

Plant Genomics Congress

13-14 May 2013

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 1st Plant Genomics Congress, which will be held on May 13-14 in London, UK at the London Heathrow Marriott Hotel.

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.

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, expert led case study presentations and interactive Q&A panel discussions examining topics through four separate tracks covering:

Conference Agenda

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
- Single-molecule sequencing for plant research
- NGS Protocols
- Genome Assembly
- Sample Preparation Technology
- Standardisation

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
- Plant genotyping, SNP discovery, QTL Mapping & Marker-Assisted Selection
- Plant genetic engineering - DNA assembly , genome editing, cloning, amplification
- DNA & RNA isolation
- 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

Day 2 Stream 1 - Plant Genomic Case Studies & Epigenetics, miRNA, & ncRNAs Research in Plants

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

Day 2 Stream 2 - Bioinformatics, Data Management & Analysis

- 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
- Integration of NGS in a genomics core
- NGS data analysis & management in a small genomics core
- Challenges in setting up an NGS facility
- Experiences and lessons learnt from the first year of high-throughput sequencing

Attendees

Delegates are pre-qualified dependent on seniority, budget, responsibility & are senior-level decision makers from academic & industry institutions, mainly in Europe but also worldwide & typically include, Professors, VPs, Directors, Managers, Heads, Scientists of or working in:

Next Generation Sequencing
Plant Genetics
Plant Sciences
Plant Breeding
Plant Physiology & Biochemistry
High Throughput Technologies
Microarray

Genotyping
Epigenetics
DNA Methylation
SNP Discovery
QTL Mapping
Computational Biology

Bioinformatics
Agronomy
Botany
Metagenomics
Biological Sciences
Environmental Sciences
Food security

Agriculture
Informatics
Data Management
Data Analysis
Data Storage
Cloud Computing
Statistical Genomics

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

Confirmed Speakers 2013

- Richard Visser, Professor, Chair & Head Plant Breeding, Wageningen UR, The Netherlands
- Lukas Mueller, Assistant Professor, Boyce Thompson Institute for Plant Research, Cornell University, USA
- Michael Bevan, Professor, Programme Leader, Cell & Developmental Biology, The John Innes Institute, UK
- H  l  ne Berges, Director of the French Plant Genomic Resource Center, INRA – CNRGV, France
- Neil Hall, Professor, Director, Centre for Genomic Research, Institute of Integrative Biology, University of Liverpool, UK
- Klaus Mayer, Group Leader Plants, Institute of Bioinformatics and Systems Biology / MIPS, Helmholtz Center Munich, Germany
- Ian Bancroft, Professor Crop Genetics, John Innes Centre, UK
- Nicolas Harberd, Professor, Plant Sciences, University of Oxford, UK
- Jos   M Jim  nez-G  mez, Max Planck Institute for Plant Breeding Research, Cologne, Germany
- Tamas Dalmay, Professor of RNA Biology, School of Biological Sciences, University of East Anglia, Norwich, UK
- Zhangjun Fei, Associate Research Scientist, Boyce Thompson Institute for Plant Research, Cornell University, USA
- Massimo Delledonne, Professor Department of Biotechnology & Director Functional Genomics Center, University of Verona, Italy
- Michele Morgante, Professor of Genetics & Scientific Director of IGA University of Udine, Italy
- Mathilde Causse, Head of the Research Unit of Genetics and Breeding of Fruit and Vegetable, INRA Avignon, France
- Alan Schulman, MTT Agrifood Research and Institute of Biotechnology, University of Helsinki
- David Horner, Professor, University of Milan
- Robin G Allaby Associate Professor, School of Life Sciences, University of Warwick, UK
- Sergi Beltran Agull  , Bioinformatics Analysis Group Leader, CNAG - Centre Nacional d'An  lisi Gen  mica, Spain
- Dan Maclean, Head of Bioinformatics, Sainsbury Laboratory, UK
- Keywan Hassani-Pak, Group Leader Applied Bioinformatics, Computational and Systems Biology, Rothamsted Research, UK
- Chungui Lu, Lecturer in Post-Genomics, Faculty of Science, University of Nottingham, UK
- Etienne Delannoy, Functional Genomics Group L'Unit   de Recherche en G  n  mique V  g  tale (URGV) INRA, France
- Uwe Scholz, Group Leader Research Group Bioinformatics and Information Technology, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany
- Marzanna K  nzli-Gontarczyk, Systems Expert Genomics/Transcriptomics – Next Generation Sequencing, Functional Genomics Center Zurich, Switzerland
- Heiko Schoof, Prof. Dr. INRES Crop Bioinformatics, University of Bonn, Germany
- Mario Caccamo, Head of the Bioinformatics, TGAC
- Michiel van Eijk, Chief Scientific Officer, Keygene N.V.
- Senior Representative, Lucigen

Reserved Speakers 2013

- Toby Bloom, Director of Bioinformatics, Broad Institute
- Todd Michael, Associate Fellow & Head of Genome Analysis Center, Monsanto, USA
- Senior Representative, BioGemma
- Rob Martienssen, Professor and HHMI Investigator, Plant Biology Cold Spring Harbor Laboratory, New York, USA
- Ulf Lagercrantz, Professor, Dept. of Plant Ecology and Evolution, Evolutionary Biology Centre, Uppsala University, Sweden
- Stanis  law Karpi  ski, Professor, Dept. of Genetics, Breeding and Plant Biotechnology, Warsaw University
- Juliette De Meaux, Professor, Plant Molecular Evolution, University of M  nster, Germany
- Arjen van Tunen, CEO Keygene N.V. and President Keygene Inc

Sponsors



1st Annual Plant Genomics Congress

Day 1 – Monday May 13th 2013, London Heathrow Marriott Hotel, UK

08.00-08.50	Registration & Coffee	
08.50-09.00	Global Engage Welcome Address & Chairman's Opening Remarks	
09.00-09.30	Keynote Address: Advances In Plant Genome Sequencing CONFIRMED: Richard Visser, Professor, Chair & Head Plant Breeding, Wageningen UR, The Netherlands	
09.30-10.00	Solution Provider Presentation For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk	Solution Provider Presentation For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk
	Conference Room 1 NGS Technologies for Plant Research	Conference Room 2 Plant Genomic Case Studies
10.00-10.25	Comparing And Contrasting Different Sequencing Platforms For Plant Research RESERVED: Todd Michael, Associate Fellow & Head of Genome Analysis Center, Monsanto	Case Study – Study of the Wheat Genome Using NGS - Title to be Confirmed CONFIRMED: Michael Bevan, Professor, Programme Leader, Cell & Developmental Biology, The John Innes Institute, UK
10.25-10.50	Applications Of Next-Generation Sequencing In Plant Research CONFIRMED: Hélène Berges, Director of the French Plant Genomic Resource Center, INRA - CNRGV	Wheat Genome - Title to be Confirmed CONFIRMED: Neil Hall, Professor, Director, Centre for Genomic Research, Institute of Integrative Biology, University of Liverpool
10.50-11.00	Morning Refreshments	
11.00-12.00	One-to-One Meetings x 3 Poster Presentation Sessions	
12.00-12.30	Solution Provider Presentation For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk	Solution Provider Presentation For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk
12.30-12.55	Title to be Confirmed CONFIRMED: Dan Maclean, Head of Bioinformatics, Sainsbury Laboratory, UK	Barley and Wheat Genome Study – Title to be Confirmed CONFIRMED: Klaus Mayer, Group Leader Plants, Institute of Bioinformatics and Systems Biology/MIPS, Helmholtz Center Munich, Germany
12.55-13.55	Lunch One-to-One Meeting x 1 at 13.30	
13.55-14.20	The "private" part of each cultivar/ecotype genome, by genome sequencing and then assisted assembly, and by de novo assembly of the transcriptome – Title to be Confirmed CONFIRMED: Massimo Delledonne, Professor, Department of Biotechnology & Director Functional Genomics Center, University of Verona	Associative Transcriptomics In Oilseed Rape And Wheat 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 association genetics approaches in species for which resources are more limited and for species with complex, polyploid genomes. The technology termed Associative Transcriptomics will be described, along with examples of application in oilseed rape and wheat. CONFIRMED: Ian Bancroft, Professor Crop Genetics, John Innes Centre
14.20-14.45	Single-molecule sequencing for plant research <ul style="list-style-type: none"> De novo assembly of complex crop genomes Crop Genome assembly Invitation to:	Barley Genome Sequencing Project <ul style="list-style-type: none"> Genome dynamics and the role of retrotransposons therein CONFIRMED: Alan Schulman, MTT Agrifood Research and Institute of Biotechnology, University of Helsinki
14.45-15.15	Panel Discussion – Possibilities of Plant Research with New NGS Technologies <ul style="list-style-type: none"> Nanopore sequencing Invitation to: Senior Representatives x 4	Case Study at Keygene – Title to be Confirmed CONFIRMED: Michiel van Eijk Chief Scientific Officer, Keygene N.V.

15.15-15.45	<p align="center">Solution Provider Presentation Title to be Confirmed</p> <p align="center">Sponsored by</p> 	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk</p>
15.45-15.55	Afternoon Refreshments	
15.55-16.35	One-to-One Meetings x 2 Poster Presentation Sessions	
16.35-17.00	<p>Case Study at BioGemma</p> <p>RESERVED: Senior Representative, Biogemma</p>	<p>NGS For Tomato Genetic Studies</p> <ul style="list-style-type: none"> • An overview on the tomato genome sequence • Resequencing for SNP discovery and map construction: we fully resequenced 8 accessions and discovered more than 4 million SNPs that were then used to genotype a segregating population and map QTL for fruit quality traits • NGS for association studies: we used 454 to resequence a set of candidate genes in 96 accessions and then look for associations between polymorphisms and fruit development traits. <p>CONFIRMED: Mathilde Causee, Head of the Research Unit of Genetics and Breeding of Fruit and Vegetable, INRA Avignon, France</p>
17.00-17.30	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk</p>	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk</p>
17.30-17.55	<p>Case Study at Syngenta</p> <p>Invitation to: Mark Forster, Team Leader, Chemical Indexing Unit, Syngenta</p>	<p>NGS in rice (joint with China) and barley (cold stress)</p> <p>CONFIRMED: Chungui Lu, Lecturer in Post-Genomics, Faculty of Science, Nottingham University, UK</p>
17.55-18.20	<p>Learning & Teaching NGS - Experiences from a Lab</p> <p>CONFIRMED: Marzanna Künzli-Gontarczyk, Systems Expert Genomics/Transcriptomics – Next Generation Sequencing, Functional Genomics Center Zurich, Switzerland</p>	<p>Dynamic Reprogramming Of Tomato Methylome During Fruit Development And Ripening</p> <p>Ripening is a developmental process that evolved to foster animal mediated seed dispersal of flowering plants. Tomato ripening is triggered by the plant hormone ethylene but is restricted to matured fruits with viable seeds by an unknown developmental cue. Here we show that tomato fruits exposed to the methyltransferase inhibitor 5-azacytidine ripen prematurely in advance of seed maturation. We then performed genome-wide bisulfite sequencing of tomato fruits at four different stages and of two ripening mutants, and tomato leaves. Our data reveals that the tomato genome is highly methylated, with 44% of cytosine sites being targeted for methylation and the majority in the asymmetrical CHH context. Our analyses also show that the 5' end of ripening-associated genes remain methylated in leaves, immature fruits and ripening-deficient mutants, but become substantially demethylated in association with fruit growth coinciding with seed maturation. Furthermore, binding sites for one of the main ripening transcription factors, RIN, are frequently localized at the demethylated regions in the promoters of numerous ripening genes and binding occurs in concert with demethylation. In summary, our data show that the methylome plays an important role in the regulatory process that coordinates tomato fruit growth and ripening and may have been selected to insure the fidelity of ripening processes.</p> <p>CONFIRMED: Zhangjun Fei, Associate Research Scientist, Boyce Thompson Institute for Plant Research, Cornell University, USA</p>
18.20	Chairman's Closing Remarks and End of Day 1	
18.30-19.30	Drinks Reception	

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Day 2 – Tuesday May 14th 2013, London Heathrow Marriott Hotel, UK

08.00-08.40	Coffee & One-to-One Meetings x 2	
08.40-09.10	<p align="center">Keynote Address Bioinformatics for Biologists</p> <p align="center">RESERVED: Toby Bloom, Director of Bioinformatics, Broad Institute</p>	
09.10-09.40	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk</p>	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk</p>
	Plant Genomic Case Studies	Bioinformatics, Data Management & Analysis
09.40-10.05	<p>Reducing ligation bias of small RNAs during library preparation for NGS and its impact on plant small RNA sequencing</p> <ul style="list-style-type: none"> • 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 <p>CONFIRMED: Tamas Dalmay, Professor of RNA Biology, School of Biological Sciences, University of East Anglia, Norwich, UK</p>	<p>Next Generation Sequencing In Next Generation Plant Breeding</p> <p>CONFIRMED: Lukas Mueller, Assistant Professor, Boyce Thompson Institute for Plant Research, Cornell University, USA</p>
10.05-10.35	<p align="center">Solution Provider Presentation Sponsored by Lexogen</p> <p align="center"></p>	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at ashley@globalengage.co.uk</p>
10.35-10.50	Morning Refreshments	
10.50-11.10	One-to-One Meetings x 1 Poster Presentation Sessions	
11.10-11.35	<p>Use of smallRNA deep sequencing to describe the variety of "RNA biogenesis profiles" associated with genomic loci producing miRNA-like products</p> <p>While the most deeply conserved plant miRNA families behave as "textbook" miRNAs - producing essentially only the miRNA and miRNA* sequences - younger and more lineage specific miRNA-like genes seem to show a much less fixed pattern of smallRNA biogenesis (despite data suggesting that they are foldback dependent and thus "miRNA-like"). This has some implications for how miRNAs and miRNA-like loci should be annotated, and indeed, the type of bioinformatics algorithms we should build to look for such loci. It can also potentially help us to gain insight into the evolutionary pathways followed by miRNA loci.</p> <p>Furthermore, I have some (for now very preliminary) evidence that some important smallRNAs are conserved at the level of sequence, but differ in biogenesis mechanism between different plants.</p> <p>CONFIRMED: David Horner, Professor, University of Milan</p>	<p>Strategies for Efficient NGS Data Management And Analysis</p> <p>CONFIRMED: Sergi Beltran Agulló, Bioinformatics Analysis Group Leader, CNAG - Centre Nacional d'Anàlisi Genòmica, Spain</p>
11.35-12.00	<p>Using Archaeogenomic Approaches To Unravel The History Of Local Adaptation In Crops</p> <p>CONFIRMED: Robin G Allaby Associate Professor, School of Life Sciences, University of Warwick</p>	<p>Panel Discussion: Panel Discussion – Data Analysis, Management and Storage Strategies – Title to be Confirmed</p> <p>CONFIRMED: Chaired by – Mario Caccamo, Head of the Bioinformatics, TGAC</p> <p>RESERVED: Arjen van Tunen, CEO Keygene N.V. and President Keygene Inc</p> <p>Invitation to: Senior Representative x2</p>

12.00-12.30	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at</p> <p align="center">ashley@globalengage.co.uk</p>	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at</p> <p align="center">ashley@globalengage.co.uk</p>
<p align="center">Lunch One-to-One Meeting x 1 at 13.00</p>		
13.30-14.00	<p>Small RNA in Norway Spruce We have some interesting data concerning siRNA degradation of plant resistance genes that seems to be surprisingly abundant in some plant species (long lived perennials). One hypothesis is that this is part of a counter counter-defence system against pathogens.</p> <p>RESERVED: Ulf Lagercrantz, Professor, Dept. of Plant Ecology and Evolution, Evolutionary Biology Centre, Uppsala University, Sweden</p>	<p>Efficient Management of NGS Data and Analysis Results at a Plant Research Institute</p> <p>CONFIRMED: Uwe Scholz, Group Leader Research Group Bioinformatics and Information Technology, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany</p>
14.00-14.25	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at</p> <p align="center">ashley@globalengage.co.uk</p>	<p align="center">Solution Provider Presentation</p> <p>For sponsorship opportunities please contact Ashley Taylor at</p> <p align="center">ashley@globalengage.co.uk</p>
14.25-14.50	<p>On Mutation: Darwin's 'whatever the cause' It has long been known that DNA sequence mutation is fundamental to biological evolution. However, mutation remains a mysterious phenomenon. This is because mutation is a relatively infrequent event, rendering attempts to understand it on a systematic basis problematic. As a result, we have until recently known little of how mutations originate on a genome-wide basis. However, whole-genome DNA sequence analysis now enables sampling of new mutations in sufficient numbers to enable meaningful analysis. Using the genetic model plant <i>Arabidopsis thaliana</i>, I will first show that exposure of plants to ionising fast-neutron irradiation generates a specific spectrum of mutations that differs substantially from that characteristic of mutations accumulating spontaneously in laboratory 'mutation accumulation' (MA) lines. Next, I will show that the intriguing phenomenon of 'somaclonal variation' (the heritable variation characteristic of plants regenerated from in vitro cultured plant cells) is in part explicable by specific classes of de novo DNA sequence mutation. Finally, I will address the question of whether or not 'natural' environments are mutagenic. I will show that plants growing in experimental 'stressful' environments (e.g. on saline soil) accumulate a spectrum of mutations that differs from that seen in MA lines (which are grown in benign environments). Interestingly the mutational spectrum of single nucleotide polymorphisms found in wild <i>Arabidopsis</i> populations reflects more closely the 'stressed' spectrum than the benign MA line spectrum. Does this mean that growth in nature is detectably mutagenic to plants? And, that environmental factors induce many of the mutations that fuel the evolution of flowering plants?</p> <p>CONFIRMED: Nicholas Harberd, Professor, Plant Sciences, University of Oxford</p>	<p>Structural Variants – Title to be Confirmed</p> <p>CONFIRMED: Michele Morgante, Professor of Genetics & Scientific Director of IGA University of Udine</p>
14.50-15.15	<p>eQTL analysis in plants using RNA-seq</p> <p>CONFIRMED: José M Jiménez-Gómez, Max Planck Institute for Plant Breeding Research, Cologne, Germany</p>	<p>A billion reads assembly: Building a comprehensive reference transcriptome for bread wheat & QTLNetMiner – Demonstration of candidate gene discovery in integrated plant and animal knowledge networks</p> <p>CONFIRMED: Keywan Hassani-Pak, Group Leader Applied Bioinformatics, Computational and Systems Biology, Rothamsted Research, UK</p>
<p align="center">Afternoon Refreshments Poster Presentation Sessions</p>		
15.45-16.10	<p>Epigenetics Case Study - Title to be Confirmed</p> <p>RESERVED: Rob Martienssen, Professor and HHMI Investigator, Plant Biology Cold Spring Harbor Laboratory, New York, USA</p>	<p>Bioinformatics Case Study at Dow AgroSciences - Title to be Confirmed</p> <p>Invitation to: Clive Evans, Team Lead, Dow AgroSciences</p>

