



The Plant Genomics Congress Asia

UTILIZING NEXT GENERATION SEQUENCING AS A TOOL FOR PROGRESSING PLANT RESEARCH

Global Engage are pleased to announce as part of their Next Generation Sequencing series of events the Plant Genomics Congress Asia, which will be held on February 24-25, 2014 in Kuala Lumpur, Malaysia. The event is the sister meeting to the European Plant Genomics Congress which took place in London this May which had over 260 registered attendees and the American meeting held in St Louis this September which went equally well.

Attracting experts working in areas such as plant sciences, next generation sequencing, genomics, epigenetics, bioinformatics and data management the conference will examine the latest NGS platforms and technologies suitable for progressing plant based research as well as tools to enable successful analysis. Presentations concentrate on, but are not limited to, regional crops such as wheat, maize, barley, rice, soybean, canola, rapeseed, palm oil, etc in order to attract delegates across the Asia Pacific region and beyond.

Plant research has transformed dramatically over the last 5 years as a result of the revolutionary breakthroughs and reduction in cost in sequencing. Plants including rice, papaya, maize and most recently tomato, banana and barley have been successfully sequenced and a wide range of biological data sets made available. Plant scientists are therefore making use of state of the art sequencing platforms to help explain biological principals, advance research and therefore enable benefits such as crop improvement by harnessing the greater understanding of plant genomes.

Should you be either an expert already using NGS for plant analysis with a desire to extend your knowledge or for researchers 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, interactive Q&A panel discussions and case study presentations from experts from a range of disciplines.

Confirmed Speakers Include:



Tomohiro Ban

Professor, Kihara Institute for Biological Research, Yokohama City University, Japan



John Manners

Chief, CSIRO Plant Industry, Australia



Dave Jackson

Professor, Cold Spring Harbor Laboratory, USA

Conference Synopsis

Day 1 Stream 1 - NGS Technologies for Plant Research

- NGS Platform comparison
- Best practice and guidelines for current technology
- Future uses of new generation technologies
- NGS Protocols
- Sample Preparation Technology
- Standardisation
- Plant genotyping, SNP discovery, QTL Mapping & Marker-Assisted Selection
- Plant genetic engineering - Genome / DNA assembly , genome editing, cloning, amplification
- DNA & RNA isolation

Day 1 Stream 2 - Plant Genomic Case Studies

- Applications of next-generation sequencing in plant research
- Using NGS to enhance-
 - Molecular marker development, Breeding, Crop improvement, Hybridization, Conservation, Evolution studies
- Case studies using:
 - De novo Seq; Resequencing; Targeted resequencing, Exome Seq; Transcriptome Seq, RNA seq; mRNA Seq, non-coding RNA, ChIP-Seq; Whole Genome Seq Targeted Sequencing / Sequence enrichment

Day 2 Stream 1 - Epigenetic Case Studies & Biofuel Research

- Applications of next-generation sequencing in plant research
- Case studies using:-
 - Epigenetics
 - DNA methylation
 - ChIP seq
 - Regulatory elements in RNA
 - miRNA
 - ncRNA
- Biofuel Case Studies

Day 2 Stream 2 –

Bioinformatics, Data Management & Analysis / Maize Case Studies

- Bioinformatic analysis and challenges
- Bioinformatics from a biologist's perspective
- Sequencing pipelines and assembly
- Gene expression analysis
- Improving error rates
- Cloud computing and storage solutions
- Compressive technologies
- NGS data analysis, management & integration in a genomics core
 - Maize Case Studies

Confirmed Speakers



John Manners, Chief, CSIRO Plant Industry, Australia



Wen-Hsiung Li, Director and Distinguished Research Fellow, Biodiversity Research Center, Academia Sinica, Taiwan



Graham King, Director, Southern Cross Plant Science and Professor of Plant Genomics and Epigenetics, Southern Cross University, Australia



Julie Law, Assistant Professor, Plant Molecular and Cellular Biology Laboratory, Salk Institute, USA



Sachiko Isobe, Head Applied Plant Genomics, Kaduza DNA Research Institute (KDRI), Japan



Yuan-Ming Zhang, Professor of Statistical Genomics, State Key Lab. of Crop Genetics and Germplasm Enhancement, Nanjing Agricultural University



Tomohiro Ban, Professor, Kihara Institute for Biological Research, Yokohama City University, Japan



Sean Mayes, Associate Professor Crop Genetics & Theme Director; Biotech., Breeding and Seeds, Crops for the Future Research Centre, Nottingham University, Nottingham and Kuala Lumpur



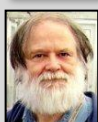
José Crossa, Distinguished Scientist, International Wheat and Maize Improvement Centre, CIMMYT, Mexico



Ek Han Tan, Postdoctoral Research Associate, Laboratory of Simon Chan, Department of Plant Biology, HHMI/GBMF, UC Davis, USA



Charles Chen, Scientist, Statistical Geneticist for Seeds of Discovery, International Maize and Wheat Improvement Center (CIMMYT) Mexico



Steve Haber, Research Scientist, Agriculture and Agri-Food, Canada



Dave Edwards, Principal Research Fellow, School of Agriculture & Food Sciences, University of Queensland, Australia



Dave Jackson, Professor, Cold Spring Harbor Laboratory, USA



Ryan Lister, Professor/ARC Future Fellow, Plant Energy Biology ARC CoE, School of Chemistry and Biochemistry, The University of Western Australia



Shi Ying Yang, Research Officer, School of Agriculture Food and Wine, The University of Adelaide & Gene Function Lab South Australian Research and Development Institute, Australia



Yue-le Hsing, Distinguished Research Fellow, Institute of Plant and Microbial Biology, Academia Sinica, Taiwan



Kenneth Olsen, Associate Professor Department of Biology, Washington St Louis University, USA

Also:

Rob Martienssen, Professor and HHMI Investigator, Cold Spring Harbor Laboratory, USA

Nagendra Singh National Professor-BP Pal Chair, National Research Centre on Plant Biotechnology, Indian Council of Agricultural Research, India

Han Zhao, Professor of Biology and Biotechnology, Institute of Biotechnology Jiangsu, Academy of Agricultural Sciences, China

Rajeev K. Varshney, Principal Scientist (Applied Genomics) & Director, Centre of Excellence in Genomics, ICRISAT, India

Kenneth McNally, Senior Scientist, The International Rice Research Institute, The Philippines

Shailajah Hittalmani, Professor and Head, Genetics and Plant Breeding Dept., Principle Investigator and Head, DNA Marker-Assisted Selection Laboratory, University of Agricultural Sciences, GKVK, India

Trushar Shah, Bioinformatics Scientist, ICRISAT, India

Silin Zhong, Assistant Professor, School of Life Sciences, The Chinese University of Hong Kong

Shancen Zhao, Senior Project Consultant, BGI

Norman Warthmann, Senior Post Doc, Borevitz Laboratory, ANU College of Medicine, Biology and Environment, Australian National University, Australia

Chungui Lu Lecturer in Post-Genomics, Faculty of Science, Nottingham University, UK

Meilina Ong Abdullah, Breeding and Tissue Culture Unit, The Advanced Biotechnology and Breeding Centre, Malaysian Palm Oil Board (MPOB) Malaysia

Harish Gandhi, Head Genetics and Trait Projects- Rice, Syngenta, India

Nandini Krishnamurthy, Computational Biologist, DuPont Pioneer, India

Kimberly Sampson, Principal Scientist, Trait Discovery, Bayer CropScience, USA

Chia-Lin Wei, Group Leader - Sequencing Technologies Group, Joint Genome Institute (JGI), USA

Parveen Chhuneja, Geneticist, Bioinformatics Centre School of Agricultural Biotechnology, Punjab Agricultural University, India

Amitabh Mohanty, Lead Trait Discovery, E.I. DuPont India Pvt Ltd.

Senior Representatives, Keygene

Clive Brown, Chief Technology Officer, Oxford Nanopore Technologies

Yijun Ruan, Professor and Director, Systems Biology Center, HuaZhong Agricultural University, Wuhan, China

Huaan Yang, Department of Agriculture and Food (DAFWA), Australia

Cuixia Chen, Professor, Shandong Agriculture University, China

Nickolai Alexandrov, Senior Scientist, The International Rice Research Institute, The Philippines

Antonio Costa de Oliveira, Associate Professor of Genetics and Plant Breeding, Plant Genomics and Breeding Center, CGF, Brazil

Jizeng Jia, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences (CAAS) China

Festo Massawe, Head of School of Biosciences (UNMC), Faculty of Science, University of Nottingham Malaysia Campus, Malaysia

Kanika Kumar, Senior Scientist, National Research Centre on Plant Biotechnology, Indian Council of Agricultural Research, India

Jacqueline Batley, Associate Professor, ARC QEII Research Fellow - School of Agriculture & Food Sciences, Faculty of Science, The University of Queensland, Australia

Shengyi Liu, Professor and Head, The Key Lab of Oil Crops Biology, the Ministry of Agriculture, PRC Department of Genomics, Oil Crops Research Institute, Chinese Academy of Agricultural Sciences, China

Agenda: Day One – Monday 24th February 2014

08.00-08.50 Registration & Morning Coffee

08.50-09.00 Global Engage Welcome Address
Stream Chair's Opening Remarks – **Sean Mayes, Associate Professor Crop Genetics & Theme Director; Biotech., Breeding and Seeds, Crops for the Future Research Centre, Nottingham University, Nottingham and Kuala Lumpur**

09.00-09.30 Keynote Address:
Genome to Phenome (G2P). The Challenge of Harnessing Big Data in Crop Improvement

- Revolutions in genomics and phenomics allow new approaches for gene discovery and trait-gene association, as well as applications in breeding, e.g. genomic selection. Large scale genotyping is getting easier, sophisticated phenotyping at scale remains challenging.
- Genomics approaches have been successfully applied in gene discovery in model species and crop plants with simple genetics like rice. However, many important crop plants are polyploid, e.g. wheat, sugarcane, cotton where tailored strategies are required such structured populations to facilitate G2P analysis.
- The soil and rhizosphere microbiome are highly influential on plant performance and the microbiome is now accessible via metagenomics. The concept of the 'hologenome' where the plant genome and microbiome are considered as a system is emerging as a new horizon in plant improvement.

CONFIRMED:
John Manners, Chief, CSIRO Plant Industry, Australia

09.30-10.00 **Solution Provider Presentation**
Title to be Confirmed
Clive Brown, Chief Technology Officer, Oxford Nanopore Technologies



Track 1 - NGS Technologies for Plant Research

Stream Chair - **Sean Mayes, Associate Professor Crop Genetics & Theme Director; Biotech., Breeding and Seeds, Crops for the Future Research Centre, Nottingham University, Nottingham and Kuala Lumpur**

Track 2 - Plant Genomic Case Studies

Stream Chair - **Shi Ying Yang, Research Officer School of Agriculture Food and Wine, The University of Adelaide & Gene Function Lab, South Australian Research and Development Institute, Australia**

10.00-10.25 **Next Generation Genomics and Integrated Breeding: A Case Study in Chickpea**
Advances in genomics are enhancing precision and efficiency in breeding for crop improvement to ensure food and nutritional security in developing countries. In the case of chickpea, an important legume crop for South Asia and Sub-Saharan Africa, a draft genome sequence of CDC Frontier variety and re-sequence data of 90 additional lines have been assembled (Nature Biotechnology 31:240-246). In addition, large-scale molecular markers, high-density genetic maps, transcriptome assembly have been generated. These resources together with precise phenotyping of specialized genetic populations led identification of a genomic region harbouring QTLs for several drought tolerance traits. Introgression of this QTL region in three leading chickpea varieties by using marker-assisted backcrossing (MABC) approach have generated superior lines with up to 12% higher yield than the recurrent parents.

3000 Rice Genome Project – Title to be Confirmed

CONFIRMED:
Kenneth McNally, Senior Scientist, The International Rice Research Institute, The Philippines

CONFIRMED:
Rajeev K. Varshney, Principal Scientist (Applied Genomics) & Director, Centre of Excellence in Genomics, ICRISAT, India

10.25-10.50 **Using NGS To Enhance Crop Improvement Or Plant Genetic Engineering - DNA Assembly, Genome Editing, Cloning, Amplification**

CONFIRMED:
Amitabh Mohanty, Lead Trait Discovery, E.I. DuPont India Pvt Ltd.

Evolutionary Genomics of Weedy Rice
Since the time of Darwin, crop domestication has been recognized as a model for understanding evolutionary change. Genome-enabled species such as rice are particularly well suited for studying the genetic and genomic changes during domestication and subsequent crop improvement. In the case of rice, weedy strains have evolved that aggressively compete with the crop and compromise productivity worldwide. In this talk I describe recent work characterizing the evolutionary relationship of weedy rice (also called red rice) to domesticated rice, the role of 'de-domestication' in the emergence of weed strains around the world, and the genetic and genomic changes associated with the evolution of weedy phenotypes

CONFIRMED:
Kenneth Olsen, Associate Professor Department of Biology, Washington St Louis University

10.50-11.40 **Morning Refreshments**
Poster Presentation Sessions

11.40-12.10 **Solution Provider Presentation**
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Title to be Confirmed

CONFIRMED:
Senior Representative, Keygene

12.10-12.35 **NGS Technologies**

CONFIRMED:
Harish Gandhi, Head Genetics and Trait Projects- Rice, Syngenta, India

Rice Blast And Drought Sequencing – Title to be Confirmed

CONFIRMED:
Shailajah Hittalmani, Professor and Head, Genetics and Plant Breeding Dept., Principle Investigator and Head, DNA Marker-Assisted Selection Laboratory, University of Agricultural Sciences, GKVK, India

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12.35-13.00	Panel Discussion – Possibilities Of Plant Research With New NGS Technologies	Case Studies With Our Experience With Rice, Tomato, Rhizobium, Pigeonpea And Wheat Genome Sequencing – Title to be Confirmed
	<p>CONFIRMED: Sean Mayes, Associate Professor Crop Genetics & Theme Director; Biotech., Breeding and Seeds, Crops for the Future Research Centre, Nottingham University, Nottingham and Kuala Lumpur</p> <p>Antonio Costa de Oliveira, Associate Professor of Genetics and Plant Breeding, Plant Genomics and Breeding Center, CGF, Brazil</p> <p>Kanika Kumar, Senior Scientist, National Research Centre on Plant Biotechnology, Indian Council of Agricultural Research, India</p>	<p>CONFIRMED: Nagendra Singh, National Professor-BP Pal Chair, National Research Centre on Plant Biotechnology, Indian Council of Agricultural Research, India</p>
13.00-14.00	Lunch	Lunch
14.00-14.25	Genomic And Evolutionary Analysis Of Oranges Oranges are an important nutritional source for human health and have immense economic value. Citrus fruits also have some unique botanical features such as nucellar embryony, which hindered the study of citrus genetics and breeding improvement. Complete genome sequences would provide valuable genomic knowledge for understanding the genetic basis and evolutionary biology of diverse resources, and thus improving citrus crops. We have applied advanced genomic and computational technologies to comprehensively analyze the sweet orange genomes, reconstituted the evolutionary history of sweet orange origin and characterized the genomic basis of orange-specific features. We are now applying the similar approaches to analyze other important crops.	Utilization Of Wild Relatives Of Wheat For Germplasm Enhancement Using Genomics Interventions
	<p>CONFIRMED: Yijun Ruan, Professor and Director, Systems Biology Center, HuaZhong Agricultural University, Wuhan, China & Professor and Director, Genomic Sciences, The Jackson Laboratory for Genomic Medicine, USA</p>	<p>CONFIRMED: Parveen Chhuneja, Geneticist, Bioinformatics Centre School of Agricultural Biotechnology, Punjab Agricultural University, India</p>
14.25-14.50	Transcriptome Analysis Of Barley In Response To Cold Stress And An Approach To Predict Functional Genes Associated With Complex Traits In Rice Using Next-Generation Sequencing Technology <ul style="list-style-type: none"> • Microarray/RNA Seq analysis in parallel of the changes on expression of thousand of genes associated with cold stress in barley. • Using RNA-Seq, differential expression of annotated genes and novel transcribed units has been investigated between wild-type and mutant rice which showed high N/P use efficiency. • We use an integrative systems biology approach to infer and model the regulatory network to facilitate understanding biological processes related to cold stress and nutrient use efficiency. 	Genomic Characterization of Afghanistan Wheat Landraces <ul style="list-style-type: none"> • Genome wide basic screening of Afghan wheat landraces • Molecular evaluation of interesting phenotypic characters • Genome-wide association mapping of essential elements • Concept of landrace characterization and utilization
	<p>CONFIRMED: Chungui Lu, Lecturer in Post-Genomics, Faculty of Science, Nottingham University, UK</p>	<p>CONFIRMED: Tomohiro Ban, Professor, Kihara Institute for Biological Research, Yokohama City University, Japan</p>
14.50-15.15	Gene discovery platform for pest and herbicide tolerance based on our microbial collection – Title to be Confirmed	Wheat Genomics
	<p>CONFIRMED: Kimberly Sampson, Principal Scientist, Trait Discovery, Bayer CropScience, USA</p>	<p>CONFIRMED: Jizeng Jia, Institute of Crop Sciences, Chinese Academy of Agricultural Sciences (CAAS) China</p>
15.15-15.45	<p style="text-align: center;">Solution Provider Presentation</p> <p>Understand Domestication and Breeding by Sequencing</p> <p>Dr. Shancen Zhao, Senior Project Consultant, BGI Sponsored by</p> <div style="text-align: center;">  </div>	<p style="text-align: center;">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk</p>
15.45-16.30	Afternoon Refreshments Poster Presentation Sessions	
16.30-16.55	NGS Technologies For Adaptive Trait Variation Neglected and underutilized crop species to inform conservation and prebreeding efforts.	Polyploid Genome Plasticity And Selection Potential: A Case From Brassica Crops
	<p>CONFIRMED: Norman Warthmann, Senior Post Doc, ANU College of Medicine, Biology and Environment, Australian National University, Australia</p>	<p>CONFIRMED: Shengyi Liu, Professor and Head, The Key Lab of Oil Crops Biology, the Ministry of Agriculture, PRC Department of Genomics, Oil Crops Research Institute, Chinese Academy of Agricultural Sciences, China</p>

16.55-17.20 Keygene Workshop



Rapid Development Of Molecular Markers By Next-Generation Sequencing Linked To A Gene Conferring Phomopsis Stem Blight Disease Resistance For Marker-Assisted Selection In Lupin

CONFIRMED:

Huaan Yang, Molecular Geneticist, Department of Agriculture and Food (DAFWA), Australia

17.20-17.45 Keygene Workshop Continued

Comparison Of The Genomes Of Octoploid Strawberry (*Fragaria ×ananassa*) And Its Wild Species

De novo whole genome sequencing was performed for octoploid cultivated strawberry (*F. × ananassa*) and its wild species, *F. iinumae* (2X), *F. nubicola* (2X), *F. nipponica* (2X) and *F. orientalis* (4X) by using Illumina and Roche sequencing platforms. A vertical 'hybrid genome' was constructed in *F. × ananassa* by eliminating heterozygous bases on the genome instead of constructing chromosome specific alignments. Total length of the non-redundant sequences and N50 of the hybrid genome was 173,229,572 bp and 5,137bp, respectively. Genome structure of the hybrid genome was compared with the four wild species and previously published genome of *F. vesca*.

CONFIRMED:

Sachiko Isobe, Laboratory Head Applied Plant Genomics, Kazusa DNA Research Institute (KDRI), Japan

17.45-18.20 Keygene Workshop Continued

Next Generation Genome And Transcriptome Sequencing Approaches In Underutilised Crops - Title to be Confirmed

- (Bambara groundnut and winged bean) – Roche 454, DaT-seq and Mi-seq.
- Marker development (SSR, SNP), mapping, allele mining.

CONFIRMED:

Festo Massawe, Head of School of Biosciences (UNMC), Faculty of Science, University of Nottingham Malaysia Campus, Malaysia

18.20-18.55 Keygene Workshop Continued

Extreme Chromosome Rearrangements In Arabidopsis

- Haploid breeding technology based on centromere-mediated uniparental genome elimination represents the future of plant breeding. However, segregation errors during haploid induction often lead to genome instability and aneuploidy.
- Using next generation sequencing and bioinformatics analysis, biological insight can be gained by studying the genomes of aneuploid plants that result from faulty haploid induction. In some cases, extreme chromosomal shattering is observed.
- De novo assembly and reconstruction of the massive chromosome rearrangements reveal the underlying mechanisms behind complex genome rearrangements and hints at the crucial role of centromeres in genome evolution.

CONFIRMED:

Ek Han Tan, Postdoctoral Research Associate, Laboratory of Simon Chan, Department of Plant Biology, HHMI/GBMF, UC Davis, USA

Chairman's Closing Remarks and End of Day 1

Chairman's Closing Remarks and End of Day 1

18.55-20.00

Drinks Reception

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Agenda: Day Two – Tuesday 25th February 2014

08.40-09.10	Keynote Address Epigenetics – Title to be Confirmed CONFIRMED: Rob Martienssen, Professor and HHMI Investigator, Cold Spring Harbor Laboratory, USA	
09.10-09.40	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
	Track 1 - Plant Genomic Case Studies & Epigenetics, Methylation Research in Plants	Track 2 - Bioinformatics, Data Management & Analysis
09.40-10.05	Exploring Epigenetic Marks in Complex Crop Genomes <ul style="list-style-type: none">Epigenetic marks such as DNA cytosine methylation and histone proteins modifications alter chromatin structure and dynamics, providing considerable agility in terms of modulating gene expression, ontogeny, and response to the environment.Many plant developmental processes and crop agronomic traits are affected to some extent by stably inherited epigenetic modifications. With high levels of DNA methylation, complex crop genomes may have adopted a range of strategies that provide plasticity in terms of crop performance.High throughput sequencing enables us to determine the extent and distribution of epiallelic variation in crop genomes, and to understand the interaction with patterns of snRNA and transcriptional regulation. Such data may be integrated with number of analytical approaches including genetical genomics. CONFIRMED: Graham King, Director, Southern Cross Plant Science and Professor of Plant Genomics and Epigenetics, Southern Cross University, Australia	Rice Bioinformatics CONFIRMED: Nickolai Alexandrov, Senior Scientist, The International Rice Research Institute, The Philippines
10.05-10.30	Chromatin Readers And The Epigenetic Landscape In Arabidopsis Thaliana <ul style="list-style-type: none">Identification of SHH1 as a master regulator of siRNA production at genomic loci actively targeted by the RNA-directed DNA methylation pathwayCharacterization of the SHH1 sawadee domain as a novel chromatin binding motif with a specificity for repressive H3K9me modifications.Demonstration that SHH1, and more specifically its sawadee domain, are required for the chromatin association of RNA polymerase IV--the polymearse responsible for initiating siRNA biogenesis. CONFIRMED: Julie Law, Assistant Professor, Plant Molecular and Cellular Biology Laboratory, Salk Institute, USA	Characterising Complex Crop Genomes Using Next Generation DNA Sequencing We have developed novel analysis pipelines for the assembly, validation and characterisation of complex crop genomes and applied these to Brassica, chickpea and wheat. Using combinations of isolated chromosome sequencing and skim genotyping by sequencing of populations, we have validated genome assemblies, identified structural variations and discovered candidate genes for important agronomic traits CONFIRMED: Dave Edwards, Principal Research Fellow, School of Agriculture and Food Sciences, University of Queensland, Australia
10.30-11.15	Morning Refreshments Poster Presentation Sessions	
11.15-11.45	Solution Provider Presentation High Efficiency Long Insert Mate Pair Library Preparation for NGS Platforms Sponsored by 	Solution Provider Presentation For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
11.45-12.10	Cell Type Specific DNA Methylomes Of The Arabidopsis Root Within the Arabidopsis genome, DNA methylation plays a critical role in suppression of transposable elements, while its role in cell type specific transcriptional regulation remains poorly understood. Most comprehensive studies of this modification have analyzed heterogeneous populations of cells within complex tissues, complicating the characterization of cell-type specific DNA methylation patterns. Here we present whole-genome single-base resolution DNA methylomes, in addition to mRNA and smRNA transcriptomes, for several distinct cell types isolated from Arabidopsis root tips. We identified numerous loci within the genome that were differentially methylated between cell types, in addition to extreme hypermethylation of transposable elements in a subset of the cell types analyzed. Overall, these maps provide new insights into the modulation DNA methylation between distinct cell types within complex plant tissues. CONFIRMED: Ryan Lister, Professor/ARC Future Fellow, Plant Energy Biology ARC CoE, School of Chemistry and Biochemistry, The University of Western Australia	Association And Linkage Mapping Methodology Improve the methodology in the utilization of NGS. One is to adopt new methods in statistics and the other is to use techniques in computer science CONFIRMED: Yuan-Ming Zhang, Professor of Statistical Genomics, State Key Lab. of Crop Genetics and Germplasm Enhancement, Nanjing Agricultural University, China

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12.10-12.35	<p>Tissue Specific Hormone Response And Epigenome Reprogramming Ethylene regulates many aspects of the plant life cycle and its biosynthesis and signaling pathways have been well characterized. However, little is known about how ethylene causes these distinct physiological responses in different tissues or even in the same tissue at different developmental stages. We adopted a systematic approach to investigate how ethylene signaling changes during tomato plant growth and development. We first compared ethylene responsive genes in different tissues using RNA-seq, identified the ethylene transcription factor binding sites using ChIP-Seq and profile the tomato methylome at different tissues using BS-Seq. We found that transcription factor bindings are not constant during development, and their tissue specific activities are associated with specific DNA methylation changes, suggesting a possible role of epigenetic factors in shaping tissue-specific hormone signaling network.</p> <p>CONFIRMED: Silin Zhong, Assistant Professor, School of Life Sciences, The Chinese University of Hong Kong</p>	<p>International Consortium of Rice Insertional Mutagenesis and the Utilization in Taiwan</p> <ul style="list-style-type: none"> • Introduction of the current international resources, including T-DNA, AC/Ds, En/Spm, Tos17, nDART/aDART, and RNAi. • The coverage and limiting factors • Creation of new and improved resources <p>CONFIRMED: Yue-le Hsing Distinguished Research Professor, Institute of Plant and Microbial Biology, Academia Sinica, Taipei, Taiwan</p>
12.35-13.00	<p>A Tool for Making Epigenetics Serve Genetics: Harnessing the Variation in Trait Expression Induced in Response to Virus Infections of Cereal Hosts</p> <ul style="list-style-type: none"> • Disease-resistant lines can be derived in direct descent from susceptible progenitors • Genetic resources in existing adapted, elite germplasm may be richer than currently realized • Tools for pursuing epigenetics-driven crop improvement are simple, safe and available to programs with modest means <p>CONFIRMED: Steve Haber, Research Scientist, Agriculture and Agri-Food Canada</p>	<p>Panel Discussion: Data Analysis, Management and Storage Strategies – Title to be Confirmed</p> <p>CONFIRMED: Charles Chen, Scientist, Statistical Geneticist for Seeds of Discovery, International Maize and Wheat Improvement Center (CIMMYT) Mexico Invitation to: Senior Representative x 3</p>
13.00-14.00	<p>Lunch</p>	<p>Lunch</p>
	<p>Track 1 - Biofuels</p>	<p>Track 2 - Bioinformatics, Data Management & Analysis</p>
14.00-14.25	<p>Algae Epigenetics – Title to be Confirmed</p> <p>CONFIRMED: Chia-Lin Wei, Group Leader - Sequencing Technologies Group, Joint Genome Institute (JGI), USA</p>	<p>Bioinformatics And Data Management On Crops For The Semi-Arid Tropics</p> <p>CONFIRMED: Trushar Shah, Bioinformatics Scientist, ICRISAT, India</p>
14.25-14.50	<p>Epigenetics – Palm Oil - Title to be Confirmed</p> <p>CONFIRMED: Meilina Ong Abdullah, Breeding and Tissue Culture Unit, The Advanced Biotechnology and Breeding Centre, Malaysian Palm Oil Board (MPOB) Malaysia</p>	<p>Title to be Confirmed</p> <p>CONFIRMED: Nandini Krishnamurthy, Computational Biologist, DuPont Pioneer, India</p>
14.50-15.15	<p>Identification and characterisation of candidate blackleg resistance genes in Brassica napus using next generation sequencing Recent advances in next generation sequencing (NGS) enable much quicker identification of candidate genes for traits of interest. Here we demonstrate this with the identification of candidate disease resistance genes from Brassica napus for its most devastating fungal pathogen, <i>Leptosphaeria maculans</i> (blackleg fungus). Analysis of the complete genome sequence of the diploid progenitor of <i>B. napus</i>: <i>B. rapa</i>, identified candidate CC-NBS-LRR and TIR-NBS-LRR family genes implicated in disease response, several of which were clustered around a region syntenic with major loci for blackleg resistance in <i>B. napus</i>. Molecular analyses of four of these candidate genes, Rlm1, 2, 3 and 4 using Next generation sequencing and ultra-high throughput SNP genotyping in diverse cultivars and segregating populations, along with initial validation, will be presented.</p> <p>CONFIRMED: Jacqueline Batley, Associate Professor, ARC QEII Research Fellow - School of Agriculture & Food Sciences, Faculty of Science, The University of Queensland, Australia</p>	<p>Genomic Prediction In Maize And Wheat Breeding Programs</p> <ul style="list-style-type: none"> • 50% of the breeding values is due to parent average component (best prediction at birth is the average of two parents breeding value). • Another 50% of the breeding value is due to Mendelian sampling component (sampling of parents genes). • Response to selection is driven by the accuracy of and time taken to estimate of Mendelian sampling term. • Several prediction results using different statistical models using real data are presented. <p>CONFIRMED: José Crossa, Distinguished Scientist, Biometrics and Statistics Unit, International Wheat and Maize Improvement Centre, CIMMYT, Mexico</p>
15.15-15.40	<p>Miscanthus Case Study- Title to be Confirmed</p> <p>CONFIRMED: Cuixia Chen, Professor, Shandong Agriculture University, China</p>	<p>Regulatory Modules Controlling Maize Inflorescence Architecture Inflorescences of maize and other grasses such as wheat, rice and sorghum, have complex architectures, which limits direct translation from eudicot models. Here we report the most comprehensive systems-level analysis of inflorescence development in a higher crop plant, which can be directly leveraged for targeted crop improvement. Significant highlights include: 1) A novel use of mutant alleles to couple dynamic changes in morphology with spatiotemporal expression signatures, and 2) The first report of genome-wide occupancy for a grass-specific transcription factor, RAMOSA1, which is encoded by a key maize domestication locus, and its regulation of target genes based on spatiotemporal context.</p> <p>CONFIRMED: Dave Jackson, Professor, Cold Spring Harbor Laboratory, USA</p>

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	Afternoon Refreshments Poster Presentation Sessions	Afternoon Refreshments Poster Presentation Sessions
15.40-16.05		
16.05-16.30	Soybean Case Study- Title to be Confirmed RESERVED: Matthew Hudson, Associate Professor, Department of Crop Sciences, University of Illinois, USA	Comparative Transcriptomics Of Developing Maize And Rice Embryonic Leaves To understand the differences between C4 and C3 plant leaf development, we have studied the transcriptional dynamics of maize (a C4 model plant) and rice (a C3 model plant) embryonic leaves during seed germination, using the Next Generation Sequencing technology. We have obtained time course transcriptomes of both maize and rice embryonic leaves from dry seeds to 72 hours post imbibition. Comparative bioinformatics analyses of these transcriptomes have shed much light on the developmental differences between the two types of leaves and also revealed genes involved bundle sheath and vein development. We have also obtained transcriptomes of bundle sheath cells and mesophyll cells of newly mature maize leaves and the data revealed functional and regulatory differentiation between the two types of cell. The data and some detailed results will be presented in the talk. CONFIRMED: Wen-Hsiung Li, Director and Distinguished Research Fellow, Biodiversity Research Center, Academia Sinica, Taiwan
16.30-16.55	Nitrogen-Responsive Long Noncoding RNAs In Maize <ul style="list-style-type: none"> • Long noncoding RNAs in maize genome • Coordinated transcription of long noncoding RNAs responsive to nitrogen • Transcription regulation in trans and cis CONFIRMED: Han Zhao, Professor of Biology and Biotechnology, Institute of Biotechnology Jiangsu, Academy of Agricultural Sciences, China	Chairman's Closing Remarks and Conference Close

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For more information please contact Nick Noakes, Marketing Director, Global Engage Ltd.

nnoakes@globalengage.co.uk

+44 (0) 1865 849841

How To Register

Phone: +44 (0) 1865 849841

Fax: +44 (0) 1865 598989

Email: info@globalengage.co.uk

Web: www.globalengage.co.uk/events

Mail: Global Engage,
Suite B, The Kidlington Centre,
Kidlington, Oxfordshire, OX5 2DL
United Kingdom

QR:



Delegate	One	Two	Three (this place is free)
Mr, Mrs, Ms, Dr, Prof:			
First Name			
Family Name			
Position			
Email			

Contact

Organization

Address

Cell:

Tel:

Email:

Conference Fees

Industry Delegate

\$1299

Discount Code:

Academic Delegate

\$699

Discount Code:

Payment Details

Total: \$ Cheques should be made out to: Global Engage Ltd. Please tick here to receive an invoice in advance of payment

Bank transfer * IBAN: GB17 MIDL 40353462665360 Credit Card: VISA AMEX MASTERCARD

Card No: 3 digit security code: Expiry Date:

VENUE

www.globalengage.co.uk/pgcasia/venue.html

ACCOMMODATION

Hotel accommodation is not included in your fee. To reserve a room at the conference hotel, please send an email to Scott Taylor at scott@globalengage.co.uk.

OTHER DETAILS:

Full Terms & Conditions are set out at www.globalengage.co.uk/terms.html

THE DELEGATE BOOKING FEE INCLUDES:

All meals and refreshments throughout the conference day, conference presentations, open workshop and general panel sessions and networking/social events, conference and speaker notes.

QUESTIONNAIRE:

Each Delegate must complete and return a "Personal and Company Details Questionnaire" issued by the Organiser on receipt of the Delegate Booking Form.

CONFIRMATION:

If you have not received confirmation of your booking prior to the event, please call Global Engage on +44 (0) 1865 849841. Your delegate place is not confirmed until payment is acknowledged. Payment must be received before the conference date. If payment has not been received before the conference date Global Engage reserves the right to ask for a credit or debit card guarantee of payment when you arrive at the conference venue.

*BANK TRANSFER PAYMENTS:

When paying by Bank Transfers quote this reference: PGCA

(Please ensure ALL bank charges are met by your organisation)

CANCELLATIONS/SUBSTITUTIONS:

Delegates cancelling more than one calendar month prior to event receive a full refund, one calendar month or less prior to event there is no refund. A substitute delegate of equal standing can be nominated within a week of the event and must be approved by the Organiser in advance in order to avoid cancellation charges.

ORDER CONFERENCE DOCUMENTATION:

I cannot attend the conference but wish to buy the event documentation pack, which includes the speakers presentations
Full documentation costs \$199.

To order, complete the registration form and method of payment. Payment must be received before the documentation and password can be despatched.

PROGRAMME CHANGES:

Global Engage reserves the right to make any necessary alterations/changes to the programme. Personal Data is gathered in accordance with the Data Protection Act 1998.

If you do not wish to receive promotional material from Global Engage, please tick here

If you do not wish to receive promotional material from the Event Sponsors, please tick here

If you do not wish to receive promotional material from any other 3rd party, please tick here

Please return this form with the address and customer code, clearly visible if you wish us to remove your records from our database.