The 2nd Plant Genomics Congress

12-13 May 2014

The European Round of the Global Engage NGS Series

London, UK

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 2nd Plant Genomics Congress, which will be held on May 12-13, 2014 in London, England. The successful event which attracted over 260 attendees last year is the sister meeting to both the US and Asian Plant Genomics Congresses which take place each year in September and February respectively.

Attracting experts working in all areas of 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 in aspects such as molecular marker development, crop/ trait improvement, breeding, hybridization, conservation, evolution studies and pathology. Presentations concentrate on, but are not limited to plant, crop and forestry research ranging from wheat, barley, maize and rice to potato, tomato, arabidopsis, spruce and ash in order to attract delegates across the Europe 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. Many plants 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 / breeding etc. 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 a 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, expert led case study presentations and interactive Q&A panel discussions examining topics through six separate tracks covering:

Day 1 Stream 1 – NGS/Genomic Technologies for Plant Research
- NGS Platform comparison / Best practice guidelines
- Future uses on new generation technologies
- NGS protocols / standardisation
- Genome assembly
- Sample preparation technology
- Genotyping by sequencing
- Genotype and phenotype connections - Genomics of domestication
  - High throughput phenotyping technology
  - Selective sweep mapping
- High resolution scanning
- Plant genotyping, SNP discovery, QTL mapping, alternative splicing, marker assisted selection
- Use of genomic data for candidate genes
- Mapping multiple traits simultaneously
- Application of TALENs and CRISPRs in plants

Day 1 Stream 2 - Plant Genomic Case Studies (Cereals)
- Applications of NGS in plant research / Using NGS to enhance:-
  - Molecular marker development,
  - Crop / trait improvement –e.g. plant stress resilience
  - Breeding e.g. novel breeding techniques
  - Hybridization,
  - Evolution studies e.g. evo devo biology, polyploid studies, transposable elements
  - Pathology

Day 1 Stream 3 – RNA Seq Case Studies
- RNA profiling by sequencing
- Plant Genomics Case Studies using RNA seq
  - miRNA

Day 2 Stream 1 - Bioinformatics, Data Management & Analysis & Forestry Research Case Studies
- Bioinformatic analysis and challenges
- Bioinformatics from a biologist's perspective
- Gene network studies
  - Identifying novel functional genes /networks / knowledge from data
- NGS data analysis
- Gene expression analysis
- Genomic selection / technologies
- Sequencing pipelines and assembly
- Improving error rates
- Cloud computing and storage solutions
- Panel Discussion - NGS data analysis &management
- Forestry Research Case Studies

Day 2 Stream 2 – Epigenetic / DNA Methylation Case Studies & Genomic Evolution Case Studies
- Case studies using:-
  - Epigenetics
  - DNA methylation
- Genomic Evolution Case Studies

Day 2 Stream 3 - Plant Genomic Case Studies
- Applications of next-generation sequencing in plant research
- Genome project updates
- Metagenomics –Microbe interaction / root systems

Plant Genomics Series

Plant Genomics Asia – February 24-25, 2014, Kuala Lumpur, Malaysia http://www.globalengage.co.uk/plantgenomicsasia.html
2nd Plant Genomics Europe – May 12-13, 2014 London, UK   http://www.globalengage.co.uk/plantgenomics.html
2nd Plant Genomics USA – September 11-12, 2014, St Louis, USA   http://www.globalengage.co.uk/plantgenomicsusa.html

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

2nd Plant Genomics Congress - Confirmed Speakers

- Richard Michelmore, Professor and Director, The Genome Center, University of California, Davis, USA
- Sophien Kamoun, Senior Scientist and Head, Sainsbury Laboratory, UK
- Cristobel Uauy, Project Leader, Department of Crop Genetics, John Innes Centre, UK
- Andrew Leitch, Professor of Plant Genetics, School of Biological and Chemical Sciences, Queen Mary University of London, UK
- Frederic Choulet, Research Scientist, INRA Clermont-Ferrand, France
- Andreas Wachter, Head Emmy Noether Research Group, Center for Plant Molecular Biology, Universität Tübingen, Germany
- Dirk Walther, Group Leader Central Infrastructure Group Bioinformatics, Max Planck Institute for Molecular Plant Physiology, Germany
- Riccardo Velasco, Head of Genomics and Biology of Fruit Crop Department, The Research and Innovation Centre (CRI), Fondazione Edmund Mach, Italy
- Martin Trick, Senior Scientist, Department of Computational and Systems Biology, John Innes Centre, UK
- Ian Bancroft, CNAP Chair of Plant Genomics, Department of Biology, University of York, UK
- Dan Maclean, Head of Bioinformatics, Sainsbury Laboratory, UK
- Stéphane Hacquard, Research Associate, Schulze-Lefert Group, Max Plank Institute for Plant Breeding, Germany
- Ales Pecinka, Group Leader, Max Planck Institute for Plant Breeding, Germany
- Jaroslav Dolezel, Scientific Director, Centre of Plant Structural and Functional Genomics, Institute of Experimental Botany, Olomouc, Czech Republic
- Ulrich Schurr, Professor, IBG-2: Plant Sciences, Forschungszentrum Jülich, Germany
- Giovanni Giuliano, Head of the Green Biotechnology Laboratory, ENEA, Casaccia Research Center, Italy
- Arthur Korte, Postdoctoral Fellow, Nordborg Group, Gregor Mendel Institute, Austria
- Saskia van Wees, Associate Professor, Plant-Microbe Interactions, Department of Biology, Faculty of Science, Utrecht University, The Netherlands
- Sandra Smit, Bioinformatics Group, Wageningen University, The Netherlands
- Serena Varotto, Professor, Laboratory of Plant Genetics and Breeding of the Department of Environmental Agronomy and Crop Productions (DAAPV), University of Padova, Italy
- Dan Bolser, Ensembl Plants Project Leader, European Bioinformatics Institute, UK
- Nathaniel Street, Assistant Professor, Umeå Plant Science Centre, Sweden
- Jürgen Logemann, Managing Director, Global Head Technology Acquisition and Innovation Management, BASF Plant Science, Germany
- Andy Greenland, Professor, Research Director, National Institute of Agricultural Botany (NIAB), UK
- Søren K. Rasmussen, Professor in Molecular Plant Breeding, Department of Plant and Environmental Sciences, University of Copenhagen, Denmark
- Glenn Bryan, Group Leader, Potato Genetics and Breeding Group, The James Hutton Institute, UK
- Scott Jackson, Georgia Research Alliance Eminent Scholar and Professor, Center for Applied Genetic Technologies, University of Georgia, USA
- Henrik Toft Simonsen, Associate Professor, Department of Plant and Environmental Sciences, Faculty of Science, University of Copenhagen, Denmark
- James Birchler, Curators' Professor Biological Sciences, University of Missouri, USA
- Sachin Rustgi, Assistant Research Professor, Department of Crop & Soil Sciences, Washington State University, USA
- Dirk Hays, Associate Professor and Chair Molecular and Environmental Plant Sciences, Texas A&M University, USA
- Venu Kalavacharla, Associate Professor, Molecular Genetics & EpiGenomics, Department of Agriculture & Natural Resources, Director, Center for Integrated Biological & Environmental Research (CIBER), Delaware State University, USA
- Burkhard Steuernagel , Research Associate, 2Blades Group, The Sainsbury Laboratory, UK
- Roosa Laitinen, Research Group Leader, Molecular Mechanisms of Plant Adaptation, Max Planck Institute for Plant Physiology, Germany
- Federico Valverde, PI. Molecular Plant Development and Metabolism Group, Institute for Plant Biochemistry and Photosynthesis, CSIC – University of Seville, Spain
- Elvira Hörandl, Professor for Systematics, Biodiversity and Evolution of Plants, University of Göttingen, Germany
- Hong-Qing Ling, Professor & Director of the State Key Laboratory of Plant Cell and Chromosome Engineering, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China
- Tamas Dalmay, Professor of RNA Biology, School of Biological Sciences, University of East Anglia, Norwich, UK
- Peter Wenzl, Project Lead, Seeds of Discovery (SeeD) Initiative, CIMMYT, Mexico
- Jonathan Jones, Professor & Senior Scientist, Sainsbury Laboratory, UK
- Ian Small, Director, ARC Centre of Excellence in Plant Energy Biology, The University of Western Australia, Perth, Australia
- Chengzhi Liang, Professor, Director of Genomics and Bioinformatics Facility, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China
- Jose Gutierrez-Marcos, Associate Professor, University of Warwick, UK
- Rowan Mitchell, Joint Leader, Cell Wall Research Group, Rothamsted Research, UK
- John MacKay, Professor of Forestry, Université Laval Wood Professor of Forest Science, University of Oxford, SmarTForests, Project co-director, UK
- Eric Schranz, Professor of Biosystematics, Wageningen University, The Netherlands
- Hélène Berges, Director of the French Plant Genomic Resource Center, INRA – CNRGV, France
- Christian Fankhauser, Professor, Center for Integrative Genomics, University of Lausanne, Switzerland
- Keita Suwabe, Associate Professor, Laboratory of Plant Molecular Genetics and Breeding, Graduate School of Bioresources, Mie University, Japan
- Gerard Bishop, Principal Research Scientist, East Malling Research, UK
- Ewen Mullins, Senior Research Officer, Crop Science Department, Teagasc Crops, Environment and Land Use Programme, Ireland
- Steve Hanley, Rothamsted Research, UK
- Patrick Zhao, Associate Professor of Bioinformatics, Samuel Roberts Noble Foundation, USA
- Gail Taylor, Professor of Plant Biology, Southampton University, UK
- Edwin van der Vossen, VP Field Crops, Keygene
- Senior Representative, Neogen/GeneSeek
- Senior Representative, Lucigen
- Senior Representative, Cergentis
- Senior Representative, Life Technologies

Reserved Speakers

- Herman van Eck, Assistant Professor, Laboratory for Plant Breeding, Wageningen University, The Netherlands
- Bas Zwaan, Professor, Laboratory of Genetics, Wageningen University, The Netherlands

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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:** **Genomics and Strategies for Resistance Gene Deployment (So many genes…. & so little time….)** • A review of current and emerging technologies for sequencing and high throughput genotyping • How these are revolutionizing our understanding of plant-pathogen interactions • Characterization of downy mildew pathogens • Molecular genetic dissection of the lettuce-*Bremia lactucae* interaction • Implications for resistance gene deployment to provide more durable disease resistance CONFIRMED: **Richard Michelmore, Professor and Director, The Genome Center, University of California, Davis, USA**

09.35-10.05	**Solution Provider Presentation** **Sponsored by Life Technologies**	**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk

10.05-10.10	**Stream Chair**	**Stream Chair**	**Stream Chair**
	NGS/ Genomic Technologies for Plant Research	**Plant Genomic Case Studies - Cereals**	**RNA Seq Case Studies**
10.10-10.35	**Plant Genome Editing Made Easy** Targeted genome engineering (also known as genome editing) has emerged as an alternative to classical plant breeding and transgenic (GMO) methods to improve crop plants. Until recently, available tools for introducing site-specific double strand DNA breaks were restricted to zinc finger nucleases (ZFNs) and TAL effector nucleases (TALENs). However, these technologies have not been widely adopted by the plant research community due to complicated design and laborious assembly of specific DNA binding proteins for each target gene. Recently, an easier method has emerged based on the bacterial type II CRISPR (clustered regularly interspaced short palindromic repeats)/Cas (CRISPR-associated) immune system. The CRISPR/Cas system allows targeted cleavage of genomic DNA guided by a customizable small noncoding RNA, resulting in gene modifications by both non-homologous end joining (NHEJ) and homology-directed repair (HDR) mechanisms. In this talk I will summarize and discuss recent applications of the CRISPR/Cas technology in plants. CONFIRMED: **Sophien Kamoun, Senior Scientist and Head, Sainsbury Laboratory, UK**	**Unravelling the Genetics of Yield in Polyploid Wheat** CONFIRMED: **Cristobel Uauy, Project Leader, Department of Crop Genetics, John Innes Centre, UK**	**RNA-seq provides novel insight into the regulation and implications of alternative splicing in Arabidopsis** Alternative splicing (AS) generates multiple transcript variants from one type of precursor mRNA and plays a pivotal role in gene expression control. AS has been found to be widespread in higher eukaryotes, however, many questions about the regulation and functions of this process remain to be answered. The enormous advances in next generation sequencing have provided the basis to address these questions systematically and on a transcriptome-wide level. Here I will present two case studies using RNA-seq, which analyzed the regulation and functional implications of AS in Arabidopsis thaliana. First, the role of Polypyrimidine tract-binding proteins as a component of the plant splicing regulatory code was investigated. Second, transcriptome-wide coupling of AS and the RNA surveillance pathway nonsense-mediated decay (NMD) was analyzed. These and future studies will help to explore the enormous regulatory potential of AS in plant development and responses. CONFIRMED: **Andreas Wachter, Head Emmy Noether Research Group, Center for Plant Molecular Biology, Universität Tübingen**

10.35-11.00	**NGS-Based Linkage Map Construction and Gene Mapping in Plants**	**Plant Chromosome Genomics** Isolation of individual chromosomes by flow sorting provides opportunities to study plant genomes in more detail and more effectively. Reduction in DNA sample complexity simplifies genome mapping and sequence assembly. This is particularly attractive when dealing with large and polyploid genomes. Chromosome-specific BAC libraries facilitate gene cloning and construction of physical maps as demonstrated in hexaploid wheat. In non-sequenced species, chromosome shotgun sequencing by NGS identifies a majority of genes and facilitates their ordering along chromosomes. In sequenced genomes, chromosome sequencing permits validation of genome assemblies at chromosomal level. Moreover, suitability of isolated chromosomes for mapping on nanochannel arrays has been demonstrated recently.	**Insights into terpenoid biosynthesis in Apiaceae through transcriptome analysis of *Thapsia* L.** *Thapsia* species (Apiaceae) produces irregular and regular sesquiterpenoids with thapsane and guaiene carbon skeletons, as also found in other Apiaceae species (see figure for biosynthesis). Transcriptomic analysis utilizing both 454 and Illumina next-generation sequencing enabled the identification several novel genes involved in the biosynthesis of terpenoids in *Thapsia*. So far we have identified and characterized 5 terpene synthases, and we have identified at least 4 four more in just two species, along with more than 30 cytochromes P450 with the CYP71 clade, where several of them are in new sub-clades. These transcriptome data provide the foundation for current and future research into the molecular basis for terpenoid biosynthesis in *Thapsia* and on the evolution of terpenoids in Apiaceae.
	CONFIRMED: **Chengzhi Liang, Professor, Director of Genomics and Bioinformatics Facility, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China**	CONFIRMED: **Jaroslav Dolezel, Scientific Director, Centre of Plant Structural and Functional Genomics, Institute of Experimental Botany, Olomouc, Czech Republic**	CONFIRMED: **Henrik Toft Simonsen, Associate Professor Department of Plant and Environmental Sciences Faculty of Sciences, University of Copenhagen, Denmark**
11.00-12.00	**Morning Refreshments** **Poster Presentation Sessions**		
12.00-12.30	**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk	**Solution Provider Presentation** **Title to be Confirmed** CONFIRMED: **Edwin van der Vossen, VP Field Crops, Keygene**	
12.30-13.00	**Panel Discussion – Title to be Confirmed**	**Harnessing next generation sequencing for crop improvement** Recent advances in sequencing technology and associated computational methods have brought greater analytical power to bear on crop plants, whose genomes are often complex and polyploid, enabling candidates for genes controlling key agronomic characters to be rapidly identified. The development of such techniques in oilseed rape and wheat will be presented, together with their application to other systems, along with a look forward to how we might best use the emerging sequence data from bread wheat	**COMET: COMparative Expression analysis of Transposable elements using RNA-sequencing data** • Transposable elements are frequent and potentially mobile components of eukaryotic genomes • Analyzing transposon expression using next-generation sequencing is challenging due to read multi-mapping, mapping across families and different transposon sizes and copy numbers between populations and species • We developed the method for intra- and inter-specific expression analysis of transposable element using RNA-sequencing data
	invitation to – **Senior Representatives x 4**	CONFIRMED: **Martin Trick, Senior Scientist, Dept of Computational and Systems Biology, John Innes Centre, UK**	CONFIRMED: **Ales Pecinka, Group Leader, Max Planck Institute for Plant Breeding, Germany**
13.00-14.00	**Lunch**		

Time			
14.00-14.25	**Overcoming the phenotyping bottleneck – networks and implementations:** • Phenotyping is increasingly a bottleneck for knowledge-oriented research as well as for breeding • Significant phenotyping concepts are developed in cross-disciplinary approaches integrating the biological question with sensor development, automation and informatics • Networks of major phenotyping centres provide options to overcome the phenotyping bottleneck CONFIRMED: **Ulrich Schurr, Professor, IBG-2: Plant Sciences, Forschungszentrum Jülich, Germany**	**A Reference Sequence of Wheat Chromosome 3B** We produced the first reference sequence of the hexaploid wheat chromosome 3B which represents 774 Mb carrying 7264 protein-coding genes and 85% of transposable elements. Sequence comparisons with related grasses revealed that wheat has recently undergone massive inter- and intra-chromosomal gene duplications. In addition, distribution of structural and functional features highlighted a striking compartmentalization in which the chromosomal extremities concentrate most of recombination events and genes originating from recent duplications, expressed in specific conditions, and with functions related to adaptation. CONFIRMED: **Frederic Choulet, Research Scientist, INRA Clermont-Ferrand, France**	**RNA-seq based transcriptomics and computational modeling of hormone-regulated plant immune responses** CONFIRMED: **Saskia van Wees, Associate Professor, Plant-Microbe Interactions, Department of Biology, Faculty of Science, Utrecht University, The Netherlands**
14.25-14.50	**High throughput phenotyping in arabidopsis** • Harness the ever increasing genomics/ transcriptomics data. • Genome-wide gene expression and/or ChiP analysis (for transcription factors) CONFIRMED: **Christian Fankhauser, Professor, Center for Integrative Genomics, University of Lausanne, Switzerland**	**Wheat A genome sequencing and physical mapping** CONFIRMED: **Hong-Qing Ling, Professor & Director of the State Key Laboratory of Plant Cell and Chromosome Engineering, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, China**	**ncRNA in maize stress response** CONFIRMED: **Serena Varotto, Professor, Laboratory of Plant Genetics and Breeding of the Department of Environmental Agronomy and Crop Productions (DAAPV), University of Padova, Italy**
14.50-15.15	**Use of high throughput remote sensing tools to introgress global climate change adaptive traits in wheat and sorghum.** • High throughput remote sensing tools such as ground penetrating radar, terrestrial laser scanning and spectral radiometry are being used to phenotype, and genotype such adaptive traits as ideal root and above ground biomass architecture, and increased leaf epicuticular wax or trichome density to name a few. • Progress in the utilization of these tools in field screening platforms and identification of regulating genetic loci will be discussed. CONFIRMED: **Dirk Hays, Associate Professor and Chair Molecular and Environmental Plant Sciences, Texas A&M University, USA**	**Title to be Confirmed** CONFIRMED: **Andy Greenland, Professor, Research Director, National Institute of Agricultural Botany (NIAB), UK**	**The effect of ligation bias on profiling plant small RNAs** • cDNA libraries of small RNAs for NGS are biased and this is based on the ability of individual small RNAs to form stable secondary structures with the adapters • Adding degenerated nucleotides to the adapters reduce the ligation bias by allowing different sequences to form a stable structure with the adapters • The impact of this ligation bias on sequencing plant small RNAs will be presented CONFIRMED: **Tamas Dalmay, Professor of RNA Biology, School of Biological Sciences, University of East Anglia, Norwich, UK**
15.15-15.45	**Solution Provider Presentation** **Sponsored by** GENESEEK Europe a Neogen Company		**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk

15.45-16.00	**Solution Provider Presentation** **Title to be Confirmed** **Sponsored by Cergentis** ![Cergentis logo] CERGENTIS COMPLETE GENE SEQUENCING	**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
16.00-16.50	**Afternoon Refreshments** **Poster Presentation Sessions**	
16.50-17.15	**Title to be Confirmed** CONFIRMED: **Jonathan Jones, Professor & Senior Scientist, Sainsbury Laboratory, UK**	**Seeds of Discovery (SeeD): Unlocking the genetic potential of maize and wheat to accelerate the development of high-yielding, climate-ready cultivars** The Seeds of Discovery (SeeD) project (http://seedsofdiscovery.org) strives to unlock the value of genetic resources by assisting breeders to develop better cultivars more quickly. We are using the DArTseq, and to a less degree the Cornell-University genotyping-by-sequencing (GbS) platforms to characterize 160,000 wheat and 40,000 maize accessions in the genebanks at CIMMYT and partner institutions. We link molecular data to breeding-relevant traits by evaluating, under field conditions, accession subsets for selected traits, such as heat/drought tolerance, P and N efficiency, grain-quality characters, and resistance to diseases and pests. Genetically diverse 'donor accessions' with favorable traits are used to develop 'bridging germplasm' harboring novel, favorable alleles in breeder-ready genetic backgrounds, to facilitate the mobilization of novel variation into ongoing breeding programs. CONFIRMED: **Peter Wenzl, Project Lead, Seeds of Discovery (SeeD) Initiative, CIMMYT, Mexico**	**Exploiting wheat RNA Seq to understand cell wall synthesis in grasses** CONFIRMED: **Rowan Mitchell, Joint Leader, Cell Wall Research Group, Rothamsted Research, UK**
17.15-17.40	**Innovation Yields Results** CONFIRMED: **Jürgen Logemann, Managing Director, Global Head Technology Acquisition and Innovation Management, BASF Plant Science, Germany**	**Gene-discovery by genome-wide association scan of quality traits in cereals** - grain quality; - biomass improvement to reduce recalcitrance - nutrient use efficiency CONFIRMED: **Søren K. Rasmussen, Professor in Molecular Plant Breeding, Department of Plant and Environmental Sciences, University of Copenhagen, Denmark**	**Using RNA-seq and a periclinal chimera to detect layer specific expression in plants** We have shown how it is possible to use a tomato periclinal chimera that has the epidermal L1 layer derived from *Solanum Pennellii* and the internal tissues from *Solanum Lycopersicum* to identify those genes that are preferentially expressed in the L1 or L2/L3 layers. This is based on RNA-seq, read-mapping and SNP detection. From the 13,000 genes expressed in the samples analysed we identified 382 genes that are preferentially expressed in L1 tissues and 1195 genes in L2/L3 tissues. Gene ontology analysis indicates many of the L1 genes are involved in cutin and wax biosynthesis whereas L2/L3 genes are involved in chloroplastic processes. CONFIRMED: **Gerard Bishop, Principal Research Scientist, East Malling Research, UK**

17.40-18.05	**GWAS**	**Genomic analysis of the transposable element structural diversity between different maize lines, using BAC libraries approach and NGS.**	**Cell type-specific transcriptome of stigmatic papilla cells from a combination of laser microdissection and Next Generation Sequencing** In plant reproduction, pollination is the initial key process in bringing together the male and female gametophytes. It consists of many sequential processes, including adhesion of pollen grains onto the surface of stigmatic papilla cells, foot formation to strengthen pollen-stigma interaction, pollen hydration and germination, and pollen tube elongation. To understand the molecular systems of pollination, from three representative species of Brassicaceae (Arabidopsis thaliana, A. halleri and Brassica rapa), stigmatic papilla cells were isolated precisely by laser microdissection and cell type-specific gene expression in papilla cells was determined by the SOLiD system. This study provides fundamental biological knowledge to dissect the molecular mechanisms of pollination in papilla cells and will shed light on our understanding of plant reproduction mechanisms.
	CONFIRMED: **Arthur Korte, Postdoctoral Fellow, Nordborg Group, Gregor Mendel Institute, Austria**	CONFIRMED: **Hélène Berges, Director of the French Plant Genomic Resource Center, INRA – CNRGV, France**	CONFIRMED: **Keita Suwabe, Associate Professor, Laboratory of Plant Molecular Genetics and Breeding, Graduate School of Bioresources, Mie University, Japan**
18.05	**Chair's closing remarks and End of Day 1**		
18.05-19.05	**Drinks Reception**		

2nd Plant Genomics Congress Europe

UTILIZING NEXT GENERATION SEQUENCING AS A TOOL FOR PROGRESSING PLANT RESEARCH

Day 2 – Tuesday, May 13, 2014, London

	Morning Coffee	
	Stream Chair	
08.30-09.00	**Keynote Address:** **How evolutionary theory can guide plant research** RESERVED: **Bas Zwaan, Professor, Laboratory of Genetics, Wageningen University, The Netherlands**	
09.00-09.30	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

09.30-09.35	Stream Chair	Stream Chair	Stream Chair
	Bioinformatics, Data Management & Analysis	**Epigenetic / DNA Methylation Case Studies**	**Plant Genomic Case Studies**
09.35-10.00	**Towards understanding regulatory processes in plants utilizing sequence variation information** CONFIRMED: **Dirk Walther, Group Leader Central Infrastructure Group Bioinformatics, Max Planck Institute for Molecular Plant Physiology, Germany**	**Combining ChIP-seq, RNA-seq, and smRNA-seq approaches to understand the epigenetics of biotic and abiotic stresses, as well as developmental regulation in crop plants** CONFIRMED: **Venu Kalavacharla, Associate Professor, Molecular Genetics & EpiGenomics, Department of Agriculture & Natural Resources, Director, Center for Integrated Biological & Environmental Research (CIBER), Delaware State University, USA**	**Developing a modern potato genetics and genomics programme** CONFIRMED: **Glenn Bryan, Group Leader, Potato Genetics and Breeding Group, The James Hutton Institute, UK**
10.00-10.25	**Title to be Confirmed** CONFIRMED: **Patrick Zhao, Associate Professor of Bioinformatics, Samuel Roberts Noble Foundation, USA**	**Genetic and epigenetic variation in legume crops** CONFIRMED: **Scott Jackson, Georgia Research Alliance Eminent Scholar and Professor, Center for Applied Genetic Technologies, University of Georgia, USA**	**Autotetraploid crop species - Potato** RESERVED: **Herman van Eck, Assistant Professor, Laboratory for Plant Breeding, Wageningen University, The Netherlands**
10.25-11.10	**Morning Refreshments** **Poster Presentation Sessions**		
11.10-11.40	**Solution Provider Presentation** **Sponsored by** **Lucigen®** **Simplifying Genomics**		**Solution Provider Presentation** For sponsorship opportunities please contact Steve Hambrook at steve@globalengage.co.uk
11.40-12.05	**Ensembl Plants: Tools for visualising, mining and analysing crop genomics data** Ensembl Plants is a genome centric platform for visualisation and analysis of plant genomics data. It hosts assembly, sequence, expression, variation and comparative datasets for a growing number of plant species (currently 26) covering a range of economically important crops, including brassica, tomato, grape, barley, potato, maize and wheat, and taxonomically diverse model organisms. The web-based genome browser visually integrates sequence and assembly information with genes, markers, probes, repeats and other public or user-supplied datasets. It includes a web-based data mining tool, allowing specific sets of data to be queried and downloaded for offline analysis. In addition to the browser, all data can be accessed computationally via extensive Perl and REST APIs and is available for FTP download or direct database access. CONFIRMED: **Dan Bolser, Ensembl Plants Project Leader, European Bioinformatics Institute, UK**	**Epigenetic memory in plants** CONFIRMED: **Jose Gutierrez-Marcos, Associate Professor, University of Warwick, UK**	**Re-sequencing 150 tomato genomes** CONFIRMED: **Sandra Smit, Bioinformatics Group, Wageningen University, The Netherlands**

	Bioinformatics, Data Management & Analysis	Epigenetic / DNA Methylation Case Studies	Plant Genomic Case Studies
12.05-12.30	**Utilising sequence capture to accelerate cloning of R genes** CONFIRMED: **Burkhard Steuernagel, Research Associate, 2Blades group, The Sainsbury Laboratory, UK**	**Centromere Epigenetics: On, Off, On Again and De Novo Activity** Centromeres of maize, as with other plants, consist of large arrays of repetitive sequences but their activity is not necessarily conditioned by these sequences. Numerous examples of inactive centromeres have been molecularly analyzed as well as reactivated cases. Further, de novo active centromeres have been found over unique sequences containing active genes. The circumstances of inactivation or de novo formation suggest that these changes occur within the time frame of a single, or at most a few, cell cycles but the changed state is then perpetuated over generations. CONFIRMED: **James Birchler, Curators' Professor Biological Sciences, University of Missouri, USA**	**Applications of Associative Transcriptomics** Association genetics approaches, such as genome-wide association scans, link trait variation with allelic variation and enable the rapid development of molecular markers to assist breeding. Until recently, the approach has been limited to those species for which extensive genomics resources, such as genome sequences, are available. However, technologies that exploit transcriptome sequencing have led to the deployment of the technology termed Associative Transcriptomics in species for which resources are more limited. Examples of the application of Associative Transcriptomics in oilseed rape, wheat and ash will be described. CONFIRMED: **Ian Bancroft, CNAP Chair of Plant Genomics, Department of Biology, University of York, UK**
12.30-12.55	**Crowdsourcing for Ash Dieback Project** CONFIRMED: **Dan Maclean, Head of Bioinformatics, Sainsbury Laboratory, UK**	**Developing natural dietary therapies for gluten syndrome using next-generation tools for genome manipulation** CONFIRMED: **Sachin Rustgi, Assistant Research Professor, Department of Crop & Soil Sciences, Washington State University, USA**	**Exploiting apple biodiversity by NGS and its application to molecular breeding** CONFIRMED: **Riccardo Velasco, Head of Genomics and Biology of Fruit Crop Department, The Research and Innovation Centre (CRI), Fondazione Edmund Mach, Italy**
12.55-14.00	**Lunch**		
	Forestry Case Studies	Genomic Evolution Case Studies	Plant Genomic Case Studies Continued
14.00-14.25	**Sequencing the 20 Gbp Norway Spruce Genome** Conifers have been dominating forest species for more than 200 million years and remain of significant ecological and economical importance. We sequenced the 20 Gbp Norway spruce (Picea abies) genome, identifying 28,354 well-supported genes, a gene content similar to that of Arabidopsis thaliana. There was no evidence of a recent whole-genome duplication with repeat analysis showing that the large genome resulted from the slow and steady accumulation of a diverse set of LTR TEs that are shared among extant conifers. 24nt sRNAs, which are known to silence TEs via methylation, were present at much lower than in other plants, while the 21nt sRNA population was highly diverse. The spruce genome contained numerous long (>50,000 bp) introns that resulted from TE insertions. CONFIRMED: **Nathaniel Street, Assistant Professor, Umeå Plant Science Centre, Sweden**	**Biodiversity studies using high-throughput sequencing of high copy-number DNA** DNA sequencing is an attractive solution for identifying plants in biodiversity assessments - but which sequences to use? We are sequencing total DNA to provide multiple sequence 'barcodes' simultaneously, obtaining quasi-complete sequences for the nuclear rDNA repeat, the chloroplast genome, much of the mitochondrial genome and many high copy number nuclear DNA regions (retrotransposons for example). The data is perfect for species identification but also valuable for phylogenetic studies and for comparative genomics. The major challenges we have overcome are a) optimising automated sequence assembly from heterogeneous, low coverage samples and b) establishing automated and accurate annotation pipelines. The approach has been successfully trialled with 96 *Acacia* accessions, including herbarium specimens CONFIRMED: **Ian Small, Director, ARC Centre of Excellence in Plant Energy Biology, The University of Western Australia, Perth, Australia**	**The Arabidopsis root microbiome: a functional extension of the host genome** • Establishment of a pure culture collection of Arabidopsis root microbiota members • Plant growth promoting activities and indirect protection against soil-born pathogens by root microbiota members • Large scale genome sequencing and population genomics of plant growth promoting rhizobacteria. CONFIRMED: **Stéphane Hacquard, Research Associate, Schulze-Lefert Group, Max Plank Institute for Plant Breeding, Germany**

14.25-14.50	**Forestry Case Study**	**Genome Evolution**	**The coffee genome sequence suggests polyphyletic origin of caffeine in eudicot evolution** Coffee is an immensely valuable beverage crop principally grown in developing countries. Here we present a high-quality draft genome of Robusta coffee, Coffea canephora, produced from a doubled haploid plant. The sequence does not show signs of the whole genome triplication described in Solanum species such as tomato and potato, indicating that the last common ancestor between C. canephora and Solanum predated this event. Coffee displays the most conservative chromosomal gene order among asterid angiosperms. The coffee genome contains a relatively low number of genes (25,574), but includes some noteworthy species-specific gene family expansions, among them N-methyltransferases (NMTs), defence-related genes, and alkaloid and flavonoid enzymes involved in secondary compound synthesis. Coffee NMTs that are involved in caffeine production expanded through sequential tandem duplications independently of those from cacao and tea, suggesting that caffeine in eudicots is of polyphyletic origin.
	CONFIRMED: **John MacKay, Professor of Forestry, Université Laval Wood Professor of Forest Science, University of Oxford, SmarTForests, Project co-director, UK**	CONFIRMED: **Andrew Leitch, Professor of Plant Genetics, School of Biological and Chemical Sciences, Queen Mary University of London, UK**	CONFIRMED: **Giovanni Giuliano, Head of the Green Biotechnology Laboratory, ENEA, Casaccia Research Center, Italy**
14.50-15.15	**Understanding trait-gene associations in black poplar for sustainable non-food bioenergy crops'**	**Diversification, Polyploidy and Comparative Genomics in the Brassicales**	**What can *A. thaliana* hybrids tell us about plant adaptation?** Studies of natural genetic variation not only provide a direct understanding of the molecular mechanisms underlying adaptive traits, but can also be used to explain adaptive evolution. Several reports of reduced fitness in hybrids (hybrid incompatibility) of *Arabidopsis thaliana* have already suggested molecular mechanisms of reproductive isolation. However, the different mechanisms resulting in hybrid incompatibilities as well as their contribution to evolution among natural populations remain still largely unknown. We use bioinformatic, genetic and metabolic tools to study *A. thaliana* hybrids, among local populations and accessions in order to understand the role of epistatic interactions in adaptation and how causal alleles could have evolved.
	CONFIRMED: **Gail Taylor, Professor of Plant Biology, Southampton University, UK**	CONFIRMED: **Eric Schranz, Professor of Biosystematics, Wageningen University, The Netherlands**	CONFIRMED: **Roosa Laitinen, Research Group Leader, Molecular Mechanisms of Plant Adaptation, Max Planck Institute for Plant Physiology, Germany**
15.15-15.45	**Afternoon Refreshments** **Poster Presentation Sessions**		

15.45-16.10	**Willow Case Study** CONFIRMED: **Steve Hanley, Rothamsted Research, UK**	**Asexual genome evolution in polyploid plants: Insights from transcriptomics studies in *Ranunculus auricomus*** Asexual genome evolution in plants combines effects of polyploidy, hybridity, and of loss of sex. Apomixis (= asexual seed production) is expected to result in accumulation of deleterious mutations as purifying selection is less efficient (Muller's ratchet). We performed a SNP and indel analysis mined from RNAseq data from three sexual diploid species and two apomictic hexaploid hybrids of the *Ranunculus auricomus* complex. Comparison of ratios of non-synonymous versus synonymous substitutions between sexuals and apomicts revealed no genome-wide mutation accumulation in asexuals, which is probably due to the evolutionarily young age of lineages and to purifying selection acting via facultative sexuality. Gene ontology analysis revealed significant enrichment of genes associated to meiosis, sporogenesis and gametogenesis, following predictions of divergent selection between sexuals and apomicts. CONFIRMED: **Elvira Hörandl, Professor for Systematics, Biodiversity and Evolution of Plants, University of Göttingen, Germany**	**Ensifer-Mediated Transformation (EMT) a novel gene transfer platform for the genetic improvement of crop varieties** Genetic transformation is a powerful research tool and is now widely adopted to expand the functionality of existing crop species. EMT is a novel non-Agrobacterium-based system to facilitate the transfer of single/multiple genes of interest into target crop genomes. Applicable to both monocots and dicots, the associated bacterium, *Ensifer adhaerens*, can be successfully substituted into existing Agrobacterium protocols with minimal requirement for protocol optimization. Applying NGS, the genome of *E. adhaerens* has been sequenced annotated and compared against that of A. tumefaciens C58. Significantly, genes that are non-essential but exert a positive influence on transformability were identified in OV14. This study has increased our understanding of T-DNA transfer by non-Agrobacterium species and creates a platform for the continued uptake and improvement of EMT. CONFIRMED: **Ewen Mullins, Senior Research Officer, Crop Science Department, Teagasc Crops, Environment and Land Use Programme, Ireland**
16.10-16.35	**Forestry Case Study** Invitation to:	**A transcriptomic approach to study the evolution of plant photoperiod pathway** Transcriptomics is revolutionizing the study of gene expression in plants. We have compared the transcriptional profiles of the photoperiod response in algae and modern plants with an evo-devo perspective. Co-expression network and Genome Wide Associative Studies (GWAS) suggest that genes have evolved within close functional niches with strong mutual influences. This helps explain gene duplication and diversity, as well as gene functional homology among very different species. Our approach could help understand global gene regulation networks in order to identify key regulators of important agricultural traits susceptible of transgenic and breeding programs. CONFIRMED: **Federico Valverde, Senior Scientist, Institute for Plant Biochemistry and Photosynthesis, CSIC – University of Seville, Spain**	**Plant Genomics Case Study** Invitation to:
16.35	**Chair's closing remarks and end of conference**		

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