

5TH PLANT GENOMICS & GENE EDITING CONGRESS: ASIA

BANGKOK, THAILAND

— 26-27 March 2018 —



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#PlantGenomicsGE

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Welcome to Global Engage's **5th Global Engage Plant Genomics and Gene Editing Asia Congress 2018**. This congress aims to look into the latest scientific findings in plant genomics and technological advancements in gene editing across various crops in Asia such as NGS platforms and omics to establish crop traits, epigenetics, phenotyping and plant microbial and microbiome. The recent years had shown soaring global demand for crops exposing the limitations of traditional farming. Plant breeding productivity has improved dramatically to serve the consumption of a larger number of people with better understanding of plant genomics.

Presentations concentrate on regional model crops in Asia such as rice, wheat, maize, barley, soybean, canola/ rapeseed, palm oil, cocoa, rubber trees and many more. Plant research and its associated technologies have improved drastically over the recent years as a result of revolutionary breakthroughs such as new gene editing technology and the reduction in the cost of sequencing. Many plants have now been successfully sequenced and a wide range of biological data sets are made available. As a result, plant scientists are now making use of state of the art technology platforms to help explain biological principals, advance research and therefore enable benefits such as crop improvement and breeding techniques.

Global Engage is pleased to announce that the next edition will be taking place on the 26th and 27th of March in Bangkok. This event is part of our highly respected Plant Genomics Series, which includes a European meeting each May and US meeting each September.

Should you be either an expert already using gene editing, NGS, or other genomic technologies for plant analysis with a desire to extend your knowledge, or a researcher keen to invest in sequencing / omic technology and looking to learn which platform/technology best suits your requirements - the conference will provide an interactive networking forum to answer your queries through a vibrant exhibition room full of technology providers showcasing their technologies and other solutions and expert led case study presentations through four separate tracks.

EXPERT SPEAKERS Include:



JOHN MANNERS

Director, CSIRO Agriculture and Food, Australia



MICHAEL JONES

Professor of Agricultural, Biotechnology,
Murdoch University, Australia



DAVE BERGER

Professor, Forestry and Agricultural
Biotechnology Institute (FABI), University of
Pretoria, South Africa



PRAKASH KUMAR

Professor - Department of Biological
Science, National University of Singapore,
Singapore



SEAN MAYES

Associate Professor in Crop Genetics,
Plant and Crop Sciences, University of
Nottingham, UK, Biotechnology and Crop
Genetic Lead, Crops for the Future, Malaysia



M.L. CHYE

Wilson and Amelia Wong Professor in Plant
Biotechnology, The University of Hong
Kong, Hong Kong

DAY 1 TRACK 1 – PLANT ENGINEERING TECHNOLOGIES:

- NGS platforms and future uses
- Genome editing – Application of TALENs and CRISPRs in plants
- Phenomic and high-throughput phenotyping technologies
- Updates on gene editing technologies
- Genotyping by sequencing and genome / DNA assembly
- High resolution scanning
- SNP discovery, QTL mapping, Alternative splicing & Marker-assisted selection

DAY 1 TRACK 2 – PLANT GENOMIC CASE STUDIES

- Plant microbiome studies
- Plant-pathogen interactions
- Plant metabolism / Pathway manipulation
- Metabolic engineering
- Molecular marker development / Marker assisted selection
- Plant breeding – Novel breeding techniques, hybridization

DAY 2 TRACK 1 – TROPICAL CROPS CASE STUDIES

- Genome Editing
- Epigenetics
- DNA methylation
- Trait improvement
- Gene silencing, Gene expression
- RNA, miRNA and ncRNA analysis
- Plant resistance

DAY 2 TRACK 2 – BIOINFORMATICS AND ITS APPLICATION IN PLANT BIOTECHNOLOGY

- Gene network studies
- NGS data analysis
- Application for bioinformatics software for DNA / RNA analysis
- Sequencing pipelines and assembly
- Data mining techniques
- Genome-wide association studies
- Bioinformatic tools and databases

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CONFIRMED SPEAKERS



JOHN MANNERS
Director, CSIRO Agriculture and Food, Australia



PRAKASH KUMAR
Professor, Department of Biological Science National University of Singapore, Singapore



SEAN MAYES
Associate Professor in Crop Genetics Plant and Crop Sciences, University of Nottingham, UK, Biotechnology and Crop Genetic Lead, Crops for the Future, Malaysia



CHAN PEK LAN
Group Leader Molecular Genetics Malaysian Palm Oil Board, Malaysia



EUNYOUNG CHAE
Assistant Professor, National University of Singapore, Singapore



BARRY POGSON
Leader, Pogson Lab, Australia National University, Australia



AMITABH MOHANTY
Senior Research Manager, DuPont Pioneer, India



HILA BEN HAMO
Senior Sales Manager, APAC Region, NRGene, Israel



TEH CHEE KENG
Manager, Molecular Breeding and Bioinformatics, Biotechnology & Breeding Department, Sime Darby Plantation R&D Centre, Malaysia



ENRIQUE CASTAÑO
Professor & Principle Investigator, CICY, Mexico



DAVE BERGER
Professor, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, South Africa



M.L. CHYE
Wilson and Amelia Wong Professor in Plant Biotechnology, The University of Hong Kong, Hong Kong



CHIEW FOAN CHIN
Associate Professor, University of Nottingham, Malaysia



APARNA DAS-PADALKAR
Asia Africa Discovery Lead & Plant Health System Lead - Row Crops, Monsanto, Thailand



ZHANG BAOHONG
Professor, East Carolina University, USA



RAJ KUMAR JOSHI
Assistant Professor & Group Leader (Plant Functional Genomics), Siksha O Anusandhan University, India



LONG-XI YU
Research Plant Geneticist USDA-ARS/Washington State University, USA



KULDANA PATHOMPITAKNUKUL
Researcher, Laboratory of Plant Immunity, Graduate School of Biological Science, Nara Institute of Science and Technology, Japan



FENG GUO ZHONG
Principle Investigator, China National Rice Research Institute, China



SUHAILA SULAIMAN
Senior Researcher - Bioinformatics, Felda Global Ventures Research and Development, Malaysia



JEFF WRIGHT
Director, Araya Bumi Indonesia (subsidiary of Djarum)



K. K. SABU
Senior Scientist, Jawaharlal Nehru Tropical Botanic Garden and Research Institute, India



WILLIAM JOHN FOLEY
Professor, The Australia National University, Australia



SANG-TAE KIM
Research Fellow, Center for Genome Engineering, Institute for Basic Science, South Korea



PAO-YANG CHEN
Assistant Professor, Institute of Plant and Microbial Biology, Academia Sinica, Taiwan



DARUSH STRUSS
Group Biotechnology Head, East-Seed West, Thailand



VINAY BHARDWAJ
Senior General Manager (R&D) Reliance Industries Limited, India



ROSLINA BINTI MOHD SHAH
Research Officer, Malaysian Cocoa Board, Malaysia



LIN YANN-RONG
Professor & Chair, Department of Agronomy, National Taiwan University, Taiwan



MIO TONOUCHI
Director of Marketing, PacBio APAC, PacBio, Japan



ZHANG BAOHONG
(Chair)
Professor, East Carolina University, USA



CHIEW FOAN CHIN
(Chair)
Associate Professor, University of Nottingham, Malaysia

08:00-08:50

Registration & Refreshments

PLANT GENOMICS & GENE EDITING CONGRESS

08:50-09:00

Global Engage Welcome Address and Track Chair's Opening Remarks:
Zhang Baohong Professor, East Carolina University, USA



KEYNOTE ADDRESS:
JOHN MANNERS

Director, CSIRO Agriculture and Food, Australia

Taking Plant Genomics Innovations to Market

The food and agribusiness sector is buoyant. Demand is growing with ongoing population expansion and rapidly growing wealth in the Asian region that is creating new markets for diverse, high quality, healthy and nutritious food products. There are challenges such as climate change, a scarcity of new arable land, reduced soil fertility and constraints on inputs such as water and fertilisers that threaten sustainable production. However there are many new technologies available to scientists and industry that can help overcome these challenges and unlock new value for the sector by bringing products to market. Plant genomics and biotechnology is being transformed by new technologies such as big genome data analytics, phenomics, robotics, gene editing and synthetic biology. However, for many publically-funded laboratories doing high quality science, generating quality papers, comes naturally but the pathway for taking that science to market seems very arduous, sometimes mysterious. Mergers and acquisitions have recently led to a reduction in number of large multinational biotechnology companies and an increase in their net size. Are these newly formed agri-tech behemoths the appropriate vehicle to deliver new technologies to market? Perhaps not and there are opportunities for more agile mid-tier, small and medium sized enterprises and start-ups to play a role, and potentially disrupt the establishment. At CSIRO we have developed a range of agri-technologies that are either commercialised or are on a commercial runway. Traditional licensing has led to new GM food products in the USA and seed establishment bioactives globally. Relationships with mid-tier companies are delivering growth stimulating bioactives for shrimp aquaculture and on a commercial runway are new biotech crops such as omega-3 canola, a new terrestrial source of essential polyunsaturated long-chain fatty acids. In addition, two CSIRO spin off companies are now marketing healthy cereals to Australian, USA and Japanese consumers. As well as outlining the technologies in our commercial pipeline I will discuss the many lessons that have been learnt in this journey of taking laboratory discoveries to consumers.

09:00-09:30



SOLUTION PROVIDER PRESENTATION:
OMID ANSARI

Ecofibre, Australia

Title TBC

09:30-10:00

SOLUTION PROVIDER PRESENTATION

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10:00-10:30

10:30-11:30

Morning Refreshments / Poster Presentations / One-to-One Meetings

PLANT ENGINEERING TECHNOLOGIES

Track Chair: Zhang Baohong Professor, East Carolina University, USA



M.L. CHYE

Wilson and Amelia Wong Professor in Plant Biotechnology, The University of Hong Kong, Hong Kong

The effect of 3-hydroxy-3-methylglutaryl-CoA synthase extends beyond the isoprenoid pathway

The mevalonate (MVA) pathway generates isoprenoids including phytosterols. Dietary phytosterols are important because they can lower blood cholesterol levels. In the MVA pathway, 3-hydroxy-3-methylglutaryl-CoA synthase (HMGS) catalyses the condensation of acetoacetyl-CoA and acetyl-CoA to form HMG-CoA. Previous studies have shown that the recombinant *Brassica juncea* HMGS1 (BjHMGS1) mutant S359A displayed 10-fold higher enzyme activity than wild-type (wt) BjHMGS1 while transgenic tobacco S359A-overexpressors (OE-S359A) accumulated sterol content, and possessed higher growth rate and seed yield than OE-wtBjHMGS1. Herein, omics methods were employed to understand the differences brought about by HMGS overexpression. Comparative transcriptomics analysis verified that the improved effect of OE-S359A resulted from an increase in downstream isoprenoid biosynthesis-, primary metabolism- and plant hormone-related gene expression. Proteomics and metabolomics data will be discussed to demonstrate that HMGS links the MVA pathway to the central metabolic pathways.

11:30-11:55

PLANT GENOMICS CASE STUDIES

Track Chair: Chiew Foan Chin Associate Professor, University of Nottingham, Malaysia



SEAN MAYES

Associate Professor in Crop Genetics, Plant and Crop Sciences, University of Nottingham, UK, Biotechnology and Crop Genetic Lead, Crops for the Future, Malaysia

Developing new crops through genomics and breeding – an example from a drought tolerant African legume, bambara groundnut

World agriculture faces significant challenges if it is to produce sufficient nutritious and safe food for the coming century. An increasing and increasingly affluent world population will put major demands on food supplies, without access to additional land or water, while climate change threatens to undermine efforts to achieve food and nutritional security. One important route to improving the resilience of agriculture is to diversify the number of crops currently grown, with rice, wheat and maize currently accounting for 60% of all calories consumed. Identifying crops which are still grown (often at low levels) and which have specific trait values beyond those of the major crops (e.g. drought tolerance) could be one approach. However, many such 'underutilised' crops also have problems across the supply chain. The revolution in genomics and genetics based particularly on Next Generation Sequencing technologies is poised to remove some of these constraints, if it even exists. These problems can range from lack of breeding, to lack of acceptable products and markets. We present recent progress in the genomics and genetics of bambara groundnut, a drought tolerant African

11:30-11:55

11:30-11:55

Continued



ZHANG BAOHONG

Professor, East Carolina University, USA

microRNA-mediated gene regulation in plant response to environmental stress

MicroRNAs (miRNAs) are an extensive class of endogenous, small RNA molecules that sit at the heart of regulating gene expression in multiple developmental and signalling pathways. Recent studies have shown that abiotic stresses induce aberrant expression of many miRNAs, thus suggesting that miRNAs may be a new target for genetically improving plant tolerance to certain stresses. These studies have also shown that miRNAs respond to environmental stresses in a miRNA-, stress-, tissue-, and genotype-dependent manner. During abiotic stress, miRNAs function by regulating target genes within the miRNA-target gene network and by controlling signalling pathways and root development. Generally speaking, stress-induced miRNAs lead to down-regulation of negative regulators of stress tolerance whereas stress-inhibited miRNAs allow the accumulation and function of positive regulators. Currently, the majority of miRNA-based studies have focused on the identification of miRNAs that are responsive to different stress conditions and analysing their expression profile changes during these treatments. This has predominately been accomplished using deep sequencing technologies and other expression analyses, such as quantitative real-time PCR. In the future, more function and expression studies will be necessary in order to elucidate the common miRNA-mediated regulatory mechanisms that underlie tolerance to different abiotic stresses. The use of artificial miRNAs, as well as overexpression and knockout/down of both miRNAs and their targets, will be the best techniques for determining the specific roles of individual miRNAs in response to environmental stresses.

11:55-12:20

11:30-11:55



EUNYOUNG CHAE

Assistant Professor, National University of Singapore, Singapore

Diversification of the Plant Immune System and its Contribution to Hybrid Performances

Individuals of a species respond differently to environmental perturbations and the genetic makeup is largely responsible for the variation in responses. Now is the most exciting time to investigate phenotypic variation in adaptive traits governed by genotype by environment (G x E) and G x G, as the advent of new sequencing tools made tremendous genomic information available in a given species [1]. Numerous genome sequencing projects revealed that genetic variability in plant immune components is exceptional, reflecting complex defence strategies that plants employ to fend off myriad pathogens. The extreme variation sometimes makes a fatal outcome. Hybrid necrosis is the best-known example of genetic incompatibility in plants in that autoimmune responses are triggered by deleterious interactions of independently evolved immune alleles [2]. My postdoctoral research exploited genetic and genomic tools available in the model plant species *Arabidopsis thaliana* to systematically investigate intraspecific hybrid necrosis [3]. The species-wide work identified several incompatibility hot spots in the genome, often in regions densely populated by NLR immune receptor genes with high variability in the populations. A particularly dangerous locus is a highly variable cluster of NLR genes, DANGEROUS MIX2 (DM2), which causes multiple, independent incompatibilities with genes that encode a range of biochemical functions, including other NLRs. Our findings suggest that deleterious interactions of immune components at the front lines of host-pathogen co-evolution limit the combinations of favorable disease resistance alleles accessible to plant genomes. This systems genetics work provides a unique platform to further investigate molecular mechanisms of immune receptor activation [4] and to dissect tradeoffs between immunity and growth in plants [5].

11:55-12:20

12:20-12:50



SOLUTION PROVIDER PRESENTATION: HILA BEN HAMO

Senior Sales Manager, APAC Region, NRGene, Israel

Title TBC



12:50-14:00

Lunch / Poster Presentations / One-to-One Meetings

PLANT ENGINEERING TECHNOLOGIES



PRAKASH KUMAR

Professor - Department of Biological Science, National University of Singapore, Singapore

RNAseq analysis reveals a molecular regulatory module of how desalination barriers are established in the roots of mangrove trees

Mangrove trees such as *Avicennia officinalis* exhibit remarkable ability to grow in saline environment by means of various adaptations. The key adaptations include salt exclusion at the roots and excess salt removal (secretion) through salt glands at the leaves. We employed RNAseq analysis to study the underlying molecular mechanisms of these two adaptations. The roots of *Avicennia* can exclude ~95% salt with the help of enhanced hydrophobic root barriers (Casparian bands and suberin lamellae). Cytochrome P450s play a key role in biosynthesis of suberin precursors. Based on an RNAseq analysis, we identified several cytochrome P450 (CYP) genes that were differentially expressed upon salt treatment in the roots of *A.officinalis*. Using an *Arabidopsis* mutant, *atcyp86b1* we characterized the function of CYP86B1 in regulating suberin biosynthesis. The *atcyp86b1*

14:00-14:25

PLANT GENOMICS CASE STUDIES



CHIEW FOAN CHIN

Associate Professor, University of Nottingham, Malaysia

Omic technologies for investigating the fruit ripening process of tropical mango *Mangifera indica*

Fruit ripening is a complex process coordinated at the cellular, physiological and biochemical levels. For climatic fruits, ripening is defined by the sudden rise in respiration of the fruit known as respiratory burst. Mango (*Mangifera indica*) has a well-defined respiratory burst, which can be as high as up to 6 fold. Much preparations and energy are channelled in the ripening process in order to produce an attractive and palatable fruit for seed dispersal. Once the peak of respiration has reached, the fruit will enter into fruit senescence phase whereby the fruit tissue will start to disintegrate. Therefore, it is important to understand the mechanisms of fruit ripening in order to prolong the shelf life of fruits so that postharvest losses can be minimised. In this study, we used two-dimensional gel electrophoresis (2DE) proteomic technique to separate the proteins extracted from the fruit mesocarp of the three ripening stages of tropical mango,

14:00-14:25

14:00-14:25

mutant seedlings showed salt sensitivity with reduction in root elongation. When treated with salt, their roots exhibited reduced suberin lamellae and Casparian bands, indicating the involvement of CYP86B1 enzyme in suberin biosynthesis. Further, we identified specific WRKY transcription factors as the upstream regulators of CYP genes. These findings reveal how hydrophobic barrier formation is controlled to confer salt tolerance in plants. Further, using a combined proteomic and transcriptomic approach, we identified several differentially expressed ion transporters in the roots. Functional studies of selected proteins are underway using heterologous systems such as yeast and Arabidopsis.



ENRIQUE CASTAÑO

Professor & Principle Investigator, CICY, Mexico

RNA in phloem involved in stress response of *Carica papaya*

Plants respond to stress conditions through different mechanism to increase their ability to survive and grow. To this end several families of transcription factor are responsible to carry out the signals required for the adaptation processes. Here show how members of the transcription super family AP2/ERF in particular the RAP2.4 from *Carica papaya* cv. Maradol are induced during stress.) Expression levels indicate that each CpRap2-type gene is differentially expressed under stress conditions as extreme temperatures. Moreover, genetic transformation of tobacco plants overexpressing CpRAP2.4a- and CpRAP2.4b-type genes, show a high level of tolerance to cold and heat stress, compared to untransformed plants. Microscopy analysis of transgenic plants showed that CpRAP2.4a- and CpRAP2.4b-type proteins were mainly localized in the nuclei of cells from leaf, root, and also onto the sieve elements. Moreover, the movement of CpRap2.4a-type RNA in tobacco grafting was analyzed indicating a particular signal required for the transport. Our results indicate that CpRAP2.4a and CpRAP2.4b RNA has a functional role in response to stress conditions as a result of exposure to extreme temperatures in papaya tree by direct translation outside the parental RNA cell.

14:25-14:50



CHAN PEK LAN

Group Leader Molecular Genetics, Malaysian Palm Oil Board, Malaysia

Oil Palm Early Nodulin 93 Protein Gene (EgENOD93): An Overlap Between Somatic Embryogenesis And Nodulation

In this study, oil palm cDNA microarrays were co-hybridized with cDNA probes of reference tissue and embryo forming or non-embryo forming leaf explants sampled at three time points (Day7, Day14 and Day21) across two tissue culture media treatments (T527 and T694). Analysis of the normalized datasets resulted in the identification of 77, 115 and 127 significant differentially expressed genes at Day7, Day14 and Day21, respectively. One of the genes coding for an early nodulin 93 protein (ENOD93), which was highly expressed at Day7, Day14 and Day21 in leaf explants from media T527. The expression of this gene was also up-regulated in the callus obtained from the same media. The full-length sequence of EgENOD93 was isolated. Phylogenetic analysis revealed that the EgENOD93 was closely related to ENOD93 of *Phoenix dactylifera* and *Potamogeton distinctus*. Furthermore, cis-acting elements such as endosperm expression, abscisic acid responsiveness, methyl jasmonate responsiveness, defense and stress responsiveness were identified in the upstream region of the EgENOD93 promoter. In situ RNA hybridization studies confirmed the localization of

14:50-15:15

14:00-14:25

Mangifera indica cv. Chokanan, namely unripe, medium ripe and ripe. Proteins were extracted in triplicate from each ripening stage of the fruits using Phenol method. The extracted proteins were separated based on charge and mass. A total of 22 differential protein spots were obtained. Out of these, 14 protein spots with significant ($p < 0.05$) fold change of at least 1.4 were excised and analysed using MALDI ToF-ToF mass spectrometer. The peptide sequences were identified through the UniProtKB/Swiss-Prot database using the Mascot search engine. A total of 9 proteins were identified, with 2 and 4 proteins having the same identities namely desiccation-related protein PCC13-62 and 3-ketoacyl-CoA thiolase B respectively. The peptide sequences were subsequently compared to the NCBI *Mangifera indica* customised database. The peptides of all 14 protein spots were identified. In particular, 3-ketoacyl-CoA thiolase B was found to have 100% identity with high significant (E value = 4×10^{-66}). The identified proteins were found to be associated with metabolic processes, photosynthesis, respiratory chain and glycolysis indicating their roles in providing high energy that enable the respiratory burst to occur in the fruit ripening process of tropical mango. In addition, the differential gene expression between the ripe and unripe Mango samples were analysed using RNAseq. The results in relation to the proteomic analysis will be discussed.

14:25-14:50



LONG-XI YU

Research Plant Geneticist, USDA-ARS/ Washington State University, USA

Application of genomics tools for enhancing resistance to biotic and abiotic stresses in autotetraploid alfalfa (*Medicago sativa* L.)

Quantitative traits such as biotic and abiotic stress resistance are most likely under the control of multiple genes and interact with environmental factors. Identification of resistance loci that contribute to variation in such complex traits, is a primary challenge in plant breeding and population genetics. In the present study, we used an integrated framework that merges a QTL mapping approach called "genome-wide association (GWA)" with high-throughput genome sequencing methodology called "genotyping by sequencing (GBS)" to map disease and abiotic stress resistance loci in alfalfa. This framework provides a statistical basis for analyzing marker-trait association using linkage disequilibrium. We have identified a group of SNP markers and candidate genes associated with *Verticillium* wilt resistance and drought and salt tolerance. Validation of the markers is in progress. Once validated, these SNP markers can be used for marker-assisted selection.

14:50-15:15



SUHAILA SULAIMAN

Senior Researcher - Bioinformatics Felda Global Ventures Research and Development, Malaysia

Muti-omics: A 'teamwork' towards the improvement of planting materials

Current scenario of rapid world population growth creates a great demand to maintain the food supply. One of the major challenges for agriculture researchers is to produce high quality product to feed people, yet manage the agriculture activities towards its sustainability. Thus, an important element is to keep producing better planting materials to drive sustainable productivity and development in agriculture. The advancement of next generation sequencing (NGS) technology has enable us to explore the genetic codes of plants to discover the secret recipe underlying the desirable traits in our plant of interest. The fact that bridging the phenotype and genotype in plants is not an easy task leads us to the implementation of multi-omics studies in the agri-genomics research. It becomes common to use bioinformatics data analysis approaches as an initiative to manage the wealth of biological data before the validation and laboratory experiments taking part. While a genome data acts as a backbone of a study in a plant, transcriptome data comes to lead to the understanding of biological expression in it. Apart from that, interactomics and plant effectoromics studies are those approaches taken to unravel the potential roles of plant

14:50-15:15

the EgENOD93 transcript in the embryogenic cells. Functional characterization of the putative orthologous *Medicago truncatula* gene, executed via the RNAi approach, provided additional evidence that ENOD93 is essential for somatic embryogenesis. Interference in the expression of *M. truncatula* ENOD93 resulted in the formation of much lower numbers of somatic embryos as compared to the control. This study enhances the understanding on the role of this gene in somatic embryogenesis and nodulation.

15:15-15:45

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14:50-15:15

components. This includes genes that contribute to traits as yield improvement, drought tolerant, diseases resistant, height and so on. Moreover, the comparative -omics studies also an important step in the discovery of biological marker in improving planting materials. Apparently, these bioinformatics approaches are completing each other to solve the biological puzzle in agri-biotechnology. Thus, the improvement of planting materials would not be a success without this 'multi-omics teamwork'

15:15-15:45

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15:45-16:35

Afternoon Break / Poster Presentations / One-to-One Meetings

16:35-17:10



AMITABH MOHANTY

Senior Research Manager, DuPont Pioneer, India
CRISPR-Cas enabled advance plant breeding
 CRISPR- Cas is one of the most important new technologies for advanced plant breeding, enabling us to help feed a growing global

population. The superior properties of CRISPR-Cas allows our scientists to develop innovative and sustainable seed products for growers similar to those realized through marker-assisted plant breeding, but with even greater efficiency, accuracy and quality. Pioneer is leading the application of this tool to develop customized agriculture solutions that help solve the real challenges farmers around the world face in growing healthy and productive crops. This presentation will share how Pioneer scientists have applied CRISPR-Cas as an advanced breeding tool to efficiently develop Waxy corn hybrids directly in elite genetic backgrounds. Waxy corn produces a high amylopectin starch content, which is milled for a number of everyday consumer food and non-food uses. This next generation of elite waxy corn hybrids is expected to be available to U.S. growers within five years, pending field trials and applicable regulatory reviews. Other potential product targets of this promising technology will also be discussed.

16:35-17:10



PAO-YANG CHEN

Assistant Professor, Institute of Plant and Microbial Biology, Academia Sinica, Taiwan
OTU5 Maintains DNA Methylation Patterns and is Critical for Interpreting Phosphate Nutrition Signals

Phosphate (Pi) starvation induces a suite of adaptive responses aimed at recalibrating cellular Pi homeostasis. Plants harboring a mutation in OVARIAN TUMOR DOMAIN-CONTAINING DEUBIQUITILATING ENZYME5 (OTU5) showed altered DNA methylation of root hair-related genes and altered Pi-responsive root traits. Unlike the wild type, homozygous *otu5* mutants did not respond to Pi starvation by increased lateral root formation and increased root hair length, but formed very short root hairs when grown on low Pi media. Under Pi-replete conditions, *otu5* plants developed more root hairs than the wild type due to attenuated primary root growth, a phenotype which resembled that of Pi-deficient plants. Growth of plants on low Pi media altered both H3K4 and H3K27 trimethylation levels at the transcriptional start site of a subset of genes encoding key players in Pi homeostasis, which was correlated with mRNA abundance changes of these genes. Pi starvation had a minor impact on DNA methylation. Differentially methylated regions were enriched in transposable elements, suggesting that DNA methylation associated with low Pi supply is required for maintaining genome integrity. It is concluded that DNA methylation and histone methylation constitute critical, interdependent regulatory components which orchestrate the activity of a subset of Pi-responsive genes.

17:10-17:25



JEFF WRIGHT

Director, Araya Bumi, Indonesia
Genetic Improvement of Eucalyptus pellita F. Muell: Important Pulp and Timber Species for the Humid Tropics

In the last twenty years, *Eucalyptus pellita* F. Muell has become a major plantation species for pulp and timber in the humid tropics. The species is native to northern Queensland Australia, Papua New Guinea and Papua Indonesia. Exceptional growth rate, wood properties, disease resistance and other factors are consistent under many forest plantation management systems. Ease of propagation from rooted cuttings, flowering sometimes as early as two years of age and an ability to hybridize with other commercial eucalypts allow rapid genetic gain in tree improvement programs and support forest plantation investments. This presentation will focus on genetic improvement of *E. pellita* under contrasting sites in Sabah Malaysia and East Kalimantan Indonesia.

17:10-17:25



DARUSH STRUSS

Group Biotechnology Manager, East-Seed West, Thailand, Adjunct Professor, Maejo University, Thailand
Developing sequence based genomic Markers for desired traits in vegetables breeding

17:25-17:50



VINAY BHARDWAJ

Senior General Manager (R&D) Reliance Industries Limited, India
Integration of genomic selection and functional breeding for pepper improvement

Novel breeding approaches are required to aid accelerate the rate of genetic gain to encounter the growing demand of food and spice crops in the face of less favorable and increasingly unpredictable environments. Genomic selection using whole-genome markers for breeding value predictions is an approach that can accelerate genetic gain through decreasing the breeding cycle time and increasing the selection intensity through larger populations. The integration of Eco physiological modeling and genomic prediction has the potential to enable more robust selection for a range of environments. Developing such approaches and making physiological measurements across the breadth of breeding programs will necessitate innovation and deployment of high-throughput phenotyping systems that can capture the temporal and spatial resolution needed to screen large sets of germplasm and build model parameters to integrate with genomic prediction.

17:50

Networking Drinks Reception and End of Day 1

08:30-08:55

Refreshments

PLANT GENOMICS & GENE EDITING CONGRESS

08:55-09:00

Track Chair's Opening Remarks: **Zhang Baohong** Professor, East Carolina University, USA

09:00-09:40



DAVE BERGER

Professor, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, South Africa

Systems biology of maize responses to the foliar fungal pathogen *Cercospora Zeina*

Maize is a staple food and animal feed source in sub-Saharan Africa, Asia and the Americas. Gray leaf spot disease caused by *Cercospora zeina* is an increasing threat in wetter regions of maize production in Africa. Maize germplasm exhibits quantitative resistance to the fungus, however the underlying processes are unclear. Microarray-based transcriptome analysis of a sub-tropical maize population grown in the field in South Africa revealed co-expression modules that correlated with resistance and susceptibility. A temperate maize line that is susceptible to GLS was grown within the same hotspot region of GLS disease in South Africa. Intriguingly, the RNAseq based transcriptome of the temperate maize line showed significant overlap with a susceptibility co-expression module from the sub-tropical maize germplasm. A model that infers possible manipulation of the host by the pathogen in this compatible interaction will be presented.

09:40-10:10

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10:10-10:50



WILLIAM JOHN FOLEY

Professor, The Australian National University, Australia

From Medicines to Jet Fuels: Genomic Improvement of Terpene Production in Eucalyptus

Trees in the genus *Eucalyptus* (Myrtaceae), the most widely planted hardwood in the world, are known as a source of terpene-dominated leaf oils that have well-known medicinal properties. In addition these terpenes have recently been identified as a suitable source for a one-step conversion to new-generation tactical jet fuels. In this talk, we will describe the genetic architecture of terpene production in *Eucalyptus* and the closely related genus *Melaleuca* by bringing together data from the *Eucalyptus* genome project together with studies using a Genome Wide Association approach in *Eucalyptus polybractea* and then a predictive Genomic Selection analysis to support a rapid enhancement of yield. Together with existing agronomic practices, this will underpin a substantial expansion of *Eucalyptus* plantations in low-rainfall regions of Australia.

10:50-11:30

Morning Refreshments / Poster Presentations / One-to-One Meetings

Tropical Crops Case Studies

Track Chair: **Zhang Baohong** Professor, East Carolina University, USA

11:30-11:55



APARNA DAS-PADALKAR

Asia Africa Discovery Lead & Plant Health System Lead - Row Crops, Monsanto, Thailand

Molecular breeding : Journey from Laboratory to the farmer fields

Bioinformatics and Its Application in Plant Biotechnology

Track Chair:



ROSLINA BINTI MOHD SHAH

Research Officer, Malaysian Cocoa Board, Malaysia

Transcriptome profiling of resistant and susceptible *Theobroma cacao* following artificial infection with cocoa pod borer insect (*Conopomorpha cramerella*) to study their hostpathogen interaction

Plants developed different mechanisms to reduce insect attack, including specific responses that activate different metabolic pathways which considerably alter their chemical and physical aspects. On the other hand, insects developed several strategies to overcome plant defence barriers, allowing them to feed, grow and reproduce on their host plants. The Cocoa Pod Borer (CPB), also known as Cocoa Moth, is caused by the insect *Conopomorpha cramerella*, causing vast losses in the cocoa industry during the 1890s and 1900s. CPB attacks both young and mature cocoa pods. A common symptom of infested pods is unevenness and premature ripening. The transcriptome was sequenced from *Theobroma cacao* tissues (pod husk and placenta) of resistant and susceptible clones, before and after infection. The unique characterisation of the differences observed; if any; in pod husk, placenta and other relevant tissues may be used to understand the molecular variations underlying the phenotypic and disease resistance characteristics, and relevant molecular markers identified can be used in downstream breeding research. P450 cytochrome gene, an aluminium detoxification genes, sugar transporter genes, defensin genes are among those found to be upregulated or downregulated in resistance or susceptible cultivar. The resistant cultivar also synthesises more enzymes for phytoalexins that was known to inhibit insect feeding. The cocoa defence is comprised of a set of chitinases for digesting the CPB larva's cuticle and possibly phytoalexins which may deter the borers with unpleasant flavours. The whole defence system for any threat appears to be more active in the resistant cultivar.

11:30-11:55

11:55-12:25



**SOLUTION PROVIDER
PRESENTATION:
SENIOR REPRESENTATIVE**
Novocraft
Title TBC

11:55-12:25



**SOLUTION PROVIDER
PRESENTATION:
MIO TONOUCHI**
Director of Marketing, PacBio APAC
PacBio, Japan
**SMRT Sequencing Highlights: Building
Better Genomes and Transcriptomes**



12:25-12:50



RAJ KUMAR JOSHI
Assistant Professor & Group Leader (Plant
Functional Genomics), Siksha O Anusandhan
University, India
**Engineering of CRISPR/Cas9-mediated
anthracnose resistance in chilli**

Anthraxnose, caused by *Colletotrichum* spp. is the most devastating disease of chilli (*Capsicum annuum*) in the tropical and subtropical regions of the world. Host resistance breeding is the most efficacious and safer management strategy for the chilli anthracnose problem. Transcriptome dynamics in chilli cultivars have revealed that the members of ethylene response factors act as major susceptibility source during anthracnose attack. We have utilized CRISPR/Cas9 gene editing system to introduce sequence specific mutation at the CaERF28 locus in *Capsicum annuum* to successfully engineer complete resistance to *Colletotrichum truncatum*, the most belligerent anthracnose pathogen. The results from this experiment will be presented to discuss the effectiveness of RNA guided engineered nuclease CRISPR/Ca9 system as a new approach for the generation of anthracnose resistance alleles in chilli cultivars.

12:25-12:50



TEH CHEE KENG
Manager, Molecular Breeding and Bioinformatics,
Biotechnology & Breeding Department, Sime
Darby Plantation R&D Centre, Malaysia
**The Oil Palm Breeding: The Past, Present
and the Future**

Oil palm (*Elaeis guineensis* Jacq.) is the most efficient oilseed crop in the world, producing 37% of vegetable oil from only 6% of global oilseed harvested area. In the past century, introduction of native pollinating weevils and thin-shelled tenera planting have significantly improved palm oil productivity in Southeast Asia. However, the yield stagnation occurred over 25 years at about 4-5 MT ha⁻¹ year⁻¹, mainly caused by limitations in conventional breeding, estate upkeep and seed production. Hence, the breeders looked to marker-assisted selection (MAS) to shorten the breeding cycle and improve genetic gain, but deployment was hindered by inconsistent QTL findings and low-throughput genotyping. Recent advances in DNA sequencing have shown us light at the end of the tunnel. An oil palm-based 200,000 SNP array, termed OP200K was derived from 59 breeding origins at Sime Darby Plantation R&D Centre. We conducted a genome-wide association study (GWAS) with 7,000 genotyped palms and successfully identified the major QTLs for yield components. Genomic selection (GS), a form of MAS that consolidates the whole-genome marker effect, was then carried out to unveil the full prediction ability. We found that GWAS-guided GS conferred higher prediction accuracy than the traditional method. For routine genotyping, smaller SNP panels (100-1,000 loci) were developed for GS, authenticity

12:50-14:00

Lunch / Poster Presentations / One-to-One Meetings

14:00-14:20



LIN YANN RONG
Professor & Chair, Department of Agronomy, National Taiwan University, Taiwan
QTLs Conferring Days to Curd Induction in Brassica oleracea by Using Genome Wide Association Study (GWAS)

Broccoli and cauliflower are belonged to Brassica genus and originated from temperate regions, which its curd formation is induced by low temperature. To uncover QTLs conferring days to curd induction is important for these two crops adapted and cultivated in Taiwan and also in Southeast Asia countries. A total of 192 breeding lines of cauliflower, broccoli and kale were used for phenotyping and genotyping. We identified 10,401 SNPs by using multiplexed shotgun genotyping (MSG) method. These germplasm could be clustered into 4 major groups and admixture populations were revealed by PCA and phylogenetic analyses. The days to curd induction (DCI) were ranged 27 to 85 d with an average of 51.4 d and ranged 29 to 78 d with an average of 49.5 d in 2014 and 2015 crop seasons, respectively. A total of 18 and 10 SNPs were strongly associated with DCI in these two crop seasons, and the significant SNPs distributed on chromosomes 2-9, for which largest SNP on chromosome 7 could contribute 13.5 d in 2015. Ten alleles could promote curding from 4.14 to 9.46 days. The candidate genes in the linkage block of the SNP were identified. The long-term objective of this study aims to establish a marker-assisted breeding system for breeding early curding varieties of *B. oleracea*. As the result, the functional markers and high throughput SNP genotyping platform will facilitate to promote breeding efficiency to breed broccoli and cauliflower new varieties which can be cultivated for shifting production season and for expanding cultivation areas.



KULDANAI PATHOMPITAKNUKUL

Researcher, Laboratory of Plant Immunity, Graduate School of Biological Science, Nara Institute of Science and Technology, Japan

Endophyte-mediated control of fungal pathogenesis in *Arabidopsis thaliana*

Plants are associated with diverse microbes from harmful pathogens to beneficial endophytes, which colonize the host plant with or without apparent disease symptoms, respectively. Plants are expected to have strategies to discriminate pathogens from endophytes. Plants accommodate beneficial endophytes which often provide the host plant with fitness benefits such as growth promotion, abiotic stress adaptation, and protection from pathogen infection. Many fungi in the genus *Colletotrichum* have been described as pathogens of agriculturally important plant. Here we report two *C. gloeosporioides* isolates, named CgP and CgE, which were both isolated from apparently healthy radish (*Raphanus sativus*) plants grown in natural soil. When infected with CgP, *A. thaliana* Col-0 accession show severe disease symptoms and is eventually killed. In contrast, CgE colonization occurs in roots of *A. thaliana* Col-0 without visible disease symptom. Remarkably, when co-inoculated with both fungi, CgE provides host protection against CgP pathogenesis. CgE colonization also protects the host from pathogenesis of *C. incanum*, a root-infecting pathogen. These data suggest that the co-occurrence of an endophyte, such as CgE, with pathogens serves to protect the host from pathogen disease, but also allows inapparent infection of potential pathogens. Importantly, our genetic studies reveal that host defenses dependent on ethylene and tryptophan-derived secondary metabolites are required for the host protection function of CgE. In the absence of these defense components, CgE displays a shift from the endophytic lifestyle to that of the pathogen. The mechanisms underlying plant protection by CgE will be discussed, based on comparative genomics studies between the two *C. gloeosporioides* isolates.

14:20-14:40



K. K. SABU

Senior Scientist, Jawaharlal Nehru Tropical Botanic Garden and Research Institute, India

Next-generation sequencing technologies and their applications for genetic studies in non-model plants

Recent technological advances in genomics have generated avenues to rapidly generate large-scale sequencing data from non-model plants at a reasonable cost. Cardamom (*Elettaria cardamomum* Maton) is a popular spice crop used all over the world, but with limited genomic information available. Cardamom cultivation is having good production potential but the plants are vulnerable to biotic and abiotic stress factors of which drought stress has a prominent role. To date, nothing is known about the regulatory roles of miRNAs and transcription factors in response to drought stress in cardamom. Ion Torrent sequencing was conducted and discovery of differentially expressed miRNAs under drought stress suggests that these miRNAs might have involved in various biological processes to improve plant tolerance to water stress. Several target genes for drought stress regulating miRNAs were identified which cleave the target mRNA involved in response to water deprivation. Transcription factors and regulators act either as activators or repressors of gene expression resulting in increased or decreased mRNA accumulation depending on tissue type or during environmental stress and knowledge on these can be utilized for metabolic engineering in plants.

14:40-15:00



SANG-TAE KIM

Research Fellow, Center for Genome Engineering, Institute for Basic Science, South Korea

Targeted genome editing using the programmable nuclease, CRISPR/Cas9 for crop research

Crop improvement is essential to attaining world food security and enhancing nutrition for human beings. Both conventional breeding and modern molecular breeding have contributed to increased crop production and quality. However, the time and resources for breeding practices have been limited. It takes a long time to bring a novel improved crop to the market, and the genetic sources from wild species cannot be always available for crops of our interests. CRISPR-Cas9 system is now widely used to edit a target genome in animals and plants. Cas9 protein derived from *Streptococcus pyogenes* (SpCas9) cleaves double-stranded DNA targeted by a single-guide RNA (sgRNA). Genome editing technology using programmable nuclease can overcome those limitations of time and resource by facilitating the specific editing of plant genomes although there is still a long-lasting argument about the safety of genetically modified organisms (GMOs). In this talk, I will briefly summarize the principle of genome editing tools, focusing on the CRISPR-Cas9 and base editing system and the application of these tools to plants in the service of crop engineering with future directions. Also I will address the off-target effect of genome editing in plant as I show two different approaches to survey potential off-targets 1) *in vitro* using whole genome sequencing data in soybean by 'Digenome-seq' and 2) *in vivo* using whole genome data from selected three generations in *Arabidopsis*.

15:00-15:20

15:20

End of Conference

MAKING A POSTER PRESENTATION

Poster presentation sessions will take place in breaks and alongside the other breakout sessions of the conference. Your presentation will be displayed in a dedicated area, with the other accepted posters from industry and academic presenters. We also issue a poster eBook to all attendees with your full abstract in and can share your poster as a PDF after the meeting if you desire (optional). Whether looking for funding, employment opportunities or simply wanting to share your work with a like-minded and focused group, these are an excellent way to join the heart of this congress.

In order to present a poster at the congress you need to be registered as a delegate. Please note that there is limited space available and poster space is assigned on a first come first served basis (subject to checks and successful registration). We charge an admin fee of \$50 to industry delegates to present, that goes towards the shared cost of providing the poster presentation area and display boards, guides etc. This fee is waived for those representing academic institutions and not for profit organisations.





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