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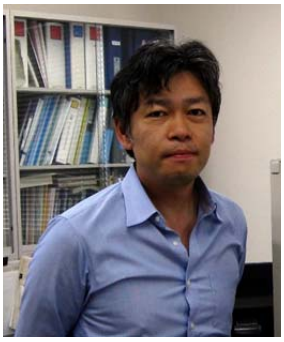
Food and agriculture in a changing world

Hunger has been rising the past three years, endangering the achievement of the second Sustainable Development Goal (SDG2), which calls for the eradication of hunger and malnutrition by 2030. Looking further into the future, our world is changing remarkably fast. Continued economic and population growth, climate change, urbanization and demographic shifts will make it challenging to produce enough food to feed the world.

However, we must do more than produce enough food. In order to lead happy, healthy and productive lives, humans need not only dietary energy, but also high quality protein and micronutrients. Thus, we must produce enough *nutritious* food, and in a sustainable manner, so that future generations will be well nourished.

Science has played an essential role in meeting past challenges in food and agriculture, including the Green Revolution. Here too the world is changing, and the burgeoning array of new technologies currently available suggests that science is likely to play a key role in the future as well. The future will see profound changes in *what* is grown, *how* it is grown, *where* it is grown and *how it moves* from one place to another. New technologies present tremendous opportunities, but these technologies also have social and economic consequences for the most vulnerable groups in society such as smallholder farmers and poor urban consumers. Everyone has a role to play in managing these consequences in a responsible manner so as to leave no one behind.



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Specialty: Conversion technology of lignocellulolytic biomass resources using microbiology

Old oil palm trunk: A sustainable bioresource for renewable energy production

Oil palm trees are replanted at an interval of approximately 20-25 years because of decreased oil productivity of old trees. Consequently, the felled trunks are the enormous amount of biomass resources in the palm oil producing countries such as Malaysia and Indonesia. We found that old oil palm trunks which were felled for replanting contained large quantity of sap with high glucose content. Oil palm sap was also found to be rich in various kinds of amino acids, organic acids, minerals and vitamins (1). Based on these findings we tried to ferment the sap to produce biofuels such as ethanol and methane, and a promising material for bio-plastics such as lactic acid and PHA using microorganisms. There products were produced from the sap without addition of nutrients at comparable rate and yield. On the other hand, we also found that sugars existing in the sap increased remarkably during storage after logging. Total sugar in the sap increased from 8.3 % (w/v) to 15.3 % (w/v), the concentration comparable to that of sugar cane juice, after 10-30 days of storage (2, 3). In addition, we prepared bio-pellet from the squeezed fiber residues of oil palm trunk (4). To encourage more sustainable oil palm industry, the project which is “Sustainable Plantation of Oil Palm by Adding Value to Oil Palm Trunk Through Scientific and Technological Innovation” will be initiated from 2019 in Malaysia under SATREPS. We believe that old oil palm trunk becomes a promising source of sugars by proper aging after logging and, thus, its sap and residues can be a sustainable feedstock of biofuels in Southeast Asia.

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Research on development of vegetables, flowers and herbs adapting climate change in Hochiminh city

Ho Chi Minh city is the important center for science and technology of Vietnam with high population density and limited agricultural land. The city’s agriculture is developing in the direction of urban agriculture and focusing on main crop groups of vegetables, flowers. Therefore, research on the development of vegetable, flower, herbs and related technological procedures is one of the important issues for the city's agriculture. This report presents some main research projects related to the development of vegetable, flower and herb varieties such as selecting pure red lines using self pollination and haploid culture; creating new varieties using irradiation, RNAi gene transfer and gene editing; analyzing genetic diversity using molecular markers; and developing procedures for propagation and obtaining bio-mass. The results show that most of the studies have achieved remarkable success. The pure red lines of *Cucumis melo* and the procedure for pollen culture of *Capsicum annuum* were created from the studies on pure red lines. Similarly, the new varieties of *Gloxinia speciosa* and the virus resistant varieties of *Dendrobium* Sonia *in vitro* were also created from the studies on breeding. In addition to the results of breeding, the procedures of propagation and obtaining biomass has been successfully established for some valuable herbs such as *Panax vietnamensis*, *Curculigo orchioides*, *Fallopia multiflora*, etc. These results are important background for the implementation of the next phase of research.

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Specialty: Plant responses to abiotic stress

Convergent evolution of desiccation tolerance across land plants

Desiccation tolerance was a critical adaptation for the colonization of land by early non-vascular plants. Resurrection plants have maintained or rewired these ancestral protective mechanisms and desiccation tolerant species are dispersed across the land plant phylogeny. Though common physiological, biochemical, and molecular signatures are observed across resurrection plant lineages, features underlying the recurrent evolution of desiccation tolerance are unknown. We utilize a systems biology approach across diverse resurrection plants to identify core sets of genes and regulatory elements associated with desiccation tolerance. Datasets include high-resolution temporal gene expression, chromatin dynamics, comparative genomics and physiology. We have identified a single gene family with dramatic expansion in all resurrection plant genomes and no expansion in desiccation sensitive species. This gene family of early light induced proteins (ELIPs) expanded in resurrection plants convergent through repeated tandem gene duplication. ELIPS are universally highly expressed during desiccation in all resurrection plants and may play a role in protecting against photooxidative damage of the photosynthetic apparatus during prolonged dehydration. We hypothesize a combination of network rewiring and localized gene duplication spurred the evolution of desiccation tolerance in land plants. Desiccation related pathways in resurrection plants may be useful for engineering improved drought tolerance and resilience into crop plants.

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Enhancing Drought Tolerance Through Directed Manipulation Of The Growth/Defense System.

Exposure to abiotic stress is one of the primary factors limiting crop productivity. Temperature, CO_2, salt, soil quality, too much water, and too little water are just some of the environmental factors limiting crop production. Among these, drought stress is the most prevalent. As a function of genotype, phenotype, and environment, plants have evolved numerous – sometimes overlapping – mechanisms to cope with limited water availability. In brief, drought resistance describes the evolved, or adapted, ability of a plant to avoid, escape, or tolerate drought stress. Conversely, and as an illustration of the functional relationship between abiotic stress and development, drought escape is used to classify a plant that can complete its lifecycle before succumbing to the effects of drought. As a function of physiological adaptation in response to limited water, drought avoidance describes the ability of a plant to maintain relatively high levels of water content despite reduced content in the soil. Lastly, drought tolerance is used to classify plants that can survive despite low relative water content.

Research in my laboratory has contributed to numerous advances in our understanding of how plants utilize basic physiological processes for immune signaling activation and pathogen resistance. In the broader context of abiotic and biotic stress signaling, we have focused on the immune signaling regulator NDR1 (non-host disease resistance-1), which is required for plant response to pathogen infection. As a function of signaling specificity, initial studies used NDR1 as a genetically-tractable model for plant response to pathogens, and from this, successfully mapped the first blueprint defining how plants specify the activation of resistance. More recent work in my lab at Michigan State University has culminated in the development of a working model based on key functional similarities between the immune regulator NDR1 and a key regulator of mammalian stress physiology, integrins – proteins required for injury, defense, and death responses in human cells. In short, published and ongoing work – presented today – demonstrates that NDR1 plays a key role in the link between cellular physiology and the activation of immune signaling. From this, we have developed the working hypothesis: Defense proteins play critical roles in non-defense-associated processes, including those associated with development and abiotic stress signaling. Here, I will present recent data demonstrating that NDR1 plays a key role in abiotic stress perception and signaling, including drought avoidance. We posit that NDR1 functions in mechanisms that allow plants to anticipate, respond to, and survive/thrive under conditions of limited water availability.

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Spatiotemporal dynamics of plant immune responses

The innate immune response is, in the first place, elicited at the site of infection. Thus, the host response can be different among the infected cells and the cells surrounding them. Effector-triggered immunity (ETI), a form of innate immunity in plants, is triggered through specific recognition between pathogen effectors and their corresponding plant cytosolic immune sensors, resulting in rapid localized cell death known as hypersensitive response (HR). HR cell death is usually limited to a few cells at the infection focus, and is surrounded by a few layers of cells massively expressing defense genes such as *Pathogenesis-Related Gene 1* (*PR1*). This virtually concentric pattern of the cellular responses observed in ETI has been proposed to be regulated by a concentration gradient of salicylic acid (SA), a phytohormone accumulated around the infection site. Recent studies demonstrated that jasmonic acid (JA), another phytohormone known to be mutually antagonistic to SA in many cases, is also accumulated in and required for ETI, suggesting that ETI is a unique case. However, the molecular basis for this uniqueness remained largely to be solved. In order to dissect spatiotemporal regulation of ETI, we have developed an intravital time-lapse imaging system of plant immune responses. Using this system, we found that the JA signaling pathway is activated in the cells surrounding the central SA-active cells around the infection sites in *Arabidopsis thaliana*. Our data revealing a dynamic pattern of plant cellular responses re-emphasizes that the spatial consideration is a key strategy to gain mechanistic insights into the apparently complex signaling cross-talk in immunity. We are further developing various genetic resources as well as imaging techniques in order to dissect plant immune active field formation around the infection foci. Our current progress will be presented.

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High-quality *de novo* genome assembly and annotation of the tomato genome using Long Read sequencing and TomExpress expression atlas

Long sequencing technology offer the possibility of dramatically improving the contiguity of genome assemblies and able to extend paths into problematic or repetitive regions. In addition to Long sequencing reads approaches, recent technologies like optical mapping and linked reads from 10X Genomics are capable to bring additional scaffolding to achieve chromosome-level assemblies.

In order to improve the actual tomato reference genome sequence, we generated 70X coverage of Pacific Biosciences (PacBio RSII) long-reads, 100X of optical mapping using two different enzymes and 100X illumina HiSeq3000 2x150b paired-reads sequencing from Chromium linked 10X Genomics libraries.

The integration of these three approaches allowed to reach a genome size of **~830 Mb** with an **N50 of 45 Mb**. The assembly contiguity reached chromosome-arm-levels. Interestingly, one full chromosome (Ch12) has been fully assembled in one scaffold. Some of the remaining scaffolds revealed large parts of some centromeric regions, even including some of the heterochromatic regions. We assessed the quality of contigs and scaffolds using Illumina mate-pair libraries and genetic map information.

The integration of the genetic map allowed to generate the 12 pseudomolecules corresponding to the 12 tomato chromosomes. Several regions corresponding to chromosome zero in the SL3.0 reference genome were included in the current assembly.

We took advantage from the large RNA-Seq data of the TomExpress platform (http://tomexpress.toulouse.inra.fr/) and use them to annotate this new genome assembly. To assess the completeness of the genome and the transcriptome assembly, busco v3.0 software has been used and shown a high percent of gene coverage (> 95%).

The genome sequence, annotation, JBrowse, and useful tools are accessible http://tomatogenome.gbfwebtools.fr/ .

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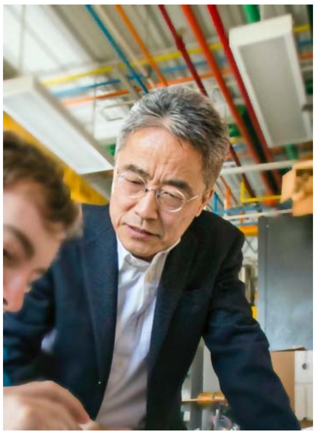
Climate-Smart Agricultural Practices: Bangladesh Perspective

Bangladesh’s agriculture has been recognized as one of the most vulnerable sectors regarding impacts of climate change due to its juxtaposing geographical position, though research to elucidate this jeopardy is still elusive. Agriculture acts as a mainstay of the economy of the millions of people, which employs around 62% of the population and contributes over 14.75% of the country’s GDP. Although agricultural production has been increased tremendously in the last couple of years due to technological development, but it is at vulnerable condition due to extreme climatic events, for instances, increasing temperature and erratic rainfall along with austere and frequent floods, droughts and cyclones in the recent years. Many research and development organizations are now doing researches in developing technologies and practices that can be useful for adaptation to climate change. Few agricultural technologies, which are considered as climate-smart practices, are being used at field levels for sustainable crop production. Some of the adaptive technologies are: stress tolerant crop varieties, conservation agriculture using mulching such as water hyacinth, floating methods of agriculture, multiple cropping/intercropping/agroforestry, *sorjan* method of cultivation, modified crop rotation, adjusted crop calendar, community seedbed, integrated homestead farming. Furthermore, rooftop gardening with fruit tree, seasonal vegetables, medicinal and ornamental plants are also found in urban area, which is getting popularity nowadays. Since climate change is a continuous process and its impacts on agriculture are versatile, both technological and non-technological issues need to be addressed. Strengthening agricultural research and collaborations with strong support systems are critically important to advocate an effective adaptation process to overcome climate change encumbers.



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Near-real-time Information System and Precision Farming

The ‘green revolution’ has been achieved by the use of modern high-yielding varieties while greater benefits have been realized from chemical fertilizers, irrigation, and pest control. However, with the increasing costs of water and chemicals plus the environmental concerns, crop-growers are facing mounting pressure to farm more efficiently. If growers can gather accurate field information efficiently, site-specific crop management could be the solution to help further increase productivity on shrinking farmlands (and reduce negative environmental impacts).

With the advent of affordable and sophisticated multirotor UAVs, there has been a rush by various companies and research organizations to develop drones for agricultural data collection applications. Despite the resources devoted to develop agricultural UAS platforms, **there has been a significant void of a knowledge-based (autonomous data collection/processing) and user-friendly interface** that will allow individual growers or farm managers to get useful information in time and so that they can manage their crops site- and time-specifically.

Working with the industry partners and utilizing algorithms derived from data collected by Illinois Laboratory for Agriculture Remote Sensing (ILARS) from over a decade of research, a smart “farmer’s personal UAS” prototype – autonomous precision farming UAS data collection system has been developed, tested on several commercial farms in 2017 growing season. The prototype uses a light-weight UAV and a low-cost high-resolution RGB camera. The system has a beta automatic UAV crop field mapping mission control app (currently for iOS smart phones and tablets), which could advice growers on data collect settings based on real-time weather/field crop conditions and allows growers to collect high-quality field data and interactively view/share data analysis results on-site.

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Intelligent Management System of Dairy Cattle Health Monitoring under Heat Stress

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During hot season, combination of fan, sprinkling and mist can lower thermal-humidity index (79 vs. 81) and increase lactating cows total daily activity 30%, milk yield 33% compared to combination of fan and sprinkling only. Heat stress also happened in cool season when daily thermal-humidity index fluctuating over 10 units. During such sudden THI fluctuation event, milk yield dropped 5-9% without changing total daily activity. However, hourly total activity showed linear decline in the afternoon and activity of feeding and rumination dropped several times in the first half day before noon. In the platform of Intelligent Management System, data of environment temperature and humidity, activity monitor, image recorder and processor, milk yield were collected, analyzed and used to control operation settings of fan, sprinkling and mist according to different degrees of heat stress. With the cross analysis of data, difference of individual lactating cow's heat stress tolerance was identified. Some cows can tolerate up to THI 82, but some cannot tolerate beyond THI 75. If THI can be controlled below their tolerable THI, milk yield can be maintained 15% higher. Drinking behavior was monitored by image system which revealed drinking frequency well correlated with the hourly incline and decline of THI during heat stress periods. Data of image and THI can be processed and linked to power distribution box of fan, sprinkling and mist operation to create varied combination settings of cooling system in according to different degrees of heat stress automatically. Indoor THI can be decreased by 3 units in average by the automatic monitor and control system, electricity energy can be saved and milk yield can be maintained 7-12% higher than manual control.

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Image-based Phenomics Approach for Discovering Abiotic Stress Tolerance Genes in Rice

Rice (*Oryza sativa*), a staple crop for the majority of the world and critical for global food security. Rice is highly sensitive to salinity and drought stress. Therefore, it is important to improve the salt and drought tolerance of rice cultivars along with better soil and water management practices. Plant responses to salinity and drought stress can be highly dynamic and difficult to quantify accurately. This is challenging for large genetics studies aimed at mapping stress tolerance genes as the scale of experiments with destructive measurements and large number of genotypes are difficult to manage. To address this issue, we are using image-based phenomics approaches to capture dynamic salt and drought responses of a rice diversity panel (~350 accessions) as a non-destructive approach with high temporal resolution. We combine this imaging approach with genome-wide association analysis to discover genes that have the potential to improve the abiotic stress tolerance in rice. Our work elucidates the rice responses to salt and drought stress from a physiological and genetic perspective.

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Bayesian genomic factor analysis and Bayesian network to characterize high-throughput phenotyping data in rice

New phenomic platforms are revolutionizing the ways in which phenotypes are collected from important crop species. The new phenomic systems deliver diverse characteristics for growth traits, detailed dynamics of abiotic stress responses, and disease development, which are not feasible through labor-intensive classical phenotyping. The rich array of available phenotypic resources offers unique opportunities to apply quantitative genetic analyses in plant breeding to build the genotype-phenotype map from a phenotype centric view. The challenge here is how to infer and interpret the complex interrelationships among a large number of phenotypes in the big data era. Therefore, this study aimed to obtain a first glimpse of the utility of graphical modeling to characterize a wide spectrum of rice phenotypes. Bayesian confirmatory factor analysis was used to derive six latent variables including grain morphology, morphology, flowering time, physiology, yield, and salt response from 48 diverse phenotypes. Causal structures were inferred for those lower-dimensional latent variables. Inferring these network structures is important because genetic selection requires causal assumptions as associations cannot be used to predict the influence of external interventions in the interrelated complex traits system. Next, we demonstrate that a Bayesian network describing putative causal relationships among multiple phenotypes can be used to infer single-nucleotide polymorphism (SNP) effects in genome-wide association studies (GWAS) through a structural equation model (SEM). We developed SEM-GWAS and applied this to rice drought responses, showing that SEM-GWAS provides important insight regarding the mechanism by which identified SNPs control traits by partitioning them into direct, indirect, and total SNP effects.

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Genomic selection and its extension to model based development in plant breeding

To feed the 9 billion by 2050, it is necessary to accelerate genetic gain in plant breeding and to unlock the genetic potential of crop plants. Genomic selection, i.e., selection based on breeding values predicted from genome-wide markers, is a promising method for the acceleration of the genetic gain, and is becoming a widely used tool in plant breeding especially for the improvement of complex traits, i.e., traits controlled by a number of genes and influence of environment and its interaction with genes. Genomic selection contributes to (1) acceleration of breeding cycles, (2) rationalization of breeding procedures, and (3) effective use of genetic resources. The combined use of other breeding technologies, such as generation advancement and genome editing, will greatly improve the potential of genomic selection. Since genomic selection in general does not take into account the effects of the environment and management, model integration between genomic prediction models and models for plant environmental responses are areas of active research. The presentation will be about the potential and future directions of genomic selection based on the results of our studies. The concept of model based development (MBD), i.e., a method for developing a complex system based on modelling and simulation, will be introduced as a future direction of genomic selection in plant breeding.

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Genomic dissection and prediction of transcriptome dynamics in field conditions

Detailed molecular mechanisms of plant environmental responses have been revealed by laboratory experiments. However, it is not enough to understand plant envrionmental responses under field condtions. To bridge between laboratory and field, we developed statistical models using extensive transcriptome data of rice leaves in the field and the corresponding meteorological data. We showed that the transcriptome dynamics of rice leaves in a paddy field were mainly governed by ambient temperature and circadian clock. The statistical model successfully predicted field transcriptome dynamics in Nipponbare, a standard cultivar. However, the effect of genomic buckground on transcriptome dynamics is not known. To establish a method of predicting the transcriptome dynamics in various genomic backgrounds, we developed several novel technologies such as automated parallel preparation of RNA-Seq library, a fast and easy-to-use R library for statistical modeling. Using these technologies, we obtained RNA-Seq data of 1,300 field samples of chromosomal substitution lines between Koshihikari and Takanari, and analyzed the transcriptome data with the corresponding meteorological and genotype data. Two statistical models describing transcriptome dynamics in Koshihikari and Takanari, respecively, were developed. We detected 2,911 genes with different expression dynamics between two cultivars by comparing with predicted transcriptome dynamics of Koshihikari and that of Takanari. Genomic regions controlling the expressional differences were successfully identified in approxmately half of the genes with different expression dynamics. Our models enable the prediction of field transcriptome dynamics not only in two parental cultivars but also in their progeny lines.