Developing practical numerical flood simulations in urban areas

Numerical simulations of floods in urban areas are useful for establishing evacuation programs and revising future city planning. In the present study, a set of shallow water equations was used to simulate the swift current on the streets to characterize horizontal flow diversion and concentration considering actual building configurations. The finite volume method was applied to an unstructured triangular mesh system to express the orientation and physical characteristics of each building based on a detailed city map. Recently, we conducted laboratory experiments and applications for actual events to develop more accurate and practical simulations of floods in urban areas.

ALB measurements of channel bathymetry for river management tasks

Recently, an airborne laser bathymetry (ALB) system using simultaneously pulsed lasers of two kinds (green and near infrared types) has attracted the attention of river and coastal engineers for use as an efficient cost-saving surveying tool. This technology is effective for high-resolution measurement of planar bathymetry including the underwater bed profile. For this study, we applied a developed ALB system and examined the accuracy in the targeted section by comparing the ALB data of 2 m horizontal resolution with existing survey data obtained using the conventional method. Then we evaluated the effects of using high-resolution ALB data in river flow analysis.

Development of a simple and compact ground survey, and in-situ test method

Since most of ground disasters occur in the unsaturated region, soil tests and ground surveys on unsaturated soils have been performed in order to measure the geotechnical characteristics in unsaturated state. In addition, because it is necessary to evaluate quantitatively the ground behavior at the time of ground disasters, the following two themes are proposed: (1) an in-situ position test on a local scale with a simple and compact test equipment, (2) a ground scale survey on a field scale using a non-destructive measurement method from the ground surface. These would be contributed to evaluate of the safety of levees and slopes.

Development of monitoring method and numerical modeling method for safety assessment of levee failure caused by seepage flow

A monitoring method of the soil water content and pore water pressure by the infiltration behavior of the river levee has been proposed for the purpose of contributing to the design and construction work of the river levee by appropriately evaluating the safety of river levee. The construction method of a simulation model that can faithfully reproduce the measurement data by saturation and unsaturated infiltration analysis is developed.
Evaluation of the shear strength and deformation characteristics of unsaturated soils

In order to prevent and reduce ground disasters in unsaturated earth structures (slope, levee, embankment, etc.) caused by a rainfall, it needs to grasp the failure mechanism of soil structures due to the rain infiltration. For this, the shear tests with the water retention test in the laboratory are carried out according to the confining stress state reproducing the state of ground as well as the deformation mode of soil structures. The shear strength and deformation characteristics of the soil structures are examined based on the obtained results.

Applicability of water repellent soil to overlayer of capillary barrier using laboratory model test

According to the past research results, since the maximum division length \( (L_D) \) in the laboratory model experiment is less than 300cm, it would be difficult to realize the application to unsaturated ground structures. Thus, laboratory model tests for the capillary barrier (CB) using the wettable and water repellent soils according to rainfall condition in this study are performed, and the applicability of the water repellent soil based on the obtained results is examined. It is expected that the more stable unsaturated ground structure would be realized by applying the water repellent soil to the sand layer of the CB system.

Development of monitoring method for disaster prevention using ICT technology

Our laboratory is developing technology to monitor variations of wide range of slopes, rivers and urban areas with high efficiency and low cost using ICT technology laser and digital images. *ICT(Information and Communication Technology)
Practical Application of Precast Concrete Member with Super-High Durability Concrete

Objectives
In order to extend the lifespan of damaged bridge girders and to shorten the period of traffic regulation during renewal construction, precast concrete member with high durability is developed with blast furnace slag sand.

1. **BFS for High Durable Concrete**
   - Establishment of Quality Standard of BFS
   - Supplying system of BFS in the Domestic

2. **PC PCa Products**
   - Strong to traffic load under water supply condition
   - High resistance to freeze and thaw with out AE agent

3. **RC PCa Products**
   - High resistance to freeze and thaw with out AE agent
   - High resistance to chloride attack

Establishing a technique for monitoring soil and groundwater contamination using Frequency Domain Reflectometry

The purpose of this study is to apply a measuring system for subsurface contamination; the FDR (Frequency Domain Reflectometry) and FDR-V (with Vector network analyzer) system are employed to measure salinity and oil contaminants.

Research Area: Evaluation of Groundwater Environment

Developing a flexible and robust communication infrastructure system for a network of sensors used to remotely monitor damage during natural disasters

When a large-scale disaster occurs, it is crucial to have stable data transfer from a network of sensors. For a region considered as high-risk, it is essential that the sensor network and data communication infrastructure be installed and configured within several hours. This study aims to develop a novel sensor network and data communication system for a test site for monitoring slope stability during intense precipitation events.

Research Area: Environmental Conscious Materials

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How to reduce greenhouse gas emissions from soil amended with organic matter?

Agriculture is responsible for emissions of greenhouse gases such as carbon dioxide (CO₂) and nitrous oxide (N₂O). Production of these gases in soil results from the biological processes like organic matter decomposition, nitrification and denitrification. These processes are regulated by easily decomposable carbon, mineral nitrogen, temperature, pH and moisture content in soil. We aim at analyzing effects of these parameters on CO₂ and N₂O emissions. In particular, we are interested in agricultural soil amended with livestock compost.

Analysis of groundwater contamination with inorganic N in Central Vietnam by using stable isotopes and microbial technologies

High concentrations of inorganic nitrogen (NH₄-N and/or NO₃-N) were found in groundwater below vegetable fields in the downstream areas of the Huong River, Central Vietnam. The objective of the study is to determine the contamination sources and mechanisms of nitrogen contamination in groundwater by using δ¹⁵N natural abundance (δ¹⁵N) and functional genes of microorganisms. We have developed a new method to collect NH₄-N, NO₃-N, and organic N in water samples for δ¹⁵N analysis. Functional genes like narG, napK, and nosZ are quantified to obtain the information on nitrogen dynamics in deep soil.

Installing artificial macropore to enhance infiltration and increase organic matter in soils.

Soil is the largest carbon storage body at terrestrial area. Our previous research showed that macroporous soils conduct surface water without clogging and that bypass flow by macropores segregated organic matter from the surface. Organic matters will be effectively conserved by these physical processes, which contributed greatly to carbon storage as well as bio-chemical processes.

Linear Macropore Installation for Reducing Red-soil Erosion at Sugarcane Field.

Red-soil erosion in sugarcane fields has been reported as a significant agricultural and environmental problems in Ishigaki Island in Okinawa, where such erosion has led to loss of nutrient-rich agriculture soil and also negatively impacted coral reefs. We introduced linear-macropore to the field. The result showed that the erosion almost cancelled the conservative land management and installation of linear macropore reduced surface water and erosion amount to 1/7.
Research Area: Agricultural Land Engineering

Observation and Modelling of Soil – Plant – Atmosphere Interaction for Sustainable Land Management

My research interest is “soil-plant-atmosphere interaction” in regional to country scale: how land surface condition affects local rainfall and climate through water and energy fluxes between land and atmosphere. Current research topics are (i) estimation of pedotransfer function and dielectric behavior of soils in regional scale to improve the algorithm of microwave satellite remote sensing of soil moisture; (ii) development of an integrated system of remote sensing, field observation, and numerical model simulations (data assimilation) for environmental monitoring & projection; (iii) process-based study on the mechanism of the soil-plant-atmosphere interaction; (iv) assessment of land-use change and global warming on food production and water resources; etc. Research methodology involves field survey, in-situ observation, laboratory experiment, satellite remote sensing, and numerical model development & simulations. Capacity building and implementation into the society especially in the developing countries are also the key.

Research Area: Irrigation and Drainage

Study on evapotranspiration and soil water content for water resources

Evapotranspiration and soil water content are very important as key factors of hydrologic cycle and water resources. In our laboratory, the following two researches on evapotranspiration and soil water are carried out: (1) There are some methods for estimating the evapotranspiration, it, however, is not so convenient to use those methods because they often needs the meteorological data at two heights. We aim to develop the simple method for estimating evapotranspiration using one height meteorological data. (2) We estimate the potential water resources for agricultural products using soil water content, evapotranspiration, and other data. The results of these researches would be contribute to not only agriculture and irrigation but also the recent variation of hydrologic cycle.

Developing a technique for estimating soil and groundwater contamination utilizing permittivity, thermal properties, and other physical properties

Soil and groundwater contamination by NAPLs (nonaqueous-phase liquids) has become a serious environmental issue in Japan and around the world. It is difficult to detect or monitor the transport rates of NAPLs under field conditions, because the NAPLs are immiscible with water. In addition, because chemical solutions are often mixed with NAPLs, the detection of contaminant is more complicated. In our laboratory, we aim to develop the fundamental techniques to detect the soil and groundwater contaminated with both NAPLs and chemical solutions using some physical properties such as permittivity, thermal properties, and self-potential.
Study on balancing agricultural practices with nature to protect water resources

Agriculture is essential to modern civilization but often has unintended negative effects upon the natural environment, especially regarding water quality. Overuse of fertilizers is costly both economically and environmentally. We evaluated regional agricultural cultivation practices to determine optimal irrigation and fertilizer, timing and amounts, to maximize production while minimizing nutrient-driven eutrophication of local water bodies.

Agricultural fields are used not only by farmers, but also by wildlife. We studied the effects of the Tundra Swan on nutrient levels in rice paddies. Tundra Swans, from Far East Russia, overwinter in flooded paddy-fields from November to March. They roost in the paddy-fields at night and forage nearby in other agricultural fields during the day. We measured Tundra Swan manure-nutrient component of paddy-field soil and water nutrient concentrations to determine optimal farmer-applied fertilizer amendments required for rice production, without over-applying.

Our ultimate goal is to find a win-win-win relationship among the environment, humans (farmers), and wildlife with respect to water quality.

Study on irrigation management for stabilizing agricultural production

Water is critical for agriculture and irrigation practice is an important part of farm management. Irrigation water is often wasted or poorly applied (i.e., amount or timing) leading to lowered agricultural production from poor crop health or damage. It is important to evaluate water resource availability to effectively manage irrigation timing and amounts required for efficient crop production.

We assessed watershed-level water availability upon a local irrigation scheme. Data were gathered through field observations and farmer questionnaires. Data were evaluated by computer modeling. At the watershed level, irrigation water allocation is spatially unbalanced among upstream, midstream, and downstream observations. We attempted to determine alternative management methods and/or improve current methods for efficiently allocating irrigation water equally to the fields.

By improving irrigation water use efficiency through better allocation management, there is an apparent increase in water availability. This will lead to an expanded cultivation area, higher production, and ultimately, better agricultural stability.

Inverse analysis/data assimilation in civil engineering

Inverse analysis/data assimilation is a methodology to assimilate observation data into numerical simulation models for realistic predictions and parameter identifications. We have developed inverse analysis methods and demonstrated the effectiveness by applying the methods to numerical experiments, model tests, and actual construction projects. Figure 1 shows conceptual illustration of cross-hole tomography which is typical inverse analysis method and is designed to visualize subsurface in a non-destructive way. Figure 2 shows a comparison between the true image of the ground and the reconstructed image by the cross-hole tomography.

Numerical Simulations using particle-based methods

We have developed simulation codes of the moving particle semi-implicit (MPS) method to predict large deformation and failure behavior in geomaterials such as clay, sand, gravel and their mixtures. Figure 3 shows a breach process of an earthen embankment due to overflow simulated by the developed MPS method.
Natural resource management in Asian countries

The commons are the cultural and natural resources accessible to all members of a community, which are not often managed by the “invisible hand” under a market system. It is the local community that uses the commons sustainably, and endogenous self-organization plays a crucial role in forming norms for sustainable resource exploitation. In this context, my research interests focus on rural communities in exploiting natural resources, with study areas including Japan, Korea, China, and Vietnam.

Roles of endogenous self-organization in rural communities

Development is a process that involves not only money and agencies but also people. The framework for organizations in a rural community can provide a clue to identifying who should be the real actors for sustainable rural development in either developed or less developed countries.

Processes of Capitalization/financialization of Nature: From Cases in Southeast Asia

In recent years, there has been discussion about approaches that procure funds through the use of financial instruments and direct payments to mitigate environmental problems. Typical examples in developing countries include the use of carbon credits (such as REDD+) and systems to pay for environmental services (PES). This study looks at the processes leading to the formulation of these funding mechanisms, and regards them as the new developments that are mainstreaming the commodification of nature—in other words the background leading to the "capitalization" and "financialization" of nature. Taking the examples in Southeast Asian cases, the study will examine the processes and mechanisms leading to the "capitalization/financialization" of nature, as well as changes in governance of society and the environment.

Photo : Vanishing Tropical Forest in Southeast Asia. Deforestation is believed to be a significant source of carbon emission. (Sarawak, Malaysia, 2008)
Study on water transport function of trees

In many tree-dominated ecosystems, drought-induced hydraulic dysfunction has been associated with the sudden death of trees exposed to critical drought stress and is one of the most important factors that determines the survival and distribution of trees. For various tree species from arid to humid regions, therefore, we aim to elucidate the mechanism of maintaining the xylem water transport under variable soil moisture conditions and the physiological properties related to it.

Study on water use properties of trees growing in dry land

Plants acquire carbon through stomata of leaf for photosynthesis, however, at the same time they lose water through the stomata. Therefore, it is essential for growth and survival to develop various properties of suppressing water loss and rapidly supplementing water loss. Water availability to plants in dry land is limited. Therefore, it is important how efficiently plants use water resources. For various species in dry land, we aim to elucidate the water use properties and survival strategy of whole tree from various organ levels through evaluation of transpiration of leaves, water transport properties of stems, water absorption properties in roots. From these aspects, we also work on research related to revegetation in the water-limited environment of dry land.

Study on evolutionary ecology using insects

All of organisms including agricultural products of material are product of evolution. All of them are influenced from environmental and ecological factors. Therefore, understanding of evolutionary ecological mechanisms is important to consider all living thing. We are grappling with researches in the mechanism of evolutionary ecology using mainly insect species. We focus on insect behaviors including anti-predator behavior, courtship and mating systems, biological interactions of insect species. Concretely, there are specialized research theme concerning mating system, sexual selection, sperm competition, insect immobility, dispersal tactics, interaction between environments and insect behaviors, using insects.

Research on insect behaviors for applied entomological techniques

In addition to the basic researches in evolutionary ecology, we can apply these results to output concerning applied entomology and insect pest control. Understanding insect behavior connect to some applied entomological techniques; for example, monitoring and detecting the beetles using lights and/or pheromone in a laboratory and a storehouse, attraction methods using ultra violet I or blue lights and lure, or breeding of flightless beetles. In addition to these researches, we concern some relationships between native and invasion insects from the world including common pill bug, sweet potato weevils, fruit flies, and broad-horned flour beetles.
Generally speaking, Japanese farmers’ scale are smaller than other countries. But, Japanese farmers’ scale are expanding now. Some rice farmers have more than 100ha paddy field, and some vegetable farmers have more than 100ha dry field. These farmers are mostly expanding by lease. And, these expansion of farm size, farmers’ management need to change. For example, some farmer need to employ worker, some farmer are forced to change selling agriculture products. In addition, one farm corporative had changed to a stock corporation. We aim to focus on changing agricultural management in Japan.

Why do Japanese farmers change? How do Japanese farmers change? And, who promotes to change Japanese agriculture management? The key to solving these questions are “policy”. After WW2, Japanese government hoped to change Japanese agriculture structure. It promoted to be established large scale farmers. Imperfectly, Japanese agriculture structure is changing now. Near the future, many Japanese old farmers will be retired. Therefore, Japanese government supports large scale farmers for accumulating these old farmers’ farmland by agriculture policy. Moreover, agriculture policy is effected by trade negotiation. We are comparing and analyzing other countries’ policy.
Transport and diffusion of dust particles by atmospheric air turbulence and highly efficient and clean combustion in internal combustion engines are themes related to environmental problems. These are multiscale/multiphysics complex flow phenomena. To solve these phenomena, a more comprehensive understanding of turbulence physics is important. By developing reliable and effective methods for direct numerical simulations (DNSs) of the Navier-Stokes equations and performing large-scale DNSs of turbulence using supercomputers, we are studying turbulence physics for various complex flow phenomena.

A method for efficiently extracting important information from huge time series datasets obtained from large-scale numerical simulations is required. Flow visualization and analysis of conditional statistics are effective for understanding turbulence phenomena. Persistent homology analysis enables us to systematically extract remarkable "changes" in the spatio-temporal space of a scalar field. By combining these, we are developing methods for detecting and understanding important events in complex turbulent flow phenomena.

Regional waste material recycling towards low carbon society: Sanitary waste treatment is a fundamental in solid waste management, moreover, it is required that "from waste to material" and "from waste to energy" to mitigate greenhouse gases emission. Solid waste processes, such as waste separation at source, segregated waste collection, optimal waste transportation, material and energy recovery treatment, and safe landfill disposal, should be combined appropriately so as to shorten the environmental burden. Our laboratory studies on designing methods to establish a sophisticated solid waste management that is suitable for sustainable regional society, specially in Asia.

Evaluation of the biomass waste recycling in university campus: From viewpoint of carbon neutral, biomass waste should be more utilized in a sound material-cycle society. By considering characteristics of various kinds of solid waste generated in our campus, such as kitchen waste, mowed grass, dead leaves, pruned branches, agriculture waste, animal dung in different seasons, our laboratory researches on effective biomass waste recycling methods.

Development of a disaster waste management training system: Japan is exposed by many risks of natural disasters such as earthquake, land sliding, tsunami, flooding and so on. Once a big natural disaster comes like the Great East Japan Earthquake, a huge amount of disaster waste generates in a short period. In order to recover the town from the damage speedy, initial countermeasure actions for disaster waste treatment by local government are quite important. Therefore, our laboratory is constructing a knowledge base of the actions and also developing a training support system for the local government.
Assessing the fate of chemicals in the environment and engineered processes

Concentration changes and dynamics of environmental chemicals are predicted and evaluated based on partition equilibrium properties of chemical compounds and their conversion/degradation kinetics. The target compounds are organohalogen compounds, PAHs, and other emerging pollutants. The target engineering processes include water treatment and gas cleaning, and solid/liquid waste treatment in such environmental media as water, air, soil, and sediment.

Safe and appropriate disposal treatment of waste water, flue gas, and solid/liquid waste, and developing further technology for recovering materials/energy from waste

Various exhausts, such as wastewater, flue gas, and other anthropogenic waste emissions should be appropriately and safely disposed. Currently, material and energy recovery is highly desired in the context of establishing a sound material recycling society.

The SWCNT photocatalyst for hydrogen production from water upon photoexcitation of (8,3) SWCNT at 680-nm light

Single-walled carbon nanotubes (SWCNTs) are potentially strong optical absorbers with tunable absorption bands depending on their chiral indices (n, m). Their application for solar energy conversion is difficult because of the large binding energy (>100 meV) of electron-hole pairs, known as excitons, produced by optical absorption. Recent development of photovoltaic devices based on SWCNTs as light-absorbing components have shown that the creation of heterojunctions by pairing chirality-controlled SWCNTs with C$_{60}$ is the key for high power conversion efficiency. In contrast to thin film devices, photocatalytic reactions in a dispersion/solution system triggered by the photoexcitation of SWCNTs have never been reported due to the difficulty of constructing a well-ordered surface on SWCNTs. Here, we show a clear-cut example of a SWCNT photocatalyst producing H$_2$ from water. Self-organization of a fullerodendron on the SWCNT core produces water-dispersible coaxial nanowires possessing SWCNT/C$_{60}$ heterojunctions, of which a dendron shell can act as support of a co-catalyst for H$_2$ evolution. Because the band offset between the LUMO levels (8, 3) SWCNT and C$_{60}$ satisfactorily exceeds the exciton binding energy to allow efficient exciton dissociation, the (8, 3) SWCNT fullerodendron coaxial photocatalyst shows H$_2$-evolving activity (QY=0.015) upon 680-nm illumination.
Incorporating a TiO\textsubscript{x} shell in single-walled carbon nanotube/fullerodendron coaxial nanowires: increasing the photocatalytic evolution of H\textsubscript{2} from water under irradiation with visible light

A custom-tailored single-walled carbon nanotube (SWCNT) photocatalyst with an electron-extracting TiO\textsubscript{x} shell, i.e., a SWCNT/fullerodendron/TiO\textsubscript{x} coaxial nanowire, has been fabricated. Due to the presence of the TiO\textsubscript{x} shell, the SWCNT/fullerodendron/TiO\textsubscript{x} coaxial nanowire shows enhanced photocatalytic activity (Φ = 0.47) for the evolution of hydrogen from water under irradiation with visible light (λ = 450 nm).

Ligand Exchange Reaction of (Me\textsubscript{4}N)\textsubscript{4}[Cd\textsubscript{10}S\textsubscript{4}(SPh)\textsubscript{16}] with Diphenyl Diselenide

The reaction of (Me\textsubscript{4}N)\textsubscript{4}[Cd\textsubscript{10}S\textsubscript{4}(SPh)\textsubscript{16}] (with diphenyl diselenide in propionitrile afforded a molecular cluster, (Me\textsubscript{4}N)\textsubscript{4}[Cd\textsubscript{10}S\textsubscript{4}(SePh)\textsubscript{16}], the structure of which was determined by X-ray crystallography. Ligand exchange proceeded in a heterogeneous reaction system, and the use of a less polar solvent appeared to be crucial for the synthesis of (Me\textsubscript{4}N)\textsubscript{4}[Cd\textsubscript{10}S\textsubscript{4}(SePh)\textsubscript{16}] to prevent degradation of the Cd\textsubscript{10}S\textsubscript{4}Se\textsubscript{16} cluster core.

Investigation of inhibition mechanism of sialidase of influenza virus and development of novel inhibitors: difluorosialic acid and sulfo-sialic acid

Development of improved influenza sialidase inhibitors is critical to prepare for potential influenza pandemics. Based on the hypothesis that Tyr406 forms an acetal intermediate in the catalytic cycle of sialidase, we synthesized 2a,3a-difluorosialic acid (1) as a suitable probe to test if a covalent intermediate can be captured. As expected, X-ray crystallographic analysis revealed that 1 forms a covalent complex with Tyr406 of influenza sialidase. This indicated that Tyr406 attacks from the b-face of the substrate, leading to hydrolysis with retention (inversion and inversion) of the configuration. In addition, 1 possessed potent anti-influenza activity (including that of Tamiflu resistant virus) with IC\textsubscript{50} inhibitory constants of 10 to 1000 nm, providing the first proof-of-concept for mechanism-based influenza sialidase inhibition.

In addition, a next-generation inhibitor, sulfo-sialic acid (2), was developed. The sialidase inhibitory activity of 2 was more potent than the corresponding carboxy and phosphono derivatives, presumably due to stronger attraction to the triarginyl binding site of the enzyme.
Activation of endogenous defense mechanisms by food constituents and their metabolites by gut microbiota

Electrophilic substances in foods possess potential to exhibit various biological activities through transcriptional regulation of cytoprotective genes involved in cellular defense against biotic stresses induced by xenobiotics, reactive oxygen species, and alcohol. We have been focusing on food-derived electrophiles such as isothiocyanates, flavonoids, and phenolic acid metabolites of quercetin 4´-glucoside, the major polyphenol in onion. Modulating effects of these compounds on cytoprotective gene expression and the underlying molecular mechanisms are investigated by the forward chemical genetics approach to elucidate their physiological significance.
Study on the molecular mechanisms that regulate environmental stress responses in plants

In nature, plants are exposed to a combination of a wide variety of environmental stresses. To sustain their growth, plants have developed robust mechanisms that integrate the stress signals and then output the optimal adaptation response. The long-term goal of our research is to uncover the molecular mechanisms of how plants achieve the signal integration and its conversion to the downstream response. In particular, our research focuses on stress signaling regulating stomatal movement. Stomatal pores, which are formed by pairs of guard cells in the epidermis especially of leaves, regulate gas exchange for photosynthesis and transpirational water loss. Guard cells can perceive various stimuli such as light, CO$_2$, pathogen infection, and various phytohormones such as abscisic acid, jasmonate, and salicylic acid, then transducing the inputs to a change in stomatal aperture. Using multidisciplinary approaches, we aim to reveal the detailed mechanisms of signaling cascading from stress sensing to stomatal aperture regulation in guard cells. We also study the basic mechanisms of heavy metal and salt stress responses in plants using model plants as well as cultured cells. Our research advance will contribute to develop new technologies that improve crop productivity and safety.

Photosynthesis and chloroplast biogenesis: Understanding to innovation

Plants perform photosynthesis in chloroplasts, where light energy is converted into chemical energy by a series of electrochemical reactions. In contrast, sessile land plants are exposed incessantly to excess light energy or harsh atmospheric environments that engender 'photodamage'. How do plants cope with such photosynthetic inactivation? What are the key elements to maintaining or even maximizing chloroplast functions?

Our group studies various aspects of chloroplast development and photosynthesis. Through understanding of the factors involved in photoprotection and chloroplast function, we aim at improving crop productivity against atmospheric stress over the long term.

Ongoing projects in Plant Light Acclimation Research Group

1. Proteolytic machineries in chloroplasts
2. Photooxidative stress and quality control of photosynthetic proteins
3. Maintenance of chloroplast envelope through protection mechanism through VIPP1
4. Behavior of chloroplast DNAs during leaf maturation and senescence
5. Quantitative trait locus (QTL) controlling stay green in sorghum
Research Area: Signaling Mechanisms

Molecular genetic studies on the mechanisms for stress sensing and response in plants.

As autotrophic sessile organism, plants have developed unique systems to regulate biological phenomena such as development, environmental stress responses, and reproduction process. Without central nervous system and sophisticated circulatory system as animals have, plant also developed unique systems to exchange information between cells or tissues. To understand and manipulate the plant behavior, we have been trying to describe the regulatory system for these molecules, deciphering the information possessed by these plant signaling molecules by molecular genetic approaches using model plants such as Arabidopsis.

Establishment of data driven crop design technology.

It has been known that useful agronomical traits of crops are dependent on both the genetic factors the crop possesses and environmental factors the crop lives. Importantly, these two factors are not independent and affect each other in a complex manner.

We have been trying to identify the genetic factors or environmental factors critical to the useful traits by describing the dynamics in physiological status of filed crop through life course concomitant with the filed environment data. Using such important factors, we will build a model that predicts the the agronomical traits. Such the model will enable us to design the crops with suitable genetic factors to a given filed conditions including the forecasted climate in near future.
Research Area : Signaling Mechanisms

Study on Molecular Physiology of Stomatal Movement against Air Pollutants

Yield loss of crops due to airborne pollutants is estimated as 30-40% near future in Japan. Plants equip the mechanism to withstand such pollutants. One of the major mechanisms is elucidated as closing stomata to prevent the entry of gaseous toxicants. To gain insight into the molecular basis of plant response to airborne pollutant, I employ molecular genetic and physiological approaches to comprehend stress signaling mechanism of stomata.

Ion Dynamics Study of Stomata, Roots and Inside of Leaves.

Although plants seem calm, silent and static, it is not real. Plants are always active and dynamic. For example, stomata move every day, every minute; tendrils move spiral around and root architecture keeps changing. These movement of plants are more or less associated with the mobilization of ions. I am an expert in ion dynamics study through electrophysiological techniques. My main research focuses are Ca²⁺ ion transport in guard cells and CO₂ transport in mesophyll cells, which play crucial roles in photosynthesis under biotic and abiotic stresses.

Plant Hormone Quantification.

In addition to physiological analysis, chemical analysis using LC-MS is one of my missions as a staff of Institute of Plant Science and Resources, Okayama University. I am taking a part of the comprehensive plant hormone quantification analysis group. Our group is having a large number of collaborators from all around the world.

Research Area : Signaling Mechanisms

Epigenetic regulation mechanisms of gene and transposon expression in plants

Genetic information is encoded in DNA base sequences. However, epigenetic information outside of the DNA sequence also has been found to play an important role in gene and transposon expression. Such epigenetic information including DNA methylation and histone modification is known to be affected by the stage of growth and changes in the environment. My research interests are: i) the molecular mechanism that controls epigenetic status in plants; ii) the ways in which epigenetic information is transmitted to the next generation; and iii) the study on the variety and the change of epigenetic regulation systems in plant evolution.

Analysis of transcriptional gene silencing mechanism in Arabidopsis

To reveal the mechanism of epigenetic gene silencing, we did mutant screening affecting transcriptional gene silencing in Arabidopsis thaliana, and recently identified new factors for transcriptional gene silencing. Arabidopsis thaliana is useful material for genetic analysis, but we also utilize several plant species for research e.g. barley, seaweed, and liverwort Marchantia polymorpha to analyze the function of epigenetic regulation in plant evolution.
Molecular mechanisms of aluminum tolerance in plants

Aluminum (Al) toxicity is a major factor limiting crop production on acid soils. However, some plant species or accessions have evolved strategies to cope with Al. Rice is the most Al-tolerant species among small grain cereal crops. We identified a transcription factor for Al tolerance (ART1) and found that it regulates at least 32 genes implicated in Al tolerance. On the other hand, barley is the most sensitive cereal to Al toxicity, but there is a large genotypic difference in Al tolerance. We identified a major Al-tolerance gene in barley, HvAACT1. Furthermore, we found that high expression of this gene is acquired by a transposon insertion in its promoter.

Transport system of mineral elements in plants

Mineral elements including essential, beneficial and toxic elements in soil affect both plant growth and human health. We are working on identification of transporters involved in uptake, root-to-shoot translocation and distribution/redistribution of these elements in plants. We have identified a number of transporters for Si, P, Mg, Mn, Zn, Cu, Fe, B, Cd and As. Especially, we found that rice has developed an efficient uptake system for mineral elements, which is mediated by both influx and efflux transporters polarly localized at the exodermis and endodermis of the roots. We also identified several transporter genes for accumulation of Cd and As in rice.
Mineral nutrients required for plant growth and development are taken up by the roots from soil solution, and then delivered to different organs and tissues depending on their requirements. In Poaceae, this selective distribution is mainly mediated in the nodes, which have highly developed and fully organized vascular systems. We found that “inter-vascular transfer” of mineral elements from enlarged vascular bundles to diffuse vascular bundles is required for their preferential distribution to developing tissues and reproductive organs.

### Studies on mineral distribution control systems in plants

A number of transporters involved in this inter-vascular transfer processes have been identified mainly in rice. They are localized at the different cell layers and form an efficient machinery in the node. These findings will be applicable to improve productivity, nutritional value and safety of cereal crops.

Representative references


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Plants are important for us, having been utilized as indispensable materials for, food, clothing and housing since ancient times. Therefore we couldn’t live without plants. I’m focusing on mineral transporters for healthy and high nutrient-efficient crop production.

#### Molecular mechanisms of Si transport

Silicon (Si) is a beneficial element for plant growth, which can alleviate many stresses by accumulation in their shoots. However, Si content of the plants varies greatly with species, and only those plants that are capable of accumulating the element can receive benefit from it. Rice is one of major Si accumulating plants. I am focusing on the study about molecular mechanisms of Si uptake and accumulation in rice for applying the beneficial effects of this element in many other plants.

#### Identification of mineral redistribution transporters

Plants require 14 mineral elements for their growth. These elements are taken up by the roots, translocated from the roots to shoots, followed by distribution/redistribution to different organs. A number of transporters for uptake and translocation of mineral elements have been identified, however, most transporters involved in mineral distribution/redistribution remain to be identified. I am working on mineral redistribution systems in rice for efficient use of mineral elements.
Research on function and structure of plant-specific malate transporters

Aluminum (Al) ion is a major inhibitory factor of plant growth in acidic soils which comprise almost 40% of the world arable land. Toxic Al cations (Al³⁺) rapidly inhibit root growth and prevent subsequent uptake of water and nutrients. The mechanisms of Al toxicity and tolerance are analyzing using a cultured cell system and whole plants. Especially Al-tolerance mechanism, wheat ALMT1 gene encoding Al-activated malate transporter was found by our group, and demonstrated as Al-tolerant as well as acidic-soil tolerant gene, for the first time in crops. In addition, since the ALMT gene and its homologues have been found only in plants, the diversity of physiological functions for individual ALMT genes was elucidated as recent studies. The molecular details of the structure and functions and the expression mechanisms of these transporters are now studied.

A gene encoding aluminum (Al)-activated malate transporter (ALMT1) regulates Al tolerance of wheat.

It was previously shown that Al tolerance in wheat (Triticum aestivum L.) is correlated with the Al-activated efflux of malate which chelates and detoxifies Al cations around root apices. To isolate the gene involved in this mechanism, Sasaki et al. (2004, Plant J.) examined a pair of near-isogenic wheat lines that differed in Al tolerance at a single genetic locus, and found a gene which shows greater expression in the root apices of ET8 (the Al-tolerant line) than that of ES8 (the sensitive line), as depicted in the photograph. The gene is named ALMT1 which encodes a novel transporter protein facilitating the Al-activated efflux of malate and is a major Al-tolerant gene of wheat.

Water and ion transport in plants under salinity stress

Salinity stress is one of major abiotic stress that limit plant productivity in global agriculture. Salinity, usually high concentration of Na⁺, reduces water and mineral uptake in plant. I study root hydraulic conductivity (Lp) using the root pressure chamber method, because regulation of Lp, is important to prevent dehydration and to cope with osmotic imbalance in initial phase of salinity stress. As for plant ion transporters, cRNAs are injected into a frog Xenopus oocytes and their properties (ion selectivity and activation mechanism) are investigated electrophysiologicaly to reveal what and how transporters regulate ion flux under salinity stress.

Aquaporins transporting water and low-molecular weight compounds

Aquaporins was first identified as a membrane protein exhibiting permeability for water when faced with an osmotic gradient. Now it is reported that several aquaporins facilitate the transport of not only water but also other low-molecular weight substrates such as glycerol, ammonia, silicic acid, arsenite, boric acid, and carbon dioxide. I study rice and barely aquaporins to improve plant growth and stress tolerance via aquaporin functions.
Study on the interaction among plant/fungus/virus toward virocontrol of phytopathogenic fungi

Using two combinations, Chestnut/chestnut blight fungus/mycoviruses and fruit trees/root rot fungi/mycoviruses, viral replication and symptom expression were investigated at the molecular and cellular levels. Obtained knowledge and achieved technical advance will be integrated into into virocontrol (a form of biological control using viruses) of the plant pathogenic fungi.

Research on neo-lifestyle of fungal viruses

Several viruses, challenging the concept or rules of viruses, have been discovered from lower eukaryotes. The objective of this project is to reveal the unique neo-lifestyle of Yado-nushi virus 1 (YnV1) and Yado-nushi virus 1 (YnV1) newly discovered from an important pathogen of perennial fruit trees, Rosellinia necatrix. We show that YKV1 hijacks the capsid of YnV1 to hetero-en-capsidate YKV1 genomic RNA and replicase and use it as the replication site. Furthermore, viruses with similar mutualistic virus/virus interactions will be found in other eukaryotic organisms to show the generality of the neo-lifestyle.

Study on viromes in crop phytobiomes

Phytobiomes refer to the complex networks between plants and their associated communities of organisms including bacteria, fungi, viruses and invertebrates. Phytobiomes are becoming increasingly recognized as important factors in plant health and productivity, but in particular, little is known about the diversities of virus communities in agricultural cropping system. Taking advances of the next generation sequencing and metagenomics, our group studies on viromes in fungi and insects that are associated with crop plants. We aim to find out whether these viral communities influence their hosts and promote the health and growth of crop plants.

Study of non-retroviral RNA virus-like elements in the genome of the plants, insects and fungi

The availability of genome sequences of a large number of eukaryotes has led to the discovery of endogenous non-retroviral RNA virus-like elements, also known as endogenous viral elements (EVEs). These elements are considered as fossil of RNA virus integrated into host genomes by as-yet-unknown mechanisms. To gain deeper insight into the long-term viral evolution and host-virus coevolution, our research is focused on identification and analysis of the EVEs in the genome of the plants, insects and fungi.
Lanthanide-dependent enzyme and motility in plant-associating methylotrophic bacteria

Plant emit large quantities of methanol through stomata as a result of their growth and pectin degradation. Methanol can be a good nutrient for bacteria and methanol-utilizing (methylotrophic) bacteria predominate on the aerial plant surface (phyllosphere). We focus on their methanol metabolism and symbiosis with plants.

*Methylobacterium* species are commonly found in phyllosphere, and they can promote plant growth. They have methanol dehydrogenase (MDH) to oxidize methanol. Not only calcium-dependent MDH encoded by *mxaF*, recently it was found that lanthanide-dependent MDH is also encoded by *xoxF* in the genomes of *Methylobacterium* species. This is the first enzyme described to date, to contain lanthanide. We investigate the mechanism of expression switching between these MDHs, depending on the availability of lanthanide.

We also study molecular mechanism of the motility and chemotaxis in methylotrophs, which is important for the bacteria to find and colonize plants. The chemotaxis is also affected by the carbon source and lanthanide.

We have found new methylotrophic bacteria belonging to novel genera. They have been isolated from rice rhizosphere using lanthanide as an essential cofactor. They are named as *Oharaeibacter diazotrophicus* SM30 and *Novimethylophilus kurashikensis* La2-4. Thus, lanthanide can be used for isolation of bacteria that contain *xoxF*, which can be found in many so-believed non-methylotrophic bacteria and novel bacteria.
Study on dynamics of Phytoplankon in environment

Our group focuses on the study of Heterosigma akashiwo, a unicellular algae that forms harmful algal bloom (commonly termed ‘red tide’). Algal bloom is typically caused by aberrant propagation of a single species, resulting in its predominance in the local population. While environmental factors including temperature and eutrophication are linked to bloom, the precise mechanism of its formation process is still obscure. We isolated a bacterial strain, Altererythrobacter ishigakiensis, a member of the class Alphaproteobacteria, that promotes growth of Heterosigma akashiwo. This is the first example of selective growth promotion of H. akashiwo by a marine bacterium, and may exemplify importance of symbiotic bacterium on algal bloom forming process in general.

Study on interaction between a giant double-stranded DNA virus and its host

H. akashiwo bloom is known to be terminated by algicidal bacteria and viruses. Heterosigma akashiwo virus (HaV) was identified as one of such bloom-terminating factors. We completed the sequencing of its genomes. The viral genome was characterized to be a linear double stranded DNA (dsDNA), with an estimated size of ~290 kbp. It is a member of Phycodnaviridae, one of the viral families regarded as “giant dsDNA viruses” that possess genomes larger than several hundred-kbp in size. We are particularly interested in studying about the infection mechanism of HaV at cellular and molecular level. The study will provide insights into infection strategies of a giant dsDNA virus, and the molecular mechanism of a major environmental phenomenon, bloom termination.

Preservation and application of genetic and genomic resources in barley

Ca. 15,000 accessions of wild and cultivated barleys and a wide range of experimental strains are preserved with a support from the National Bioresource Project. Genomic libraries and extensive cDNA resources have been developed for genomic analysis of barley which contributed to estimate gene regions on the draft barley genome sequence published in 2012. These genetic and genomic resources are used to identify agriculturally important genes on barley genome. We also found that barley and diploid wheat shared the same genomic structure and barley can be used as a diploid model of the Triticeae species, including wheat, barley and rye.

Gene isolation in barley

The study focuses on isolation and characterization of genes controlling industrially important traits using the genome diversity of barley. A recent example is a gene corresponding for barley seed dormancy (Qsd1), which is associated with pre-harvest sprouting and malting for brewing beer. Our analysis using a wild barley accession harboring a strong grain dormancy revealed novel insight into the genetic mechanism regulation grain dormancy in barley (Sato et al. 2016 Nat. Commun.). The orthologous genes are also existed in wheat genomes which will be important to control seed dormancy in wheat.
Introduction to Research

Research Area : Plant Diversity Analysis

Study on genetic diversity of crop species toward achieving sustainable crop productivity

Genetic diversity of target species is indispensable sources to breed new crop varieties to overcome food shortages under global environmental changes and population explosions. IPSR preserves more than 10,000 barley germplasm as not only for the research materials for plant science but also future resources to improve this crop species. The aims of our seed-bank activity as well as our research projects are to grasp the degree of the variation of traits associated with stress tolerance and ‘high-yield’ productivity and to understand genetic structure of the trait for mining the phenotypic diversity.

Deciphering the genetic diversity of domesticated barley spreading the entire world, we are evaluating agronomic traits such as vernalization requirement and salt tolerance at the germination stage. Genomic variation of the barley materials is explored using the next generation sequencing (NGS) technologies to make advances in our barley domestication history research. To uncover the genetic structure of the agronomic traits, multiple mapping populations such as recombinant inbred lines (RIL), chromosome segment substitution lines (CSSL) and nested association mapping population (NAM) are also developing, and the quantitative trait loci (QTL) corresponding to the agronomic traits are identifying.

Assoc. Prof. SAISHO Daisuke

Genome editing in barley

Genome editing is a new technology of genetic engineering in which DNA is inserted, replaced, or removed from a target genome sequence using artificial restriction enzymes (nucleases). We are now developing a method of mutagenesis by the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) or other techniques for future breeding and functional genomics in barley.

Research Area : Plant Diversity Analysis

Identification of the genes responsible for transformation amenability in barley

Different plant cultivars of the same genus and species can exhibit vastly different genetic transformation efficiencies. However, the genetic factors underlying these differences in transformation rate remain largely unknown. In barley (Hordeum vulgare), ‘Golden Promise’ is the most useful and well-studied cultivar for genetic transformation. By contrast, cultivar ‘Haruna Nijo’ is recalcitrant to genetic manipulation, although numerous genomic resources have been developed for this haplotype. Recently, we identified three major genomic regions on chromosomes 2H and 3H in barley important for successful transformation with Agrobacterium, utilizing the ‘Haruna Nijo’ × ‘Golden Promise’ F2 generation. We termed these loci as Transformation Amenability (TFA) responsible for Agrobacterium-mediated transformation.

The genomic regions identified herein likely include necessary factors (i.e. regeneration from callus) for Agrobacterium-mediated transformation in barley. The potential to introduce these loci into any haplotype of barley opens the door to increasing the efficiency of transformation for target alleles into any haplotype of barley by the TFA-based selection method. Now we are trying to isolate the genes responsible for TFAs.

Assoc. Prof. HISANO Hiroshi

Fig. Green shoots regenerating from callus of barley
(1) Molecular dissection of “domestication” genes in barley

- Naked caryopsis (nud)

- Short awn (lks2)
  JXB 63: 5223-5232 (2012)

(2) Molecular characterization of key genes for “food” barley

Development of remote cross breeding in rice via polyploidization

For breeding of super rice varieties with useful new genes, it is important to promote allelic exchange in existing cultivars by crossing them with wild or genetically remote cultivars. However, hybrids are rarely obtained from such distant crosses due to multitude of reproductive barriers. Interestingly, we found a fertile tetraploid progeny derived from anther culture of Asian rice cultivar, *O. sativa*, and African rice cultivar, *O. glaberrima*. Using genomic and phenotypic analyses, we now aim to clarify mechanisms involved in recovery of seed set in these plants. Furthermore, we hope to establish a novel remote cross breeding strategy in rice that overcomes reproductive barriers by introduction of polyploidization and haploidization.

Genetic dynamics in rice multiparent cross population

The expansion of genetic diversity in crossed populations is essential for faster and more efficient crop improvements. To overcome a limiting factor of biallelic gene combinations in rice breeding that depends on classical 2-way crosses, we developed a new multiparent population using 8-way cross strategy. By comparing genomic and phenotypic dynamics of this population, with those found in usual 2-way populations or parents, we aim to demonstrate the usefulness of multiparent populations for genetic improvement and development of novel breeding approaches in rice.
Introduction to Research

Research Area: Integrated Genomic Breeding

Analyses of kinetochore components of plant and its applications

We have been conducting molecular cytogenetic studies on the structure and function of nuclei and chromosomes using plant species. Kinetochores have been our main research subjects among functional chromosomal elements. We have been conducting basic research on the kinetochores, and have identified kinetochore components from various plant species including many crops. Additionally, we have conducted applied research including “construction of plant artificial chromosome (chromosome vector)” and “haploid production” using knowledge of the basic researches.

Analyses of epigenetic status in plants

Epigenetic regulation plays important roles in all aspects of plant life activities including development and stress responses. Epigenetic modifications of individual cells in plant organs/tissues are considered to be individually controlled, but it is difficult to know how each cell is modified by current methods. In order to solve this problem and to obtain epigenetic modification information of individual cells, we are developing epigenetic modification analysis methods using immunohistochemical staining, which provides a bird’s-eye view and single cell-level resolution keeping positional information of individual cells in organs/tissues.

Research Area: Integrated Genomic Breeding

Boosting up crop breeding by integrated bioinformatics and statistical genetics

Along with drastically changing our lives, computers have also brought a paradigm shift in plant breeding. “Genomic breeding” is a state-of-the-art method which integrates genome-wide genotype information to model and predict phenotypic variation in populations. Although modern computer-based methods have strong potential for accelerating the development of new varieties, statistical models used in the method still need improvements to capture in detail events happening in real nature. At present, we try to integrate all useful environmental and biological data into new statistical models for genomic breeding that will allow accurate phenotype prediction within relatively small datasets. We apply a large variety of modeling methods that also include machine learning strategies. We hope that our work will boost up breeding in the future, helping to overcome the global shortage in food production experienced worldwide.

Exploring genetic diversity for discovery of novel beneficial genes and improved crop productivity

In addition to methodological approaches, we also use real plants to discover novel genes leading to practical improvements of rice. Currently, African cultivated rice Oryza glaberrima is our main genetic target and source for variety of stress tolerance-related genes. In particular, we hope that O. glaberrima will provide us with beneficial genes to promote rice yield even under harsh environments that spread as a result of global warming in the current era.
Study on allopatric speciation in plants

Allopatric speciation is the typical process of formation of new species. The mechanisms how allopatrically distributed species established reproductive isolation is not well studied. I am interested in genetic mechanisms driving reproductive isolation between allopatrically distributed species or intraspecific lineages.

By investigating genetic variation, I have revealed intraspecific genetic divergence in various alpine plants. I focus on this genetic divergence for studying mechanisms of allopatric speciation because that such genetic divergence provides a good system to understand evolutionary processes following geographic isolation.

I am tracking the first issue by investigating genetic variation from worldwide samples of arctic-alpine plants by collaborating with several laboratories in Norway, USA and BC. I am challenging the second issue by implementing genetic and physiological approaches using model plants.

Biogeography of arctic-alpine and alpine plants

Arctic-alpine plants have enormous ranges encompassing the Arctic as well as higher mountains at lower latitude. Their ranges have been established by range shifts following the Pleistocene climatic oscillations, cycles of glacial/cold and interglacial/warm periods. I am interested in (i) when and how arctic-alpine plants established such a vast range and (ii) how they adapt to various environmental regimes such as light environments and temperature that drastically varies along latitude.

Regulation of virulence-related gene expression by Gas/Rsm-mediated quorum sensing in plant pathogenic bacteria

Understanding the mechanisms by which phytopathogens express their virulence is crucial for controlling plant diseases. Using Gram-negative phytopathogen Pseudomonas syringae pv. tabaci 6605 as a model pathogen, we have investigated important virulence factors using a large variety of virulence-related mutant strains such as ΔfliC, a defective mutant of flagellar filament protein, ΔpsyI, a defective mutant of acyl-homoserine lactones (AHL) synthetase in quorum sensing system and so on. We recently found that many isolates including P. syringae pv. tomatum DC3000 (PtoDC3000), do not produce AHL. In these strains, the open reading frames of psyI or psyR, which encodes the transcription factor PsyR were mutated. These results indicate that many isolates of P. syringae have genetically lost AHL production ability by the mutation of their responsible genes. To examine whether PtoDC3000 modulates the gene expression profile in a population-dependent manner, we carried out microarray analysis using RNAs prepared from low- and high-density cells. And then, we found that the expression of the small noncoding RNAs rsmX and rsmY were remarkably activated in high-density cells, but abolished in a ΔgacA mutant of Pta6605. These results indicate that Regardless of the ability to produce AHL, P. syringae regulates the expression of rsmX/Y by currently unknown quorum-sensing molecules. It is thought that rsmX and rsmY capture translational inhibitor RsmA, then derepress the expression of virulence-related gene. We now investigate the function and mechanism of rsmX and rsmY-regulated expression of virulence-related gene expression.
Unraveling plant disease susceptibility to fungal pathogens

Multi-layered defense barriers ensure that a plant is the host to only a few adapted pathogens. Thus, the host range of a particular plant pathogen relies on its ability to fully suppress plant defense responses such as the pattern-triggered immunity (PTI). One of the common pathogen strategies to overcome PTI is the production of a plant defense suppressor. In the case of Mycosphaerella pinodes, a causal agent of Mycosphaerella blight on pea, this fungus can avoid host defense responses by secreting at least two suppressors named supprescins A and B (Fig. 1), which manipulate the physiology of the host cells, including JA biosynthesis through targeting the host’s ATPase. In parallel, a constituent(s) similar to the fungal supprescins has been discovered in healthy leaves of pea. Such a constituent was also found in the healthy leaves of barley and Arabidopsis plants, and collectively referred to as an endogenous suppressor (ES). Actually, the purified ES can suppress or delay PTI, enabling the non-adapted pathogen to cause disease symptom on corresponding plants. Interestingly, the action of the pea ES is quite similar to that of the supprescins A and B secreted by M. pinodes (Fig. 1), which manipulate the physiology of the host cells, including JA biosynthesis through targeting the host’s ATPase. In parallel, a constituent(s) similar to the fungal supprescins has been discovered in healthy leaves of pea. Such a constituent was also found in the healthy leaves of barley and Arabidopsis plants, and collectively referred to as an endogenous suppressor (ES). Actually, the purified ES can suppress or delay PTI, enabling the non-adapted pathogen to cause disease symptom on corresponding plants. Interestingly, the action of the pea ES is quite similar to that of the supprescins A and B secreted by M. pinodes (Fig. 1). This fungus can avoid host defense responses by secreting at least two suppressors named supprescins A and B (Fig. 1), which manipulate the physiology of the host cells, including JA biosynthesis through targeting the host’s ATPase. In parallel, a constituent(s) similar to the fungal supprescins has been discovered in healthy leaves of pea. Such a constituent was also found in the healthy leaves of barley and Arabidopsis plants, and collectively referred to as an endogenous suppressor (ES). Actually, the purified ES can suppress or delay PTI, enabling the non-adapted pathogen to cause disease symptom on corresponding plants. Interestingly, the action of the pea ES is quite similar to that of the supprescins A and B secreted by M. pinodes (Fig. 1), which manipulate the physiology of the host cells, including JA biosynthesis through targeting the host’s ATPase. In parallel, a constituent(s) similar to the fungal supprescins has been discovered in healthy leaves of pea. Such a constituent was also found in the healthy leaves of barley and Arabidopsis plants, and collectively referred to as an endogenous suppressor (ES). Actually, the purified ES can suppress or delay PTI, enabling the non-adapted pathogen to cause disease symptom on corresponding plants. Interestingly, the action of the pea ES is quite similar to that of the supprescins A and B secreted by M. pinodes (Fig. 1).
For the control of crop diseases caused by a fungal pathogen *Rhizoctonia solani*

*Rhizoctonia solani* is a soil-borne fungal phytopathogen causing rice sheath blight as well as seedling damping-off or root rot in various crops. Management of this pest is difficult and it gives rise to serious damage in agriculture and economies. An experimental pathosystem using *Brachypodium distachyon*, an emerging model plant, revealed plant immunity mechanism against this pathogen leading to a novel insight into the fungal infection strategy. Fungal proteinaceous weapons called effectors are now being investigated.

Molecular basis of a biological control agent for crown gall disease in grapevine

Grape is one of the major fruits produced in Okayama. It suffers serious damage from crown gall disease which is caused by *Rhizobium vitis* Ti strain. A non-pathogenic strains of *R. vitis* have been isolated as biological control of this pest. The molecular mechanism underlying this suppression activity is investigating and we found a potential causal substance produced by this biocontrol agent.

Isolation and characterization of plant defense activators for sustainable agriculture

Plant defense activators exhibit cop protection activity by priming or inducing plant immune response. We established a quantitative assay method for plant defense response and identified potential compounds through a high-throughput screening of several commercial libraries of organic small molecules as well as a laboratory-made small cyclic peptides. They can be used for not only lead compounds to develop agrochemicals but also molecular probe to understand plant immunity.

Genetic study on instability of flowering time in wheat and barley under global warming conditions

Global climate change has a huge impact on crop production. For wheat and barley production in Japan, warm winter has been arising as a serious problem which would cause yield decrease and low quality.

So far, early-flowering (heading) varieties of wheat and barley have been developed to avoid pre-harvest sprouting and Fusarium head blight, which could often be caused by monsoonal rain during maturing and harvesting stages. However, most of early-flowering varieties show “instability of flowering time” in response to ambient temperature. They differentiate young spike primordium extremely earlier in warmer winter than in ordinary years. Unexpectedly precocious spike development will result in yield decrease due to less biomass production and frost injury caused by transient chills in early spring.

To solve the problem, it is necessary to disclose genetic mechanism underlying the instability of flowering time. For this goal, we are working on (1) identification of novel flowering-time genes and their interaction with other flowering-time genes, (2) finding genes which do not promote flowering very much even under warm winter condition, and (3) disclosing the genetic mechanism underlying the instability of flowering through molecular genetic study.
Studies on relationship between fruit constituents and its taste

A fruit contains various taste active compounds, such as sugars, organic acids, amino acids, polyphenols, and aromas. We have been studying to clarify the effects of juice constituents on the fruit taste and developing quantitative evaluation system for fruit taste.

Studies on the mechanism of gibberellic acid induced seedlessness in grapes

Gibberellic acid (GA3) is widely used in the production seedless grape in Japan. We have been studying to clarify the mechanism involved in seedlessness of gibberellic acid treated grapes.
**Effects of timing of flowering on fruit quality and incidence of physiological disorders in peach**

We are trying to clarify physiological aspects and mechanisms of various problems or improved points in high quality fruit production and to develop their solution. Stability of fruit size and Soluble solid content (SSC) level is important in high quality peach fruit production. Also, severe flesh disorder causes economic loss. We found that “the fruit from early timing of flowering” shows worst qualities and the severe flesh disorder symptom within a tree awe to inferior accumulation of mineral nutrition and assimilates during the latter half of fruit development. These results are utilized to improve the skill thinned flowers or fruit.

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**Research on the environmental control for greenhouse production using ICT**

Greenhouse production is important for supplying vegetable and ornamental plants. In our country, the environmental control in greenhouse using microcomputer has not been spread until recently. A controller for environmental control was too expensive for small scale greenhouse, which was popular in Japan. So, the low cost controller named “Yoshi Max” was developed by our laboratory. This controller is conforms to the Ubiquitous Environment Control System (UECS) communication protocol (https://uecs.jp/index-e.html). UECS is beginning to spread in Japan as an environmental control system using ICT.

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**Researches on detection of incidence of internal fruit physiological disorder and estimation of fruit maturity on the tree using an acoustic vibration method**

To accomplish the stable fruit production, removal of abnormal fruit in orchard during immature stage and information of optimal harvesting was needed. Therefore, it is important to develop nondestructive method which can be utilized on the tree. By using an acoustic vibration measurement, split-pit occurrence could be detected from the ratio of resonant frequencies ($f_3 / f_2$), and progress of fruit maturity (decrease in flesh firmness) could be associated with the decline of $f_3$ value measured without removal of fruit bag.
**Introduction to Research**

**Research Area : Crop Science**

**Studies on Salinity Tolerance Relating Grain Productivity in Cereals**

An adequate food supply from agricultural crops is essential to the quality of human life. Salinity is one of the most serious environmental stresses severely limiting crop growth and grain productivity. Salt-affected land occupies about 20% of irrigated agricultural land. Rice, a major staple food for the ever-increasing world population, is one of the most salinity-sensitive crops. As such, improving the salinity tolerance of rice is desired to increase productivity on salt-affected soil. However, genetic and physiological knowledge of salinity tolerance relating grain productivity in rice is still limited. We study salinity tolerance in rice at both physiological and molecular levels. We found several quantitative trait loci (QTLs) for salinity tolerance relating high plant dry weight and grain yield under long-term saline conditions by using chromosome segment substitution lines carrying segments from a salinity-tolerant variety in the genetic background of a salinity-sensitive variety. Our research advance will contribute to developing rice varieties with high yield under salinity stress conditions.

**Research Area : Control of Flowering**

**Development of compacted medium using heat fusion fiber**

We found that medium could be hardened using heat fusion fiber. We demonstrated that use of hardened medium could enable cell transplants production and bedding plant production without polyethylene pots. Pansy and garden-type cyclamen plants grown in compacted medium without polyethylene pots in the summer season were bigger than those grown in compacted medium with polyethylene pots. The temperature of the medium without polyethylene pots was lower than that with polyethylene pots. This could be due to the evaporative cooling effect from the surface of compacted medium without polyethylene pots.

**Improvement of growth and flowering of *Eustoma grandiflorum* by low temperature treatment**

It is important to establish a suitable method for rosette avoidance and cost reduction in *Eustoma* seedlings production in summer. We found that intermittent low temperature storage treatment could be available as a supplemental method to prevent rosette of *Eustoma* seedlings after application of low temperature treatment to imbibed seed. However, suitable temperature and cycle have not been clarified. We confirmed that the cycle of 15-15 day stored at 10˚C was a suitable treatment to avoid rosette, promote growth and decrease labor for *Eustoma* growing.
Global warming affects agriculture and food supply. In livestock industry, extraordinarily high temperature in summer season gives stress to livestock species and reduces their productivity, such as daily gain of body weight and milk production. Recently, it is becoming a big issue that the heat stress decrease pregnancy rate of dairy cows in summer not only in Japan but also all over the world.

To solve this problem, we are investigating the effect of heat stress on uterine functions of cattle.

In our current study, it is shown that the heat stress disrupts endocrine function of bovine uterus such as prostaglandins secretion and influences the mechanism for the recognition of pregnancy in cattle, resulting in low pregnancy rate.

Now we study how the heat stress affect uterine function of cattle.

Immunohistochemistry of bovine endometrium. Green signals indicate the localization of heat sensor proteins.

Oviduct is an important organ as a site for sperm capacitation, fertilization and early embryonic development. It is also the pathway of gametes and embryo connecting the ovary to the uterus. In spite of the essential organ for establishment of pregnancy, regulating mechanisms of oviductal function are unclear. Our aim is to clarify the physiological mechanisms which control the oviductal functions.

Spontaneous contraction of oviduct is necessary for transport of gametes and embryos, since it produces peristaltic movement. Oviduct contains endogeneous pulse generator for contraction called as “pacemaker”. Pacemaker cells generate rhythmic spontaneous depolarization leading to the contraction of smooth muscle cells. In our project, the factors involved in spontaneous contraction are investigated using bovine oviductal tissues. In addition, we also try to identify the pacemaker cell in mammalian oviducts.
Basic and applied research on mammalian gametes (maturation, fertilization and early development)

We are studying on gametes in mammals including humans during gametogenesis, maturation, fertilization and early development, to develop efficient systems for embryo production in vitro. We are also undertaking basic and applied studies to improve the efficiency in the production of more value-added useful animals.

Intracytoplasmic sperm injection

Development of new systems to produce embryos in vitro from oocytes collected from small diameter follicles

For in vitro embryo production in mammals, especially domestic animals, usually oocyte-cumulus complexes derived from middle follicles with a diameter of 3-6 mm have been used. However, a large number of small follicles with less than 3 mm in diameter, rather than middle follicles, dominantly exist on the surface of ovaries. On the other hand, the developmental competence of the oocytes from small follicles (in meiosis and early development following fertilization) has been known to be much lower than those from middle follicles. We're trying to make clear the molecular reasons about differences in the developmental competence and to make effort to improve the ability by various modifications.

Expression of Drp1 protein, which is a critical factor associated with the division of mitochondria, in mouse embryos and the co-distribution with mitochondria

Expression of H2B-mCherry RNA injected into porcine immature oocyte
1. Study on host-pathogen relationship and pathophysiology in parasite infection

We are exposed to the infectious diseases. We need to develop a cheaper, effective, and safety ways to control the infectious diseases because these incur a heavy economic loss. One of the problems is that we have a little information to the infectious diseases. Hence, our mission is to understand the pathophysiological and immunological mechanisms of infectious diseases. In near future, we hope that the results of our research are applied to vaccine development and new strategies for disease control.

Our targets are parasites as follows:

1. Avian coccidia: Our research is to understand 1) the molecular mechanisms of parasite invasion, 2) the pathological mechanisms in the intestine, and 3) immunological mechanisms.

2. Leishmaniasis: We are studying to understand 1) the molecular mechanisms of disease development, 2) analysis of virulence factors of the parasites, and 3) the parasitic mechanism.

2. Food Science: physiological analysis of food ingredients

Food ingredients have important roles to our health. However, we have a little knowledge of them scientifically. Our mission in this research area is to understand the physiological effects of food ingredients, especially polyphenols and carotenoids, and to develop the innovative and useful way for human and animal health.

1. Research history and analytical methods of gut microbiota
2. Gut microbiota and the bacterial composition and diversity of human gut microbiota
3. Symbiosis with the host of the gut microbiota
4. Effect of food ingredients on the human gut microbiota
5. Gut microbiota and disease (effect of gut microbiota to host)
6. Metagenome analysis and gene function of gut microbiota

Food ingredients have important roles to our health. However, we have a little knowledge of them scientifically. Our mission in this research area is to understand the physiological effects of food ingredients, especially polyphenols and carotenoids, and to develop the innovative and useful way for human and animal health.

1. Complete genome analysis of lactic acid bacteria and bifidobacteria
2. Functional bacterial genome analysis
3. Research on probiotics/prebiotics effects by using gnotobiotic mice
4. Effect of dietary fiber as prebiotics