



# AgriGenomics World Congress

**8-9 July 2010**  
**Brussels, Belgium**



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# Plant Genomics

## Day One - Thursday 8 July 2010

- 08:00 **Registration**  
**Session: Growth Optimization for Food and Biofuels**
- 09:00 **Keynote Presentation**  
**The Role of Genomics in the Future of Food Security**  
Jim Dunwell, Professor, University of Reading  
This presentation discusses the role of genomics in the search for a sustainable intensification of global agriculture in which crop yields are increased without adverse environmental impact and without the cultivation of more land.
- 09:30 **Correlation of Parental Transcriptome and Field Data for the Characterization and Prediction of Heterosis in Maize**  
Stefan Scholten, University of Oxford  
Precise prediction of hybrid performance based on the genetics of inbred lines would have great advantages for breeding. Our results suggest that transcriptome-based methods have a high potential to improve the efficiency of maize hybrid breeding programs.
- 10:00 **Exploring and Exploiting Epigenetic Variation in Crops**  
Graham King, Deputy Director, BBSRC  
Large, complex crop genomes have distinct targets and distribution of epigenetic marks compared with metazoans. Epigenetic variation, mediating regulation of genes affecting crop development and response to environment, is an under-explored and under-exploited source of variation for crop improvement.
- 10:30 **Coffee Break and Networking in the Exhibition Hall**
- 11:15 **Keynote Presentation**  
**Accelerating the Improvement of Dedicated Saccharinae Bioenergy Crops**  
Andrew Paterson, Distinguished Research Professor, University of Georgia  
Expansion of agriculture to provide plant biomass for production of fuels/feedstocks will require additions to our present repertoire of crops. Numerous avenues to leverage knowledge of botanical models to accelerate improvement of dedicated energy crops will be presented.
- 11:45 **Deconstruction Of Biomass For Biofuels Production**  
Masood Hadi, Senior Member of Technical Staff/Director, Sandia National Laboratory/Joint BioEnergy Institute  
To advance biomass deconstruction we developed transgenic plants encoding a suite of enzymes for cellulosic deconstruction. The unique aspects of our technology -rationally engineered extremophilic enzymes, targeted to specific cellular locations, -dormancy during plant proliferation, which activate under pre-treatment conditions.
- 12:15 **Technology Spotlight**
- 12:30 **Lunch and Networking in the Exhibition Hall**
- 13:30 **Poster Session**
- 14:30 **Keynote Presentation**  
**Improving Feedstock Crops for Biofuels**  
Richard Flavell, Chief Scientific Officer, Ceres  
Numerous species are attractive as feedstocks for the biofuels industries. These include the C4 grasses switchgrass, miscanthus, and sorghum. Breeding programs for each of these species are making progress which will be described. Transgenes have been selected in Arabidopsis and rice and transformed into these species to provide further yield gains. The different strategies for improving and deploying the different crops will be described.
- 15:00 **Brachypodium Distachyon and its Use for Cereals**  
Georg Haberer, Staff Scientist, Munich Information Centre for Protein Sequences  
Three subfamilies of the grasses, the Ehrhartoideae (rice), the Panicoideae (maize, sorghum) and the Pooideae (wheat, barley) provide the basis for human nutrition. The wildgrass Brachypodium distachyon, the first member of the Pooideae subfamily to be completely sequenced, holds exceptional promise as a model system for grass research. We use the complete genome sequences of rice, sorghum and Brachypodium to analyze and order chromosomal shotgun sequences of barley (Hordeum vulgare). Next generation selective sequencing and synteny projection allows to sequence tag the majority of the barley protein coding genes and to characterize individual segments on a per gene resolution. Extensions of our approach to other cereals and recent results for wheat will be presented and discussed.
- 15:30 **Coffee Break and Networking in the Exhibition Hall**
- 16:15 **Panel Discussion: Enhancing Public Acceptance of GM Crops in Europe - The Role of Scientific Community**  
While genetically modified crops are now grown in 25 countries around the globe including many in Europe, there are still major hurdles for wide spread acceptance of this technology across the EU. This panel discussion involving scientific experts drawn from both Europe and North America will identify those hurdles and then explore strategies to enhance increased acceptance of crop biotechnology across Europe  
Vivian Moses, Professor, Kings College London  
Jens Katzek, BIO Mitteldeutschland  
C.S. Prakash, Professor, Tuskegee University  
Jim Dunwell, Professor, University of Reading
- 17:00 **Drinks Reception**

# Plant Genomics

## Day Two - Friday 9 July 2010

- 08:00 **Registration**  
**Session: Enhancing Plant Resistance to Disease**
- 09:30 **Keynote Presentation**  
**Death be to Proud: Modulation of Programmed Cell Death for Disease/Stress Tolerance in Plants**  
Marty Dickman, Professor, Texas A&M University  
The recently discovered Arabidopsis family of BAG proteins are molecular chaperones influencing several plant stress responses. We have generated transgenic plants that express BAG genes. These genes have the potential to generate effective disease resistance/stress tolerance in economically important crop plants.
- 10:00 **Molecular Basis of Durable Fungal Resistance in Wheat**  
Beat Keller, Director, Institute of Plant Biology  
The Lr34 disease resistance gene in wheat confers durable resistance against several fungal pathogens. Lr34-based resistance and non-host resistance in Arabidopsis share surprising similarities, suggesting new approaches in plant breeding.
- 10:30 **Coffee Break and Networking in the Exhibition Hall**
- 11.15 **Small RNA and Selective DNA Methylation in Plant Antiviral Defence**  
Yiguo Hong, Professor, University of Warwick  
I will give a brief review on enhancing plant resistance to diseases caused by single-stranded DNA geminiviruses. Latest finding in my laboratory about the role and application of small RNA and selective DNA methylation to combat viral infection will be presented.
- Session: Systems-Based Approaches & Genomic Mapping in Plants**
- 11:45 **Beyond Bioinformatics: The Impact of Next Generation Sequencing Technologies in Agrigenomics**  
Miguel Perez-Enciso, Professor, Universitat Autònoma de Barcelona  
New sequencing technologies have revolutionized genomics research and have democratized genomics, making it accessible to small labs and non mainstream species. Although currently bioinformatics is a serious bottleneck, the main challenges in the future are to be statistical, e.g., how to incorporate such a deluge of data into current animal and plant breeding schemes.
- 12:15 **Technology Spotlight**
- 12:30 **Lunch and Networking in the Exhibition Hall**
- 13:30 **Poster Session**
- 14:30 **The Microfluidic Microarray Chip Developed for the Detection of Fungal Infection of Food Crops**  
Paul Li, Group Leader, Simon Fraser University  
A circular microfluidic microarray chip has been developed for fast hybridization of 96 samples simultaneously. Two PCR products (260 bp) with one-base-pair difference, derived from food crop fungal pathogens, *Botrytis cinerea* and *Botrytis squamosa*, have been discriminated in 3 minutes.
- 15:00 **Sequencing and Identification of the Genes Controlled Epigenetically Exploring the Homology Approach Between Model Plant Arabidopsis and Commodity Crop Theobroma cacao.**  
Vladimir Brukhin, Aberystwyth University  
We study the cocoa genes that are controlled by methylation. The genes were identified by in silico assessment of the 159 000 cocoa ESTs which were blasted against sequences of the Arabidopsis methylation-regulated genes. The data on the assessment of the methylation status of the sequenced gene promoters and coding regions under different conditions and in a various tissues, and also on the technologies that transfer the information on the methylation status of these regions from the model to the commodity organisms will be discussed.
- 15:30 **Coffee Break and Networking in the Exhibition Hall**
- 16:15 **Comparative Study of Brassica rapa and Arabidopsis thaliana Genomes: Implications on the Alpha Duplication of A. thaliana and Reshuffling of its Unit and Direction of B. rapa**  
Jung Sun Kim, Researcher, Rural Development Administration  
By comparing the order of orthologous loci between two genomes, 'conserved linkage groups' or 'colinear conserved blocks' were detected. In total, 26 conserved blocks in A. thaliana corresponding to 64 blocks in B. rapa were detected.
- 16.45 **Close of Conference**

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Prearrange meetings with other delegates or follow up with them after the event.

Check the event website for further information.

# Animal Genomics

## Day One - Thursday 8 July 2010

- 08:00 **Registration**  
**Session: Disease Resistance in Livestock**
- 09:00 **Keynote Presentation**  
**Mechanisms of Host Resistance to Trypanosomiasis**  
Steve Kemp, Professor, University of Liverpool  
Tsetse fly transmitted trypanosomiasis in African livestock has enormous economic and human health impact. By combining a range of genetic approaches, we are able to identify candidate mechanisms, genes and variants responsible for the dramatic differences in susceptibility to disease shown by different cattle breeds.
- 09:30 **Genomics of Infectious Disease: The Horse Model**  
Petr Horin, Professor, Faculty of Veterinary Medicine, University of Veterinary and Pharmaceutical Sciences  
Modern principles of genomic analyses of infectious diseases, based on data obtained from human studies, will be introduced. Results of association and evolutionary genetic analyses in domestic horses and in other equid species will be presented.
- 10.00 **Alpha-defensins of the Horse - An Insight into a Well Armed Organism**  
Oliver Bruhn, Project Leader, Research Center Borstel  
The repertoire of equine alpha-defensins, a class of antimicrobial peptides, was observed, and selected peptides were analysed regarding their antimicrobial properties against human and equine pathogens, their mode of action, their membrane selectivity, and cytotoxicity.
- 10:30 **Coffee Break and Networking in the Exhibition Hall**  
**Session: Genetic engineering to Increase Yield from Livestock**
- 11:15 **GM Animals – Another GM Crops?**  
Ann Bruce, Senior Research Fellow, University of Edinburgh  
GM crops have had a troubled passage within Europe. Can future developments in GM animals learn from these experiences? This presentation will consider some of the social context for the development of GM animals in Europe.
- 11:45 **Genome-Wide Expression QTL (eQTL) Analysis of Loin Muscle Tissue Identifies Candidate Genes in Pigs**  
Catherine Ernst, Associate Professor, Michigan State University  
Ernst and colleagues have completed a comprehensive genome-wide expression quantitative trait loci (eQTL) analysis for pigs, the first analysis of its kind reported for livestock. This work integrates genetic markers, phenotypes, transcript profiles and genomic sequence to identify candidate genes.
- 12:15 **Technology Spotlight**
- 12:30 **Lunch and Networking in the Exhibition Hall**
- 13:30 **Poster Session**  
**Session: The Use of Microarrays and Bioinformatics in Animal Genomics**
- 14:30 **Genomic Expression Evaluation: Introduction and Perspectives**  
Eve Ramery, Post-Doc, University of Liege  
Few technologies are currently available for transcriptomic studies. To date, use of microarrays appears as the technique of choice but sequencing/resequencing could compete with it in the future. Together, these techniques open new perspectives in cattle and Herd Health Research.
- 15:00 **DNA Microarray Analysis of Reproduction System in Black Tiger Shrimp (*Penaeus monodon*)**  
Nitsara Karoonuthaisiri, Head of Microarray Laboratory, National Center for Genetic Engineering and Biotechnology  
Microarray analysis of male and female reproductive systems of black tiger shrimp (*Penaeus monodon*) will be presented. Microarray comparisons reveal several potential markers relevant to the maturation of testis and ovary of this economically important animal.
- 15:30 **Coffee Break and Networking in the Exhibition Hall**
- 16:15 **The GENOTEND Chip: a Tool to Analyse Gene Expression in Muscles of Beef Cattle**  
Jean-Francois Hocquette, Senior Scientist, Director of the Herbivore Research Unit, INRA  
We have developed a chip to quantify the expression level of 3000 genes in bovine muscles, including markers of beef quality. These are specific of conditions of production but some gene families are important for beef quality in all conditions.
- 16.45 **Monitoring of siRNA Silencing in vivo by Advanced Handheld Confocal Microscopy**  
Wibool Piyawattanametha, Research Scientist, National Electronics and Computer Technology Center (NECTEC)  
We demonstrate a novel handheld near infrared fluorescence dual-axes confocal (DAC) microscope in a 10-mm diameter package for monitoring of small interfering RNAs (siRNAs) silencing in transgenic animals. The DAC microscope can reveal sub-surface morphology at depth of up to 300 µm into the tissues.
- 17.15 **Close of Conference**

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Check the event website for further information.

# Registration Form

## AgriGenomics World Congress 2010

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| <input type="checkbox"/> | Industry Delegate                             | €850 |
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<sup>†</sup> Check web site for deadline    <sup>°</sup> For non profit institutions only

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