



The 3rd Plant Genomics Congress Asia

UTILIZING NGS, OMIC AND GENE EDITING TECHNOLOGIES TO PROGRESS PLANT RESEARCH

Global Engage are pleased to announce as part of their Next Generation Sequencing series of events the 3rd Plant Genomics Congress Asia, which will be held on April 11-12 2016 at the Renaissance Kuala Lumpur Hotel, Malaysia. The successful event which was attended by over 170 people in 2015 is the sister meeting to the European Plant Genomics Congress which took place in London this May which had over 280 registered attendees and the North American meeting which drew 200 experts in September.

Attracting scientists working in all areas of plant research including molecular marker development, breeding, crop improvement, disease/stress resistance, bioenergy, evolution studies and gene editing techniques. The conference will examine the latest strategies, technologies and research techniques utilizing NGS, Omic technologies, phenotyping, epigenetics, bioinformatics and data analysis methods to further plant research. Presentations from 40+ international and regional experts concentrate on, but are not limited to, regional and model crops such as rice, wheat, maize, barley, sorghum, arabidopsis, soybean and palm oil in order to attract delegates from across Asia and beyond.

Plant research has transformed dramatically over the last few years as a result of the revolutionary breakthroughs and reduction in cost of sequencing. Many plants and crops have been successfully sequenced and a wide range of biological data sets made available. Plant scientists are making use of state-of-the-art sequencing platforms to help advance research and thus enable crop improvement by harnessing the greater understanding of plant genomics. This research is now being progressed even further by the ascension of gene editing technologies including CRISPR.

Should you be an expert already using NGS / Omic technologies for plant analysis with a desire to extend your knowledge or a researcher keen to invest in sequencing technology and looking to learn which platform 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, expert led case study presentations & interactive Q&A panel discussions examining topics through four separate tracks.

Confirmed Speakers Include:



Birger Lindberg Møller
Professor of Plant Biochemistry, Centre for Synthetic Biology, University of Copenhagen, Denmark



Robert Park
Professor, Department of Plant and Food Science, Judith and David Coffey Chair in Sustainable Agriculture, The University of Sydney, Australia



Mee-Len Chye
Wilson and Amelia Wong Professor in Plant Biotechnology, School of Biological Sciences, University of Hong Kong

Conference Synopsis

Day 1 Stream 1 – NGS/ Omic Technologies for Plant Research

- NGS platforms / new technologies / future uses
- Synthetic biology / genome editing / genome and pathway design / CRISPR and TALENs
- Phenomics and high throughput phenotyping technologies
 - Genotype and phenotype connections
 - Selective sweep mapping
 - Novel methods and imaging techniques
- Proteomics and mass spectrometry
- Metabolomics
 - Metabolic engineering / plant metabolism / pathway manipulation / systems biology
- Transcriptomics
- Genotyping by sequencing / genome and DNA assembly
- Sample preparation technology and techniques
- High resolution scanning
- SNP discovery, QTL mapping, alternative splicing, marker assisted selection

Day 1 Stream 2 - Plant Genomic Case Studies

- Crop / trait improvement e.g. stress resistance
- Molecular markers / marker assisted selection
- Plant breeding
 - Novel breeding techniques
 - Breeding by design
 - Hybridization
- Evolutionary genomics
- Plant / agricultural microbiome
- Pathology / plant-pathogen interactions

Day 2 Stream 1 – Bioinformatics, Data Management & Analysis

- Bioinformatics – analysis and challenges
- Analysis of microarray data
- NGS data analysis
- Application of bioinformatics software for DNA / RNA analysis
- Gene expression analysis
- Gene network studies
- Tools for genomic selection
- Sequencing pipelines and assembly
- Improving error rates
- Cloud computing and storage solutions

Day 2 Stream 2 - Part A) Biofuel Research; Part B) Plant Genomic Case Studies (Stress / Disease Resistance)

Using NGS in plant research to enhance:

- Molecular marker development / Marker assisted selection
- Crop / trait improvement
- Plant breeding
- Disease/Stress resistance
- Evolution studies
- Pathology

Part B) Biofuel Case Studies

Confirmed Speakers



Robert Park
Professor, Department of Plant and Food Science, Judith and David Coffey Chair in Sustainable Agriculture, The University of Sydney, Australia



David Jackson
Professor, Cold Spring Harbour Laboratory, USA



Peter Gresshoff
Professor, Plant Molecular Genetics, Director, Centre for Integrative Legume Research, University of Queensland, Australia



Yung-Fen Huang
Assistant Professor, Department of Agronomy, National Taiwan University, Taiwan



Meilina Ong Abdullah
Head of Breeding & Tissue Culture Unit, Advanced Biotechnology & Breeding Centre, Malaysian Palm Oil Board, Malaysia



Denis Murphy
Professor of Biotechnology, Faculty of Computing, Engineering and Science, University of South Wales



Mee-Len Chye
Wilson and Amelia Wong Professor in Plant Biotechnology, School of Biological Sciences, University of Hong Kong



Boon Lim
Associate Professor, School of Biological Sciences, University of Hong Kong, Hong Kong



Jennifer Ann Harikrishna
Director, Centre for Research in Biotechnology for Agriculture, Professor, Institute of Biological Sciences, University of Malaya, Malaysia



Matthew Hannah
Expert Scientist, Trait Research, Bayer CropScience, Belgium



Masaru Ohme-Takagi
Director/Professor, Institute of Environmental Research and Technology, Saitama University, Senior Researcher, National Institute of Advanced Industrial Science and Technology, Japan



Ian Godwin
Professor in Plant Molecular Genetics, School of Agriculture and Food Sciences, Centre for Plant Science, The University of Queensland, Australia



Paul Quick
Principal Scientist and Head of C4 Rice Project, International Rice Research Institute, Philippines



Birger Lindberg Møller
Professor of Plant Biochemistry, Centre for Synthetic Biology, University of Copenhagen, Denmark



Rofina Yasmin Binti Othman
Professor, Institute of Biological Sciences, Director, Centre for Innovation & Commercialisation, University of Malaya, Malaysia



Ya-Long Guo
Professor, State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, China



Matthew Paul
Professor, Rothamsted Research, UK



German Spangenberg
Director, AgriBio, Professor of Plant Genetics and Genomics, La Trobe University, Australia



Yuehui He
Professor, Shanghai Center for Plant Stress Biology, Chinese Academy of Sciences, China



Xu Jian
Assistant Professor, Department of Biological Science, National University of Singapore, Singapore



Motoaki Seki
Team Leader, Plant Genomic Network Research Team, RIKEN CSRS, Professor, Yokohama City University, Japan



Prasanna Bhat
Molecular Genetics and Genomics Team Lead, Monsanto, India



Xianzhong Feng
Professor, Deputy Director, Key Laboratory of Soybean Molecular Design Breeding, Chinese Academy of Sciences, China



Geo Velikkakam James
Research Scientist, Rijk Zwaan, Netherlands



Xuehua Zhong
Assistant Professor, Laboratory of Genetics, University of Wisconsin-Madison, USA



Jacqueline Batley
Associate Professor, School of Agriculture and Food Sciences, University of Queensland, Australia



Kazuki Saito
Group Director, Metabolomics Research Group, RIKEN, Japan



Kemal Kazan
Group Leader, Protection from Pathogens and Pests, CSIRO Agriculture, Honorary Professor, Queensland Alliance for Agriculture & Food Innovation, University of Queensland, Australia



Steven Scofield
Adjunct Associate Professor, University of Purdue, Research Geneticist, USDA-ARS, USA



Thomas Städler
Senior Scientist, Plant Ecological Genetics, Institute of Integrative Biology, ETH Zurich, Switzerland



Michael Jones
Professor of Agricultural Biotechnology, Director, Western Australian State Agricultural Biotechnology, Murdoch University, Australia



Mahmood-ur-Rahman Ansari
Assistant Professor, Department of Bioinformatics and Biotechnology, Government College University Faisalabad, Pakistan



Thomas Bureau
Associate Professor, Department of Biology, McGill University, Canada



Pao-Yang Chen
Assistant Research Fellow, Institute of Plant and Microbial Biology, Academia Sinica, Taiwan



Shavannor Smith
Associate Professor, Department of Plant Pathology, University of Georgia, USA



Raj Kumar Joshi
Visiting Professor, Dept. of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, Canada
Assistant Professor, Centre of Biotechnology, Siksha O Anusandhan University, Bhubaneswar, Odisha, India

2016 Sponsors



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Venue

Renaissance Kuala Lumpur Hotel
Corner of Jalan Sultan Ismail and
Jalan Ampang,
Kuala Lumpur
50450
Malaysia

A discounted group rate is available to all attendees. Details of how to book are available on registration. Space is limited and accommodation is available on a first come basis.



For more information please contact Steve Hambrook, Conference Director, Global Engage Ltd.
steve@globalengage.co.uk +44 (0) 1865 849841

Agenda: Day One – Monday 11th April 2016

08.00-08.50	Registration & Coffee	
08.50-09.00	Global Engage Welcome Address – Stream Chair's Opening Remarks -	
09.00-09.35	Keynote Address: Synthetic Biology in Plants	
	Confirmed: Birger Lindberg Møller, Professor of Plant Biochemistry, Centre for Synthetic Biology, University of Copenhagen, Denmark	
09.35-10.05	Keynote Address: Inflorescence architecture: genomics for enhanced maize yield	
	- Combining developmental genetics and genomics in maize inflorescences - Natural variation and weak alleles enhance yield traits genome engineering to study maize gene function	
	Confirmed: David Jackson, Professor, Cold Spring Harbour Laboratory, USA	
10.05-10.35	Solution Provider Presentation	
	For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk	
10.35-11.45	Morning Refreshments Poster Presentation Sessions	
	NGS, Omic and Gene Editing Technologies for Plant Research	Plant Genomic Case Studies
11.45-12.10	Manipulation of the plant isoprenoid pathway to enhance agriculture	Rice Case Study
	3-Hydroxy-3-methylglutaryl-CoA synthase (HMGS) is an enzyme in the mevalonate pathway of isoprenoid biosynthesis. - The ectopic expression of BjHMGS1 mutant (S359A) in tobacco caused increase in plant growth, pod size and seed yield. "Omic" technologies will be used to investigate the S359A transgenic lines to understand changes in metabolism.	
	Confirmed: Mee-Len Chye, Wilson and Amelia Wong Professor in Plant Biotechnology, School of Biological Sciences, University of Hong Kong	Confirmed: Paul Quick, Principal Scientist and Head of C4 Rice Project, International Rice Research Institute, Philippines
12.10-12.35	Phenotyping	Using NGS-Based Genotyping Platform for Genomic Discovery of Rice Introgression Lines
	Confirmed: Thomas Bureau, Associate Professor, Department of Biology, McGill University, Canada	Confirmed: Yung-Fen Huang, Assistant Professor, Department of Agronomy, National Taiwan University, Taiwan
12.35-13.05	Solution Provider Presentation	Solution Provider Presentation
	For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk	For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
13.05-14.05	Lunch	
14.05-14.30	RNAseq analysis and metabolic profiling of medicinal plants	Systems Biology and Molecular Breeding of Forage
	Confirmed: Kazuki Saito, Group Director, Metabolomics Research Group, RIKEN, Japan	Confirmed: German Spangenberg, Director, AgriBio, Professor of Plant Genetics and Genomics, La Trobe University, Australia
14.30-14.55	RNAseq to identify new pathway and novel factors that facilitate the interplay between auxin and ethylene signalling pathways in root elongation	Molecular genetic mechanisms for nodulation control of nodulation in legumes
		All legumes like soybean, pea and peanut, regulate the number of nitrogen fixing nodules through an internal Autoregulation of Nodulation (AON) mechanism. AON is initiated in the root's nodule primordia by synthesis of a CLE peptide (12 amino acids long) which is transported to the leaf where the LRR receptor kinase GmNARK perceives the systemic signal and induces a non-typical cytokinin release. This leaf signal results in the induction of expression of a miR172c, which down-regulates the expression of the AP2 transcription factor GmNINC1, which negatively regulates expression of the critical GmENOD40 gene; thus excessive nodulation after initial nodulation is suppressed. The process appears to be universal in all legumes.
	Confirmed: Xu Jian, Assistant Professor, Department of Biological Science, National University of Singapore, Singapore	Confirmed: Peter Gresshoff, Professor, Plant Molecular Genetics, Director, Centre for Integrative Legume Research, University of Queensland, Australia

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Agenda: Day One – Monday 11th April 2016

14.55-15.20	Novel Epigenetic, RNA and Peptide Regulation in Plant Abiotic Stress Responses Plants respond and adapt to drought, cold and high-salinity stresses in order to survive. Many stress-regulated genes have been identified by transcriptome and genetic analysis, and its function in the stress responses have been elucidated. However, we think that novel mechanisms involving RNAs, peptides and epigenetic regulation have additional functions in the regulation of plant stress responses and adaptation. In this congress, I will present our recent findings on the novel regulation mechanisms in the stress response and adaptation. Confirmed: Motoaki Seki, Team Leader, Plant Genomic Network Research Team, RIKEN CSRS, Professor, Yokohama City University, Japan	GmCYP78A72 regulates seed size in soybean - GmCYP78A72 heterologous expression in Arabidopsis resulted in big sepals, petals, carpel and seeds. - Over-expression of the GmCYP78A72 in soybean resulted in increase of pea size - This strategy can be effectively used to engineer large seed traits in soybean varieties. Confirmed: Xianzhong Feng, Professor, Deputy Director, Key Laboratory of Soybean Molecular Design Breeding, Chinese Academy of Sciences, China
15.20-15.50	Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk	Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
15.50-16.50	Afternoon Refreshments Poster Presentation Sessions	
16.50-17.15	DNA methylation and histone modification in developmental and environmental gene regulation Confirmed: Xuehua Zhong, Assistant Professor, Laboratory of Genetics, University of Wisconsin-Madison, USA	Cereal crop genomics Confirmed: Jacqueline Batley, Associate Professor, School of Agriculture and Food Sciences, University of Queensland, Australia
17.15-17.40	Impacts of High Energy Supply from Chloroplasts and Mitochondria on the Leaf Transcriptomes, Proteomes and Metabolomes - By modulating energy outputs from chloroplasts and mitochondria, we have generated fast-growth and high seed yield Arabidopsis with high ATP and sucrose contents in leaves. - Transcriptome, proteome and metabolome profiles of the high ATP transgenic line were compared with wild-type plants. - I shall illustrate the impacts of high energy supply from chloroplasts and mitochondria on plant physiology, from organellar genomes to primary and secondary metabolism. Confirmed: Boon Lim, Associate Professor, School of Biological Sciences, University of Hong Kong, Hong Kong	Maize Case Study Confirmed: Shavannor Smith, Associate Professor, Department of Plant Pathology, University of Georgia, USA
17.40-18.05	The Chimeric Repressor Gene Silencing Technology (CRES-T) is a Useful Tool for Functional Analysis of Transcription Factors and Manipulation of Plant Traits A number of transcription factors are known to act as master regulators of various phenotypes and are useful tool for the manipulation of plant traits. However, plant genes are frequently duplicated and such structural and functional redundancy often interferes with efforts to identify gene functions of plants. To overcome these difficulties, we developed a novel gene silencing system, called Chimeric REpressor Gene-Silencing Technology (CRES-T), in which a transcription factor is converted into strong repressor by fusion of the plant-specific repression domain (SRDX) and suppresses the target genes dominantly over the activity of endogenous and functionally redundant transcription factors. We present here that CRES-T system is useful tool for functional analysis of redundant plant transcription factors and the manipulation of various plant traits. Confirmed: Masaru Ohme-Takagi, Director/Professor, Institute of Environmental Research and Technology, and Graduate School of Science and Engineering of Saitama University, Japan	Cereal crop genomics Confirmed: Matthew Paul, Professor, Rothamsted Research, UK
18.05-18.30	Transcriptomics Reserved: Ji-Young Lee, Assistant Professor, Seoul National University, South Korea	Integrated approaches to improve crop yield This presentation will describe Bayer's Crop Efficiency research approach comprised of focused research programs complemented by key enabling technologies with the objective to increase crop yield. - These activities are supported by an extensive network of collaborations, including many public-private partnerships. We will describe selected technologies and approaches which are together aimed at gaining a better understanding of the genetic and physiological basis of yield and yield components in crops. - These activities will be exemplified using with activities in the fields of computational biology, genomics and candidate gene engineering. Confirmed: Matthew Hannah, Expert Scientist, Trait Research, Bayer CropScience, Belgium
18.30	Chair's Closing Remarks and End of Day 1	
18.30-19.30	Networking Drinks Reception	

Agenda: Day Two – Tuesday 12th April 2016

08.15-08.55	Coffee and Networking Meetings	
08.55-09.00	Stream Chair Welcome Address:	
09.00-09.40	Keynote Address Genomics to protect the world's cereal crops from rust diseases The three pathogenic rust fungi that infect wheat are the most important biotic impediments to stable wheat production in many regions. The development of our understanding of the genetic interactions between wheat and these pathogens is a remarkable chapter in the history of plant science. While these advances have translated into considerable success in using genetics to protect wheat from the ravages of rust, they continue to impact on global wheat production by virtue of their abilities to change and overcome host resistance genes. Crucially, efforts to control rust in wheat have been underpinned by long-term studies of the evolution of virulence in rust pathogens that have generated extensive historical collections of viable rust isolates that represent the best germplasm available for genomic research on plant pathogenic fungi. The presentation will give an overview of efforts in applying genome sequencing in developing new approaches to control these important plant pathogens. Confirmed: Robert Park, Professor, Department of Plant and Food Science, Judith and David Coffey Chair in Sustainable Agriculture, The University of Sydney, Australia	
09.40-10.10	Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk	
10.10-10.40	Crop pathogen resistance Confirmed: Michael Jones, Professor of Agricultural Biotechnology, Director, Western Australian State Agricultural Biotechnology, Murdoch University, Australia	
10.40-11.40	Morning Refreshments Poster Presentation Sessions	
	Bioinformatics, Data Management & Analysis	Plant Genomic Case Studies
11.40-12.10	Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk	Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
12.10-12.35	The investigation of genome wide DNA methylation DNA methylation is an important epigenetic modification involved in many biological processes. Bisulfite treatment coupled with high-throughput sequencing (BS-seq) provides an effective approach for studying genome-wide DNA methylation at base resolution. My talk will give an overview of a comprehensive pipeline for the epigenomic data analysis of genome wide DNA methylation, including the biology, alignment, and bioinformatic analysis. I will cover a few case studies with integrative (epi)genomic analyses in plants and animals. Confirmed: Pao-Yang Chen, Assistant Research Fellow, Institute of Plant and Microbial Biology, Academia Sinica, Taiwan	Genomics of Fusarium Resistance in Wheat - Reverse genetic analyses of wheat to increase disease resistance against Fusarium pathogen will be reported. - Sub-genome specific defence gene expression in wheat. Interesting new insights on relative contribution of different wheat sub-genomes (A, B and D) into plant defence against a Fusarium pathogen will be reported. - Brachypodium: as an emerging model for functional genomics of Fusarium resistance in wheat. A comparative RNA-seq analysis of wheat and Brachypodium defence responses will be reported. Confirmed: Kemal Kazan, Group Leader, Protection from Pathogens and Pests, CSIRO Agriculture, Honorary Professor, Queensland Alliance for Agriculture & Food Innovation, University of Queensland, Australia
12.35-13.00	Epigenetic control of actions of the plant defence hormone jasmonate in Arabidopsis - Jasmonate (JA)-signalling repressors known as the JAZ proteins directly interact with chromatin modifiers - JAZs and chromatin modifiers act in concert to silence JA-responsive genes in the absence of JA - Genome-wide RNA-seq analyses reveal dynamic control of JA gene expression Confirmed: Yuehui He, Professor, Shanghai Center for Plant Stress Biology, Chinese Academy of Sciences, China	Wheat pathogen resistance Confirmed: Steven Scofield, Adjunct Associate Professor, University of Purdue, Research Geneticist, USDA-ARS, USA
13.00-14.00	Lunch	

Agenda: Day Two – Tuesday 12th April 2016

14.00-14.25	Bioinformatics Approaches in Agricultural Sciences with a focus on Cotton The amount of plant genomic/proteomic data is growing exponentially, and there is a parallel growth in the demand for tools and methods of data management, visualization, integration, analysis, modeling and prediction. We have identified 8 novel genes tolerant to drought stress in cotton which have been characterized with Bioinformatics applications. The presentation will generally deal to the important biological data related to: (1) DNA, RNA, and protein sequence analysis, (2) to predict molecular structures, (3) the protein – protein analysis and (4) analysis of signaling pathways associated with stress tolerance. Confirmed: Mahmood-ur-Rahman Ansari, Assistant Professor, Department of Bioinformatics and Biotechnology, Government College University Faisalabad, Pakistan	Sorghum 'omics and biotechnology – Title to be Confirmed Confirmed: Ian Godwin, Professor in Plant Molecular Genetics, School of Agriculture and Food Sciences, Centre for Plant Science, The University of Queensland, Australia
14.25-14.50	Data to decision; enabling research and development Analysis of data includes inspection, cleaning, transforming, integrating, visualizing and finally modeling data with the goal of discovering insights that support decision making. Data for research and development is an amalgamation of data sourced from public institutes, in-house research from companies and via collaborations. Corporate organizations store data in various enterprise level tools and there is possibility that these data will become “data in silo”. Quality of data needs to be first checked before using it for analysis. Heterogeneous data is normalized using ontologies, metadata guidelines and rules and is a crucial step before using the data for any analysis. Once the relationships are built using proper ontologies and controlled vocabularies data is ready for integration or analysis. We illustrate one case study which showcases the importance of data stewardship highlighting getting and cleaning data, normalization, integration and visual analytics to enable gene prioritization for testing in our research pipeline. Confirmed: Prasanna Bhat, Molecular Genetics and Genomics Team Lead, Monsanto, India	Using Genomics to Address Agricultural Improvement and Food Security. A Case Study Using Oil Palm Modern genomics and related biotechnologies have the capacity to improve crop yield, quality and environmental footprint in order to address concerns about population growth, sustainability and climatic uncertainty. Major target traits for oil palm include oil yield, fatty acid quality, plant architecture, pest/disease tolerance, climatic resilience and nutrient use efficiency. A major challenge is the deployment of often-imperfect bioinformatic tools for the conversion of the plethora of data from genome sequencing and transcriptomics into more useful biologically relevant information. This talk will assess the nature of these challenges and will also focus on recent progress in elucidating the basis of key agronomic traits in oil palm and the translation of such knowledge into real-world crop improvement. Confirmed: Denis Murphy, Professor of Biotechnology, Faculty of Computing, Engineering and Science, University of South Wales
14.50-15.15	Novel methodology to construct and utilise chromosome substitution libraries in plants Reverse breeding is a plant breeding strategy in which the order of steps to produce new plant variety is essentially reversed. This is mainly achieved by down regulating recombination thereby reconstructing parental lines from an offspring. These parental lines are reciprocal combination of lines selected from chromosome substitution lines (CSL). Chromosome substitution line is a line in which a single or multiple chromosome of a donor genotype is substituted into the genome of a recipient genotype. So plant with a ploidy level of n will have 2ⁿ chromosome substitution lines in the library (In case of Arabidopsis, n = 5, CSL = 32). I will discuss various methodologies to develop CSL, utility of CSL to improve breeding program. Confirmed: Geo Velikkakam James, Research Scientist, Rijk Zwaan, Netherlands	Palm Oil Case Study Confirmed: Meilina Ong Abdullah, Head of Breeding & Tissue Culture Unit, Advanced Biotechnology & Breeding Centre, Malaysian Palm Oil Board, Malaysia
15.15-15.40	Afternoon Refreshments	
15.40-16.05	Exploring Genomic Imprinting and Endosperm Transcriptomes in Abortive Hybrid Wild Tomato Seeds - Hybrid seed failure represents an important postzygotic barrier to interbreeding among species of wild tomatoes (<i>Solanum</i> section <i>Lycopersicon</i>) and other angiosperm groups. Based on seed size differences in reciprocal hybrid crosses and developmental evidence implicating endosperm failure, we hypothesized that (perturbed) genomic imprinting might be involved in this strong postzygotic barrier. - We surveyed endosperm transcriptomes obtained via laser-assisted microdissection of developing seeds representing both intra- and interspecific pollinations and identified hundreds of candidate imprinted genes. - We uncovered systematic shifts of the 'normal' (intraspecific) maternal:paternal transcript proportions in hybrid endosperms; the average maternal proportion of gene expression increased in both directions of the hybrid cross but was strongly negatively correlated with 'normal' maternal proportions. Additionally, several gene families involved in transcriptional regulation exhibit either up- or down-regulation in hybrid endosperm. Confirmed: Thomas Städler, Senior Scientist, Plant Ecological Genetics, Institute of Integrative Biology, ETH Zurich, Switzerland	Palm Oil Case Study Confirmed: Rofina Yasmin Binti Othman, Professor, Institute of Biological Sciences, Director, Centre for Innovation & Commercialisation, University of Malaya, Malaysia

16.05-16.30 Evolutionary genomics in green plants

Confirmed:

Ya-Long Guo, Professor, State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, China

Association of small RNA expression and DNA methylation with altered gene expression in banana (*Musa acuminata* cv. Berangan) roots during salt stress

- Small RNA's including miRNA and siRNA regulate gene expression during development and stress responses in plants.
- Using banana and salinity as a model system, we examined the changes in levels of miRNA, siRNA, mRNA and DNA methylation between roots exposed to salinity stress (300 mM NaCl) and untreated roots.
- This presentation will discuss the use of transcriptomic data for elucidating the roles of small RNA in gene silencing at the transcriptional and post-transcriptional level.

Confirmed:

Jennifer Ann Harikrishna, Director, Centre for Research in Biotechnology for Agriculture, Professor, Institute of Biological Sciences, University of Malaya, Malaysia

16.30-16.55 Evolutionary genomics case study

Reserved:

Jeffrey Mower, Associate Professor, Department of Agronomy and Horticulture, University of Nebraska-Lincoln, USA

Long non-coding RNA responsive to *Sclerotinia sclerotiorum* infection in *Brassica napus*

The function of long non coding RNAs (lncRNAs) in the regulation of gene expression and stress responses largely remains unclear, particularly in plants. In our study, we used a stranded RNA sequencing approach to identify lncRNAs responsive to *Sclerotinia sclerotiorum* infection in *Brassica napus*. A large RNA-Seq data resulted in the identification of 3181 lncRNAs categorized as intergenic, natural antisense, exonic overlapping and novel isoforms. Several lncRNAs were differentially expressed in response to pathogen infection. Besides, forty lncRNAs were identified as precursors for numerous microRNAs that are involved in mediating plant responses to fungal phytopathogens. Additionally, the evaluation of sense/antisense transcript pairs revealed reciprocal expression patterns supporting the hypothesis that steric clashes of transcriptional machinery may lead to inactivation of sense promoter. These findings suggest that stranded RNA-seq is a potential tool for exploring lncRNAs that play crucial roles in the anti-pathogenic networks of plants

Confirmed:

Raj Kumar Joshi, Visiting Professor, Dept. of Agriculture, Food and Nutritional Science, University of Alberta, Edmonton, Canada
Assistant Professor, Centre of Biotechnology, Siksha O Anusandhan University, Bhubaneswar, Odisha, India

16.55

Chairman's Closing Remarks and Conference Close



Poster Presentations

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 all abstracts in full.

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 forum you need to be registered as a delegate. Please note that there is limited space available and posters space is assigned on a first come first served basis (subject to checks and successful registration).

For further information on submission, approval and the technical poster spec, please contact: submit@globalengage.co.uk or go to www.globalengage.co.uk/pgcasia/delegates.html

Global Engage - Plant Genomics Series

3rd Plant Genomics USA – September 14-15, 2015, St Louis, USA

<http://www.globalengage.co.uk/plantgenomicsusa.html>

2nd Synthetic Biology (Gene Editing) Congress (Plant Tracks) – October 19-20, 2015, London, UK

<http://www.globalengage.co.uk/synthetic-biology.html>

3rd qPCR & dPCR Congress (Plant Tracks) – October 19-20, 2015, London, UK

<http://www.globalengage.co.uk/qpcr.html>

3rd Plant Genomics USA – April 11-12, 2016, Kuala Lumpur, Malaysia

<http://www.globalengage.co.uk/plantgenomicsasia.html>

4th Plant Genomics Europe – May 9-10, 2016, London, UK

<http://www.globalengage.co.uk/plantgenomics.html>