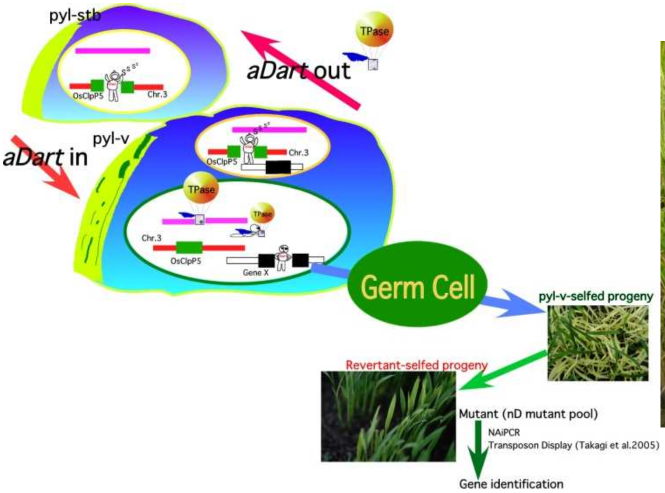
Professor	Masahiko Maekawa
Assistant Professor	Kazuhide Rikiishi
Assistant Professor	Shigeko Utsugi

Sustainable agriculture and a sufficient supply of food are important subjects for people seeking to live harmoniously in a natural environment in the 21st century. In this group, greater production efficiency of crops by functional analyses of transposon-tagged genes and introgression or genomic rearrangement from wild species and the mechanism of gene expression by phytohormones are being studied.

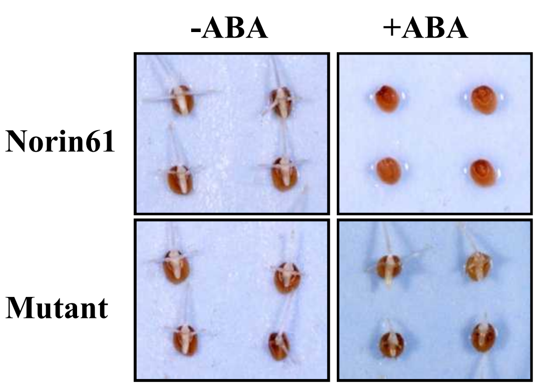
1) Breeding of DNA transposon, *nDart*-tagged lines and functional analyses of the causative genes for the tagged mutants in rice.

2) Development of vigorous rice through introgression from wild rice and analysis of the causative factors.

3) Analysis of regulatory mechanisms for seed dormancy in gramineous crops.

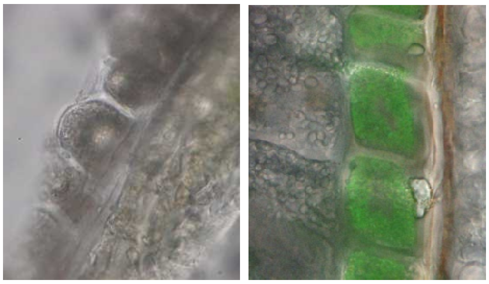


Strategy of breeding of DNA transposon, *nDart*-tagged lines and functional analyses of tagged genes.



ABA-insensitive mutant isolated from a dormant wheat cultivar, Norin61.

Development of vigorous rice (left) derived from F2 of the cross between *Oryza longistaminata* and T-65 under non-fertilized conditions. Norin 18 is shown as a control at right.



Localization of TaTIP3;1 by immunofluorescence in wheat aleurone cells during seed ripening. TaTIP3;1 was accumulated in aleurone cells at late stages of seed development (right), was not accumulated in the cells at the early stages (left).

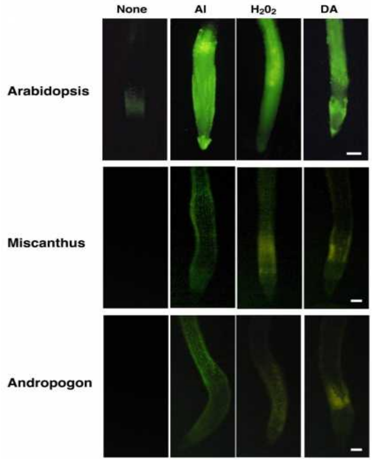
Group of Adaptation to Bioenvironmental

Associate Professor Bunichi Ezaki
Associate Professor Shigemi Tanakamaru

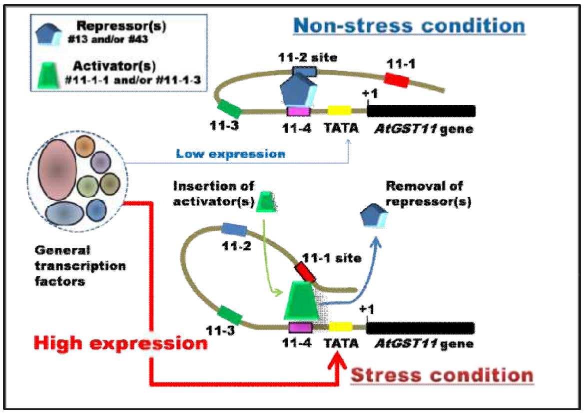
Our group has been investigating the adaptive mechanisms for bioenvironmental stresses (e.g. metal toxicities, oxidative stress, salt stress, temperature stress, and light) using wild plants, *E. coli,* and yeast as model systems.

We have been isolating the tolerant genes and induced genes for metal stresses and oxidative stresses from wild plants and characterizing their functions to clarify their adaptive mechanisms. Construction of transgenic plants carrying useful isolated genes is also expected to create new environmental stress-resistant plants in this group.

The ecophysiological interactions between plants and meteorological factors under various environmental conditions are also studied at several levels that include plant cells, whole plants and entire ecosystems. We are making and assessing observations of the atmospheric environment in the Seto Inland Sea district and on the mechanism of frost tolerance of Primula.



Lipid peroxidation in root tips of wild plants (Arabidopsis, Miscanthus and Andropogon) using Al, hydrogen peroxide, and diamide
Because the latter two plants were tolerant to these stressors, low oxidative damage was observed.



Model : How do the transcription factors control expression of *AtGST11* gene under stress?
Each of the isolated four transcription factors probably binds to the specific sites in the promoter to change the DNA conformation as activator(s) and repressor(s).

Primula plants differ in their frost tolerance.

Decolorization of morning glory petal by acid rain
Acidification of rainwater in the Seto Inland Sea district is extreamely high.

X Research Core for Future Crops

This research core includes the (1) Innovative research group and (2) International collaboration group. The objectives of this core are to exploit new research topics that are expected to be important in the near future and to advance future-oriented studies in plant stress science. Collaboration with Jomo Kenyatta University of Agriculture and Technology (Kenya, eastern Africa) will be promoted toward an ultimate goal to enable crop production in stressful conditions.

Innovative research group

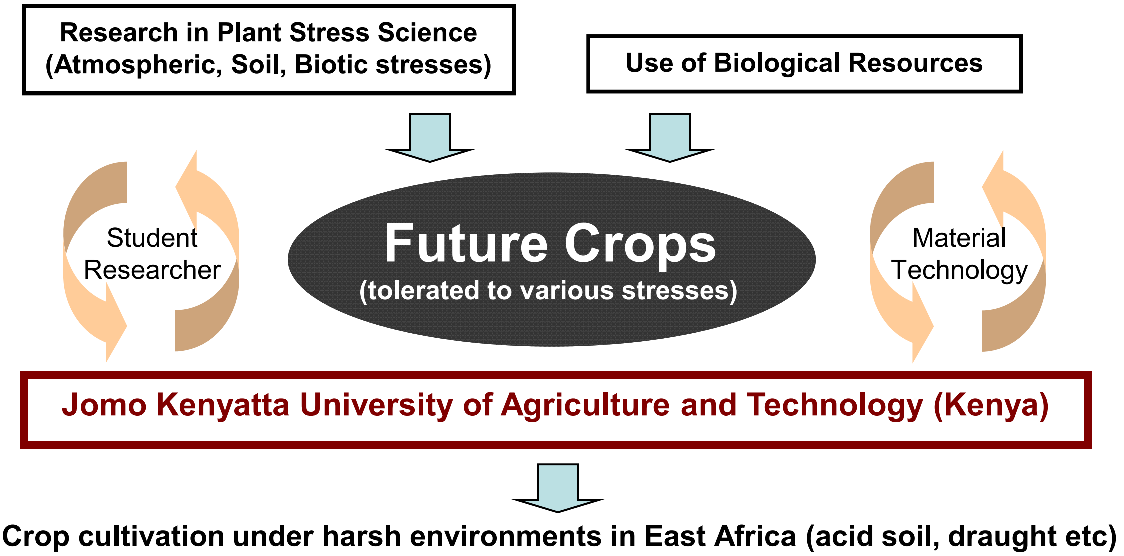
Assistant Professor Shoko Ueki

Our group focus on cell biology aspect of plant response to viral infection. For plant cell biologists, plant viruses serve as important molecular probes to study about plant cell physiology. Our groups is particularly interested in interaction of virus and plant cell during viral movement. Plant virus exploits cell wall spanning channel structure, plasmodesmata (Pd) to spread cell-to-cell. Pd is known to function as a passage way for intercellular macromolecule exchanges, and the molecular traffic through the stucture is known to be highly regulated by yet unknown regulatory system. Our group aim to scrutinize the molecular/cellular mechanism of the Pd regulation using plant viral protein as movement probe.

We also initiate a project to study about interaction between algae and algal viruses at molecular level. Viral infection is among the factors that regulate algal propagation in environment, and our study will give great insights into algal behavior in natural ecosystem. Also, since Algae is assumed to be a potent bioreactor to produce organic materials, our study may greatly advance the industrial usage of the organism.

International collaboration group

The aim of this research group is to analyze the current status of the global environmental stress and to investigate plant stress resistance for increasing future crop productivity.



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