Regulation of Freezing Tolerance and Salicylic Acid-Mediated Immunity by
Arabidopsis CAMTA Transcription Factors

*Arabidopsis thaliana* calmodulin-binding transcription factors CAMTA1, CAMTA2 and CAMTA3 function in an additive manner to regulate the expression of genes involved in freezing tolerance and salicylic acid (SA)-mediated immunity. In the case of freezing tolerance, the CAMTA proteins act rapidly to induce genes in response to low temperature (4°C). In the case of SA-mediated immunity, the CAMTA transcription factors act to repress the expression of SA-pathway genes in healthy plants grown at moderate temperature (22°C). However, this CAMTA-mediated repression of SA-pathway genes is overcome in plants exposed to low temperature (4°C) for more than one week and in plants infected by biotrophic and hemibiotrophic pathogens. Our long-term goal is to understand the mechanisms by which the CAMTA transcription factors act as inducers and repressors of gene expression and how their activities are regulated by both rapid-acting and slow-acting cold-signaling pathways. We have found that CAMTA3-mediated repression of SA pathway genes involves action of an N-terminal repression module (NRM) that acts independently of calmodulin (CaM) binding to the CaM-binding (CaMB) domain, a finding that is contrary to current models. In addition, mutational analysis has provided evidence that the repression activity of the NRM is suppressed by action of the IQ and CaMB calmodulin binding domains responding to signals generated in response to low temperature and pathogen infection. Our results indicate that current CAMTA3 structure-function models require revision and that regulation of CAMTA3 repression activity by low temperature and pathogen infection involves related mechanisms with distinct differences.
Modularity in Jasmonate Signaling for Multi-stress Tolerance

The phytohormone jasmonoyl-L-isoleucine (JA-Ile) coordinates immune and growth responses to increase plant survival in unpredictable environments. The core JA-Ile signaling pathway comprises several functional modules, including a repertoire of COI1-JAZ co-receptors that couple hormone perception to degradation of JAZ repressors, JAZ-interacting transcription factors that execute physiological responses, and multiple negative feedback loops to ensure timely termination of these responses. Emerging evidence indicates that JAZs integrate various informational cues to enhance plant resilience to both biotic and abiotic stress. Interestingly, JA-Ile-mediated defense responses are accompanied by potent growth inhibition. Despite the importance of these growth-defense tradeoffs in shaping plant productivity in natural and agricultural ecosystems, the molecular mechanisms that link growth and immunity are still poorly understood. We are using genetic approaches in Arabidopsis to understand the role of JA-Ile signaling in growth-defense balance. Our recent findings show that bHLH-type MYC transcription factors play an important role in promoting both in leaf defense and growth inhibition. We have also used genetic suppressor screens to identify mutations that uncouple growth-defense antagonism, thus allowing plants to grow and defend well simultaneously. These findings have implications for designing crops for improved performance in harsh environments.
Development of Technologies and Crops for Stable Food Production under Adverse Environments and Changing Climate Conditions

Goal 2 of the United Nations’ 17 Sustainable Development Goals (SDGs) aims to end hunger, achieve food security and improved nutrition, and promote sustainable agriculture. Currently, 215 million people in Sub-Saharan Africa are undernourished. It is well known that agricultural potential in developing regions, including Africa, has not been fully realized because their adverse environments and changing climate conditions impose abiotic stresses (e.g., low soil fertility, droughts) and biotic stresses (e.g., pests, diseases) on plant growth and development. To ensure food and nutrition security, we will endeavor to develop technologies and crops with high productivity and adaptability to adverse environments and changing climate conditions. So far, we have developed rice near-isogenic lines (NILs) with early-morning flowering trait that mitigates high temperature-induced sterility and soybean NILs with high salinity tolerance using marker assisted selection. We have shown that overexpression of an Arabidopsis galactinol synthase gene improved drought tolerance in transgenic rice and increased grain yield. We will also generate fundamental information concerning regional crops, such as yam and cowpea, needed to explore useful germplasm and develop tools to select and evaluate the materials effectively. We hope these technologies and materials could contribute to achieving food and nutrition security in developing regions.
Defining the Convergence and Interplay Between Biotic and Abiotic Stress Signaling

The activation of innate immune signaling in plants requires numerous preformed and inducible mechanisms to resist pathogen infection. Of these mechanisms, the regulation and organization of the eukaryotic actin cytoskeleton has emerged as a key platform required for a cell’s response to both abiotic and biotic stress activation. Actin, together with the more than 75 actin-binding proteins identified in plants, regulates key signaling processes, including those required for stomatal movement and immunity. The current favored model for the regulation of actin dynamics posits that actin filaments are constantly rearranged via polymerization, severing, and depolymerization. Research in my laboratory has undertaken a comprehensive and quantitative evaluation of immunity and general stress activation as a function of cytoskeletal organization. While actin is well known for its roles in defining cell shape and powering movement of organelles and macromolecules, its role as a surveillance and signaling platform during stress signaling is less defined. Recent data using plant stomatal guard cells as amenable and biologically relevant cell type will be described. Using this model, we have begun to define the relationships that link basic physiological processes (e.g., hormone signaling, PAMP perception) to the host immune response and cellular response during changes in the environment.
Leveraging Evolutionary Adaptations to Improve Crop Resilience

There is great potential to improve crop species through the identification of the genetic basis of evolutionary adaptations within those species. My research is focused on understanding the genetic basis of adaptive trait evolution in the bioenergy crop switchgrass and in common bean, a critical food staple in Africa and Latin America. For switchgrass, I am focused on understanding the genetic basis of adaptive divergence between southern lowland and northern upland ecotypes. There are large adaptive differences in heat, cold, and drought tolerance, pathogen resistance, and biomass yield between these two ecotypes. To identify adaptive loci (QTLs) responsible divergence between switchgrass ecotypes, we planted an upland x lowland F2 mapping population at 10 locations distributed over 17 degrees of latitude. Through this experiment, we have identified important genotype x environment interactions for disease resistance, flowering time, and biomass. My research on common bean is focused on identifying the genetic and physiological basis of natural variation in heat tolerance among varieties. To accomplish this goal, we are integrating physiology and gene expression studies as well as conducting genome-wide association mapping (GWAS) of heat tolerance. Together these research endeavors illustrate the great potential for studies of evolutionary adaptation to improve crop species.

Considering the forecasted world demographic growth and the global changes in climate, it is becoming a major challenge for society to provide sufficient amounts of food. Food crops are raised for human consumption and provide grains, fruit and vegetables, which are essential for life. As for other crops, production of fruit and vegetables is determined by interactions between genetic and environmental factors (GxE). While we are entering a period of increasingly rapid climate change, the overall objective of research in plant physiology is to design new strategies to maintain high yields of fruits produced in harsh temperature conditions. Fruit yield is a complex trait depending on the successful completion of different steps of reproductive organ development, known to be highly sensitive to environmental factors. The core of the project deals with mining and phenotyping a vast range of genetic resources to identify cultivars/genotypes displaying yield stability and to uncover locigenes controlling flower initiation, pollen fertility and fruit set. Moreover, since high yield and elevated temperatures can be detrimental to quality traits, TomGEM will also tackle the fruit quality issue. TomGEM gathers expert academic researchers and private actors committed to implement a multi-actor approach based on demand driven innovation. Tomato producers and breeders are strongly involved from design to implementation of the project and until the dissemination of results. TomGEM will provide new targets and novel strategies to foster the breeding of new tomato cultivars with improved yield under suboptimal temperature conditions. TomGEM will translate scientific insights into practical strategies for better handling of interactions between genotype, environment and management to offer holistic solutions to the challenge of increasing food quality and productivity. The innovative aspect of the TomGEM project is to implement trans-disciplinary approaches to investigate the impact of high ambient temperatures on tomato fruit production. The ultimate goal of the TomGEM H2020 European project will be to design plant breeding (Genetic) and cultivation (Management) strategies to maintain high yield under high ambient temperatures (Environment).
Functional Analysis of ICE1 Interacting Proteins for Cold Tolerance

ICE1, a transcription factor, plays an important role in cold signaling and cold response in plants. To investigate more detail function of ICE1, we screened interacting proteins of ICE1 by Y2H (yeast 2-hybrid assay). Y2H and BiFC (bimolecular fluorescence complementation) assay revealed that MYC-type transcription factors and CML (calmodulin-like protein) have been identified as the ICE1 interactors, whose interaction occurred in nucleus. MYC-type transcription factors were identified as negative regulators for cold tolerance. The \textit{myc} mutants were tolerant to freezing temperatures. \textit{CBF} and other cold-responsive genes were up-regulated in the \textit{myc} mutants. The interactions of the MYC proteins with the MYC-recognition sites in the \textit{CBF3} promoter were detected by ChIP assay. These results demonstrate that MYCs interact with ICE1 and with the \textit{CBF3} promoter to negatively regulate cold-responsive genes and cold tolerance. CML was one of the ICE1 interactors, too. \textit{In vitro} pull down assay demonstrated that interaction between CML and ICE1 was dependent on Ca$^{2+}$ concentration. And the interaction was enhanced by cold treatment \textit{in vivo}. CML-overexpressing plants exhibited cold tolerance compared to wild-type plants. These result suggested that \textit{CML} plays an important role in regulation of cold signaling and tolerance through interaction of ICE1.
Biological and environmental stresses have been increasing gradually by global warming in the world. Improvement of such stress tolerance is becoming more important issue in breeding program of rice. Elucidation of the association between nucleotide and phenotypic changes is a big challenge in molecular genetics and breeding of rice that has to be addressed inevitably. Toward this goal, we have been involved in the genetic and molecular dissection of traits with agronomical and economical values, such as heading date, blast resistance and root architecture, etc. These findings allowed us to developed new cultivars and lines with desirable allele at the quantitative trait loci (QTL) with major effect. A QTL-mediated resistance contributes to durable resistance to rice blast, a devastating disease caused by the fungal pathogen *Magnaporthe oryzae*. We successfully identified the genes of diverse biological functions for this resistance. Determination of precise gene location in chromosome of the blast resistance QTL, *pi21*, allowed us to overcome linkage drag, co-introduction of undesirable agricultural traits from the donors. Furthermore, we demonstrated that combining multiple genes (QTLs) in genetic backgrounds of elite cultivars by MAS is an effective strategy to further enhance QTL-mediated resistance. Several QTLs for root length and root growth angle were identified by QTL analyses. We isolated quantitative trait locus **DEEPER ROOTING 1 (DRO1)**, which controls root growth angle, in rice. It was clarified that *DRO1* is involved in cell elongation and that predominantly influences root growth angle, but shows no marked differences in other root and shoot traits. Modulation of root system architecture using these QTL alleles will enhance improvement of drought avoidance and other traits, such as nutrition uptake and lodging resistance.
Haploid Induction and Genome Elimination Mediated by Centromeric Histone 3

Genome elimination occurs in certain plant hybrids when one parental chromosome set missegregates and is lost. Using Arabidopsis, Ravi and Chan (Nature, 2010) discovered that alteration of centromeric histone 3 (CENH3, a.k.a CENP-A) induced genome elimination. We have found that modified, mutant or diverged CENH3 determine an altered epigenetic environment in the centromere. Upon hybridization to the wild-type, kinetochores fail to reassemble on centromeres specified by variant CENH3. In addition to enabling simple production of haploids, this phenomenon provides a dramatic case of genome instability. In the early embryo, missegregated chromosomes are partitioned in micronuclei and undergo endonucleolytic degradation and elimination. Rescue dependent on non-homologous end joining results in chromosome types similar to those described for human chromothripsis. Our results highlight the role of CENH3 in centromere function, genome stability, and interspecific incompatibility. At the same time they provide a genetically malleable model system.
Development of Tomato Bioresources in Japan based on cv. “Micro-Tom” as model tomato cultivar.

Tomato (*Solanum lycopersicum* L.) is one of the most important crops in terms of production and economic value. And tomato is an excellent model plant for studies of fleshy fruits and experimental genomic studies of the *Solanaceae* family including potato, eggplant, pepper, tobacco, petunia and others. In future, bioresource collection and preservation will also become increasingly important from the viewpoint of Nagoya protocol and convention on biological diversity. Thus, for facilitation of breeding and functional genomics research of tomato, we have launched on the National BioResource Project (NBRP)-tomato in Japan (http://tomato.nbrp.jp/) since 2007. The major purpose of the NBRP-tomato is collection, preservation and provision of tomato bioresources, such as major experimental lines, wild tomato species, introgression lines, T-DNA tag line, mutant lines and full-length cDNA collections based on ‘Micro-Tom’ (TOMJPF00001), which has several advantages as a model plant including small plant size and a short life cycle. We have preserved >16,000 mutagenized M3 populations which were generated by EMS treatment or gamma-ray irradiation so far. We have isolated over 2,500 individual mutant lines with visible phenotype from the mutant population, and these individual mutant lines can available through the database ‘TOMATOMA’ (http://tomatoma.nbrp.jp/). On the other hand, as DNA resources, the sequence information of Micro-Tom full-length cDNA and EST are available from database ‘KaFTom’ (http://www.pgb.kazusa.or.jp/kaftom/) and EST database ‘MiBASE’ (http://www.pgb.kazusa.or.jp/mibase/), respectively. A reference genome sequence of Micro-Tom is also available through ‘TOMATOMICS’ (http://bioinf.mind.meiji.ac.jp/tomatomics/). Our comprehensive tomato resources will help to facilitate breeding and functional genomics research of tomato.
Current Development of GM Oncidium Orchid in Taiwan: From Basic Research to Commercialization

Oncidium Gower Ramsey ‘Honey Angel’ orchid is the major exporting cut flower in Taiwan. In the past decades, although the hobby breeders and plant scientists have paid much efforts to breed new varieties with various floral pigments, the object is still far away. Owing to the pollen sterility, traditional breeding by using artificial pollen hybridization is unavailable. Therefore, a modern molecular breeding of genetic engineering is the best effective strategy to generate new Oncidium varieties. By using RNA interference technology, mRNA transcripts of phytoene synthase gene were specifically blocked down in floral tissues. The carotenoid contents of violaxanthine, 9-cis-violaxanthin and neoxanthin were predominantly decreased. It caused the disappearance of yellow hue and resulted in a new variety with white color florets.

GMO is well regulated by government in the worldwide. Although the GM Oncidium orchid is well adopted by orchid farmers, the evaluation of environmental safety is strictly performed following guideline in Taiwan. The outcome from one-year field trial revealed that stable genetic inheritance, no gene flow, no allelopathic effects, no horizontal gene transfer for the GM Oncidium orchid plant. Two rounds panel review on the environmental safety evaluation has finished during the past two years. A request for proof of the pollen sterility is raised by the committee comment of the second-round review. The evidence of meiotic abnormality in micosporogenesis of pollen cells, such as chromosome laggard, chromosome bridge, etc. is proposed to the committee. The optimistic outcome is anticipated for the GM Oncidium item in the near future.
An integrated organic livestock-plant system was initiated by the Department of Livestock Development (DLD) in Thailand to assist animal resources more efficiently, and diversify food production. Due to consumers are increasingly seeking environmentally safe, chemical residue free health foods, along with product traceability and a high standard of animal welfare. Therefore the organic production is not only a challenge for producers in Thailand but also supports ecosystems and has an ability to increase resilience of rural communities to external changes. One way to increasing the uptake of organic agriculture was to encourage a shift to integrated livestock-plant production systems. This is required changes in farmer’s attitudes, trust in organic management system and knowledge management techniques to assist farmers produce high quality, healthy food protein and increase the market opportunities.
Improving Broiler Supply Chain Traceability in Indonesia

In a normal year, Indonesian farmers produce approximately 1.285 million tons of poultry meat, representing 62 percent of total domestic meat production. In Indonesia, poultry is one of the best protein choices and is the fastest growing market. The poultry consumption per capita has been increasing since 1994 and will continue to increase until 2023. Therefore, it is very crucial to improve supply chain traceability in Indonesia to enhance food transparency and safety as the main requirements for all food stakeholders, especially consumers. This paper discusses the development and implementation issues of IT-based traceability system for broiler supply chain from broiler farmers to retailers in Indonesia. Some of tools necessary for supporting supply chain traceability, such as a DSS for selecting suitable geographical locations of broiler houses and a KMS for assisting broiler farmers to optimally utilize broiler closed-house technology for broiler production, are also presented.

**Keywords:** broiler production, food transparency and safety, spatial-based DSS, traceability system.
Azmi Yahya, PhD. P.Eng 
Professor
(former Dean of the Faculty of Engineering at University Putra Malaysia
Department of Biological and Agricultural Engineering, Faculty of
Universiti Putra Malaysia, 43400 Serdang, Selangor D.E., Malaysia
E-mail: azmiy@upm.edu.my
Specialty: Agricultural Engineering,

Issues and Challenges in Rice Production for Food Security in Malaysia

Rice is the staple food for the populace and a source of income to the majority of the rural dwellers in Malaysia. Currently, rice is grown on 673,745 ha of land with an annual production of 2.55 million tons and an average yield of 3.8 tons/hectare. With the current country’s current population of 28,401,000 and per capita rice consumption of 110 kg/year, for the country to achieve 100% self-sufficiency from the present 73% sufficiency, rice production must be at 3.22 million tons and the average yield has to be 4.8 tons/hectare. Furthermore, the local rice production is expensive as compare to what obtains in some neighbouring countries. This paper examines the various issues and challenges related to rice production and discusses the efforts undertaken by the government for country’s rice self-sufficiency. The use of the Data Development Analysis (DEA) Methodology in optimizing the energy used in rice cultivation with the ultimate purpose of reducing its total production cost in one selected study area is discussed.
Can We Feed the World in 2050?

Science, Research and Technologies for Global Food Security

The term “Food Security” was defined by the Food and Agriculture Organization of the United Nations (FAO) in 1996 as ensuring that people have access to 1) sufficient, 2) safe and 3) nutritious food; and achieving food security for all is the organization’s core mandate. A FAO study shows that approximately 793 million people suffer from chronic hunger worldwide, and an estimated 161 million people under the age of five are chronically malnourished. There is a prospect of a drastic global population growth; the current world population of 7.6 billion is expected to reach 9.8 billion in 2050. Some of the world’s highest rates of population growth are predicted to occur in areas that are highly dependent on the agriculture sector which also have high levels of food insecurity. Growth in the agriculture sector is one of the most effective means of reducing poverty and achieving food security. While basic and conventional practices in smallholders need to be focused for this challenging global goal, FAO also recognizes that some newly developed tools utilizing advanced science, research and technology can be useful in managing such food security problems. The lecture discusses these agricultural tools and biotechnologies, as well as various initiatives and activities at the FAO to support its Members in their efforts to ensure people have regular access to enough, safe and high-quality food. The key roles of research and development in the academia sector will be of a particular highlight in order to promote a multi-sectoral and collaborative approach in fighting against the world hunger.