11th-12th April 2016, Kuala Lumpur, Malaysia



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



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-theart 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, Head of Centre for Synthetic Biology, Head of VILLUM Research Center for Plant Plasticity, 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 0
- 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 0
- **Evolutionary genomics**
- 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

Plant / agricultural microbiome

Paul Quick

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



Mark Davey Group Leader, Applied Genetics, 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



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

























Principal Scientist and Head of C4 Rice Project, International Rice

Research Institute, Philippines

Birger Lindberg Møller Professor of Plant Biochemistry,

Head of Centre for Synthetic Biology, Head of VILLUM Research Center for Plant Plasticity, University of Copenhagen, Denmark

Matthew Paul Professor, Rothamsted Research, UK

Ya-Long Guo Professor, State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany,

of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, China

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

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

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



CSRS, Professor, Yokohama City University, Japan

Ji-Young Lee Assistant Professor, Seoul National University, South Korea

Geo Velikkakam James Research Scientist, Rijk Zwaan, Netherlands



Xuehua Zhong

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

Jacqueline Batley ARC Future Fellow,

ARC Future Fellow, University of Western Australia, Australia



Amit Rai Assistant Professor, Chiba University, Japan

Kemal Kazan



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



Steve Scofield USDA-ARS Research Geneticist and Adjunct Associate Professor, University of Purdue

Thomas Städler

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

Michael Jones Professor of Ag Biotechnology

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

Mahmood-ur-Rahman Ansari

Government College University

Faisalabad, Pakistan

Thomas Bureau

Assistant Professor, Department of

Bioinformatics and Biotechnology,





Pao-Yang Chen Assistant Research Fellow, Institute

Associate Professor, Department of

Biology, McGill University, Canada







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 Gold Sponsors



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.



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 plant biology: The ultimate way to 'go green' - Light-driven production of structurally complex diterpenoids With 12,000+ known structures, diterpenoids are a prime example of bio-active natural products produced by plants. Many are used as highly valuable pharmaceuticals, fragrances, natural plant growth promoters, food ingredients such as flavors or as colorants and spices. Unfortunately, they are typically produced in minute amounts in plants and their structural complexity render them difficult to prepare from fossil resources using organic chemical synthesis. We have developed an integrated biochemical and functional genomics bio-sustainable production including targeted metabolomics and single cell-type transcriptome studies to identify the genes encoding a desired pathway. The functional parts identified also enabled combinatorial assembly of new-to-nature diterpenoid pathways. The entire pathway for forskolin was elucidated. Forskolin is a cyclic AMP booster approved for treatment of glaucoma but also used as a weight loss aid. The forskolin pathway is being used as test model system for large scale light driven production of high value diterpenoids following targeting of the P450s to the thylaloid membrane and using cyanobacteria or moss as photosynthetic production hosts grown in contained photo-bioreactors. Our results pave the way for development of other large scale light driven biotechnological production systems and for synthetic biology approaches for rational expansion of diterpenoid chemical diversity. Confirmed: Birger Lindberg Møller, Professor of Plant Biochemistry, Head of Centre for Synthetic Biology, Head of VILLUM Research Center for Plant		
	Plasticity 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 Japoratory, USA 		
10.05-10.35	Solution Provid	ler Presentation	
	For sponsorship opportunities please contact S	teve Hambrook at <u>steve@globalengage.co.uk</u>	
10.35-11.45	Morning Re Poster Present	efreshments tation Sessions	
	NGS, Omic and Gene Editing Technologies for Plant Research	Plant Genomic Case Studies	
	 agriculture 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	 Using phenomics to discover high value orphaned DNA The non-coding DNA realm of genomes harbor sequences (e.g. transposons, non-coding RNA genes and regulatory elements) often neglected for downstream experimental characterization. Many protein-coding genes have also been marginalized because of their evolutionary relationship with transposons. Though bioinformatics investigations predict potentially functional regions in non-coding DNA, systematic functional analysis has been lacking. This is due in part to a bottleneck in phenotyping. In order to attain high-throughput functional validation for these regions, we have exploited a new Phenomics Platform located at McGill University. We present a systematic functional survey of marginalized DNA in the form of co-opted transposons conserved in the Brassicaceae. Our results indicate that not only do they have a phenotype but many are also potentially involved in abiotic stress responses. Confirmed: Thomas Bureau, Associate Professor, Department of Biology, McGill University, Canada 	Using NGS-Based Genotyping Platform for Genomic Discovery of Rice Introgression Lines Crop wild relatives (CWR) have contributed significantly in modern breeding, however, CWR remains under-exploited in crop breeding because of natural barriers related to interspecific hybridization. Introgression lines are appropriate material to make use of wild alleles in a breeding program. We used NGS-based high-throughput genotyping platform to characterise rice introgression lines, created through interspecific hybridization between Oryza sativa, L. ssp. <i>iaponica</i> and Oryza nivara. The genomic characterization of these rice introgression lines using high-throughput genotyping will be presented.	

12.35-13.05	Solution Provider Presentation Title To Be Confirmed	Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk	
	Senior Representative - DNAnexus		
13.05-14.05	l	unch	
14.05-14.30	De novo transcriptome studies as a tool for unveling the chemical diversity and processes involved there biosynthesis in medicinal plants Medicinal plants have been used for thousands of years as an important source of bioactive compounds, and have played major role in human health management. Bioengineering provides the solution to meet high demand of phytochemicals derived from these medicinal plants while protecting them from being extinct. Unfortunately, limited genomic information on most medicinal plants due to its complex genome structure has restricted their research and thus biosynthetic mechanisms of many important phytochemicals are still poorly understood. Recent advancement in next generation sequencing, reduced cost per base sequencing, and development of computational algorithms and resources has revolutionized the field of photochemistry. In my talk, I will present my recent research on application of <i>De n</i> ovo transcriptome studies to identify and characterization of chemical diversity in medicinal plants. Confirmed: Amit Rai, Assistant Professor, Chiba University, Japan	Systems Biology and Molecular Breeding of Forage S Confirmed: German Spangenberg, Director, AgriBio, Professor of Plant Genetics and Genomics, La Trobe University, Australia	
14 30-14 55	Title To Be Confirmed	Molecular genetic mechanisms for podulation control of podulation	
14.30-14.33	The To be commed	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 GmNNC1, 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.	
	Invitation to:	Confirmed: Peter Gresshoff, Professor, Plant Molecular Genetics, Director, Centre for Integrative Legume Research, University of Queensland, Australia	
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	 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 h, Soybean Molecular Design Breeding, Chinese Academy of Sciences, 	
15 20 15 50	RIKEN CSRS, Professor, Yokohama City University, Japan	China Solution Provider Presentation	
13.20-13.30	Title To Be Confirmed Agilent Technologies	For sponsorship opportunities please contact Steve Hambrook at <u>steve@globalengage.co.uk</u>	
15.50-16.50	0 Afternoon Refreshments		
16 50-17 15	Poster Prese	Poster Presentation Sessions	
	environmental gene regulation Epigenetic regulation of gene expression plays critical roles in maintaining genome integrity, imprinting, cellular differentiation, normal growth and development, disease formation as well as in responding versatile environmental signals. Our overall research them is to understand how epigenetic modifications of DNA and histones modulate chromatin structural dynamics to regulate gene expression. We are also interested in understanding how epigenetic modulation o chromatin structure and gene expression dictate responses to environmental changes and how environment conditions feed back to shape the epigenetic landscape. We will address these questions at the whole genome level by combining genomics, genetic, proteomic, and biochemical approaches Confirmed: Xuehua Zhong, Assistant Professor. Laboratory of Genetics.	approach Leptosphaeria maculans, the causal agent of Blackleg disease in Brassica napus is responsible for an average of 15% p.a. crop losses worldwide. Seedling derived qualitative resistance to this disease is e conferred by the recognition of an effector molecule by the product/s of a resistance gene and typically results in complete resistance. The identification of genes underlying important QTL is extremely f challenging in complex genomes such as <i>B. napus</i> . However, recent advances in next-generation sequencing (NGS) enable much quicker identification of candidate genes for traits of interest. Using an array of genomics analysis tools, the elucidation and downsteam validation of candidate genes can be accomplished in a more efficient and timely manner. Molecular analyses of candidate resistance genes using <i>B. napus</i> NGS data are presented. Confirmed:	
	University of Wisconsin-Madison, USA	Jacqueline Batley, AKC Future Fellow, University of Western Australia, Australia	

ee, Assistant Professor, Seoul National University, South	Mark Davey, Group Leader, Applied Genetics, Bayer Cropscience
	Contirmed:
omics	 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.
nme-Takagi, Director/Professor, Institute of Environmental Ind Technology, and Graduate School of Science and g of Saitama University, Japan	Confirmed: Matthew Paul, Professor, Rothamsted Research, UK
I for Functional Analysis of Transcription Factors and on of Plant Traits of transcription factors are known to act as master regulators obhenotypes and are useful tool for the manipulation of plant ever, plant genes are frequently duplicated and such nd functional redundancy often interferes with efforts to ne functions of plants. To overcome these difficulties, we a novel gene silencing system, called Chimeric REpressor cing Technology (CRES-T), in which a transcription factor is nto strong repressor by fusion of the plant-specific domain (SRDX) and suppresses the target genes dominantly tivity of endogenous and functionally redundant n factors. We present here that CRES-T system is useful tool al analysis of redundant plant transcription factors and the on of various plant traits.	 parallel approaches for crop yield improvement Use of caged trehalose 6-phosphate modifies sugar signalling chemically in plants for the first time Chemical modification of trehalose 6-phosphate abundance increases yield potential and stress resilience Chemical and genetic approaches can be used in parallel to modify trehalose 6-phosphate, which regulates a major regulatory hub for yield
ellar genomes to primary and secondary metabolism. Associate Professor, School of Biological Sciences, of Hong Kong, Hong Kong	Confirmed: Shavannor Smith, Associate Professor, Department of Plant Pathology, University of Georgia, USA
High Energy Supply from Chloroplasts and Mitochondria Transcriptomes, Proteomes and Metabolomes dulating energy outputs from chloroplasts and mitochondria, ve generated fast-growth and high seed yield Arabidopsis igh ATP and sucrose contents in leaves. riptome, proteome and metabolome profiles of the high ansgenic line were compared with wild-type plants. illustrate the impacts of high energy supply from plasts and mitochondria on plant physiology, from	Maize Case Study
	High Energy Supply from Chloroplasts and Mitochondria Transcriptomes, Proteomes and Metabolomes dulating energy outputs from chloroplasts and mitochondria, ve generated fast-growth and high seed yield Arabidopsis gh ATP and sucrose contents in leaves. riptome, proteome and metabolome profiles of the high ansgenic line were compared with wild-type plants.



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: Pachoz Park Parks Parfores a Department of Plant and Eccel Science, Judith and David Coffor Chair in Sustainable Arrivations The University			
	of Sydney, Australia			
09.40-10.10	0 Solution Provider Presentation			
	For sponsorship opportunities please contact Steve Hambrook at <u>steve@globalengage.co.uk</u>			
10.10-10.40	New approaches to crop pathogen resistance Plant pathogens contribute to preventing crops from reaching their full yield potential. Losses caused by infestation with nematodes and aphids result from direct feeding damage and transmission of virus diseases. Both pest groups use a battery of effectors to penetrate plant tissues, evade host defences and control host cell metabolism. Since nematode and aphid pests feed from cell contents they are amenable to control by host-induced gene silencing (HIGS). Remarkably they have some effectors in common. The application of RNAi technology to confer host resistance to these pests will be described. 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 & Anglysis Plant Genomic Case Studies			
	Bioinformatics, Data Management & Analysis	Plant Genomic Case Studies		
11.40-12.10	Bioinformatics, Data Management & Analysis Solution Provider Presentation	Plant Genomic Case Studies Solution Provider Presentation		
11.40-12.10	Bioinformatics, Data Management & Analysis Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk	Plant Genomic Case Studies Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk		
11.40-12.10	Bioinformatics, Data Management & Analysis Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk 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.	Plant Genomic Case Studies Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk 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.		
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11.40-12.10 12.10-12.35 12.35-13.00	Bioinformatics, Data Management & Analysis Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk The investigation of genome wide DNA methylation 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 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 	Plant Genomic Case Studies Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk 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 Adventures performing functional genomics in hexaploid wheat • We utilize virus induced gene silencing to create knockdown phenotypes in hexaploid wheat. • VIGS has been used to identify genes with critical functions in a range of disease resistance systems. • We are employing RNA-seq to identify genes likely to encode critical functions for resistance to diseases caused by Fusarium graminearum. These candidates will be confirmed by VIGS.		
11.40-12.10 12.10-12.35 12.35-13.00	Bioinformatics, Data Management & Analysis Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk 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 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	Plant Genomic Case Studies Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk 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 Adventures performing functional genomics in hexaploid wheat • We utilize virus induced gene silencing to create knockdown phenotypes in hexaploid wheat. • VIGS has been used to identify genes with critical functions in a range of disease resistance systems. • We are employing RNA-seq to identify genes likely to encode critical functions for resistance to diseases caused by Fusarium graminearum. These candidates will be confirmed by VIGS. Confirmed: Steve Scofield, USDA-ARS Research Geneticist and Adjunct Associate Professor, University of Purdue		

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	 Harnessing the sorghum genome for improved grain quality and human health Using NextGen sequencing we are now in a position to improve sorghum grain quality for specific end-uses We have identified sorghum genes and gene pathways which have major effects on grain digestibility, seed size and protein content Genomics approaches have shown the grass pollen allergens in Sorghum differ significantly from those in temperate grass species Confirmed: Ian Godwin, Professor in Plant Molecular Genetics, School of Agriculture and Food Sciences, Centre for Plant Science,
	Faisalabad, Pakistan	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.	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.
	Prasanna Bhat, Molecular Genetics and Genomics Team Lead, Monsanto, India	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 ord to produce new plant variety is essentially reversed. This is mail by down regulating recombination thereby reconstructing parent from an offspring. These parental lines are reciprocal combination selected from chromosome substitution lines (CSL). Chromosome line is a line in which a single or multiple chromosome of a donor is substituted into the genome of a recipient genotype. So plant ploidy level of n will have 2ⁿ chromosome substitution lines in the case of Arabidopsis, n =5, CSL = 32). I will discuss various met 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 R	lefreshments
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 (Solanum section Lycopersicon) 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. 	The chloroplast genome sequence of Musa balbisiana and heterogeneity among the Musaceae A detailed analyses of the complete chloroplast genome sequence of <i>Musa balbisiana</i> Colla, an important wild progenitor of cultivated banana combining molecular and phylogenomic analyses investigating the structural variation in the chloroplast genomes of the Musaceae has revealed some novel insights into the evolution of banana. Overall, its gene content, size and order are similar to that of <i>Musa acuminata</i> with extensive expansion of the IR/SSC regions. Interestingly, the IRb/SSC expansion observed in <i>Musa balbisiana</i> is absent in the sister taxon <i>Musa textilis</i> and members of Zingiberacae and Heliconiaceae. Nonetheless phylogenomic analyses of whole chloroplastomes and shared protein datasets have unequivocally supported the monophyly of <i>Musa balbisiana</i> and <i>Musa textilis</i> . The genome exhibits a typical quadripartite structural organization with a large single-copy (LSC, 87828 bp) region and a small single-copy (SSC, 11547 bp) region interspersed between inverted repeat (IRa/b,35064 bp) regions.

Confirmed:

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

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

16.05-16.30	Gene family evolution in green plants with emphasis on the origination of Arabidopsis thaliana genes	Association of small RNA expression and DNA methylation with altered gene expression in banana (Musa acuminata cv. Berangan roots during salt stress	
	 The rate of gene gains and losses in plants (0.001379) is similar to the rate in yeast, Drosophila, and mammals. 2745 gene families present in all the green plants represent the 'core' proteome of green plants; 70% of Arabidopsis thaliana genes could be traced back to 450 million years ago, and 5.3% A. thaliana genes are species-specific genes. 	 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: Ya-Long Guo, Professor, State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, China	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	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 toll 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 Rem	arks and Conference Close	

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Poster Presentations

	Title	Principal Author(s)	Affiliation
1	Allium sativum Pathogenesis related protein 5 (AsPR5) stimulates the defense response pathway and enhances the resistance to necrotrophic fungal infection.	Ellojita Rout, Satyabrata Nanda, Raj Kumar Joshi	Functional Genomics Laboratory, Centre of Biotechnology, Siksha O Anusandhan University, Bhubaneswar-751003, India
2	Molecular cloning and in silico analysis of nitric oxide associated 1 (NOA1) gene of Elaeis guineensis Jacq.	Yee-Min Kwan, Chai-Ling Ho, Sariah Meon and Mui-Yun Wong*	Universiti Putra Malaysia
3	Use of functional genomics to study the response of rice to abiotic stress	Kupusamy UPriya, Gatehouse AMR, Edwards MG	Newcastle University, United Kingdom

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3rd Plant Genomics Asia – April 11-12, 2016, Kuala Lumpur, Malaysia http://www.globalengage.co.uk/plantgenomicsasia.html

4th Plant Genomics Europe – May 9-10, 2016, London, UK <u>http://www.globalengage.co.uk/plantgenomics.html</u>

2nd qPCR & dPCR Congress USA (Plant Tracks) – July 11-12, 2016, Philadelphia, USA <u>http://www.globalengage.co.uk/digital-and-qpcr.html</u>

4th Plant Genomics USA – September 12-13, 2016, Philadelphia, USA <u>http://www.globalengage.co.uk/plantgenomicsusa.html</u>

3rd Synthetic Biology (Gene Editing) Congress (Plant Tracks) – October 20-21, 2016, London, UK <u>http://www.globalengage.co.uk/synthetic-biology.html</u>

4th qPCR & dPCR Congress (Plant Tracks) – October 20-21, 2016, London, UK <u>http://www.globalengage.co.uk/qpcr.html</u>

