6th Plant Genomics & Gene Editing Congress: Europe

Partnerships in Biocontrol, Biostimulants & Microbiome: Europe

Rotterdam, The Netherlands — 14-15 May 2018 —

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Building on the successes of our global Plant Science series of events, Global Engage is pleased to announce the co-located 6th Plant Genomics & Gene Editing Congress Europe and Partnerships in Biocontrol, Biostimulants & Microbiome Europe.

**Plant Genomics & Gene Editing**
Plant research has transformed dramatically over the last few years as a result of revolutionary breakthroughs and cost reductions in sequencing technology. Successful sequencing of many plants, along with the improvement of biological data sets, have given plant scientists the tools and knowledge to make exciting developments to benefit agriculture. Novel gene editing technologies like CRISPR will take this research even further. This conference will examine the latest NGS, ‘omic’ and gene editing technologies being used for progressing plant-based research, as well other gene-focused aspects of plant science.

**Biocontrol, Biostimulants & Microbiome**
Increasing prioritization of sustainability in agriculture has led to rapid growth in the agricultural biologicals industry. The benefits of biological products in agriculture are significant, and developments in technology and research make agricultural biologicals an exciting, dynamic industry in which to work and study. This conference will focus on the latest research, technologies, products and business strategy in the growing biologicals industry.

**Why Attend?**
A key focus of this year’s event is to facilitate collaboration between the over 300 senior representatives from industry and academia who will attend. With extensive networking time, interactive roundtable discussions and expert Q&A sessions, there is ample opportunity to meet and engage with other attendees at the meeting.

The conference will be an excellent opportunity to learn, share, discuss and engage with the most current agricultural research and technology. During the two-day conference, there will be networking breaks to promote interaction with your peers, over 60 expert led presentations, a dynamic exhibition room filled with technology providers showcasing their technologies and solutions, and several interactive panel discussions examining various topics across six separate tracks.

**EXPERT SPEAKERS Include:**
- **RICHARD VISSER** 
  Professor, Chair, and Head of Plant Breeding, Dean of Research, Wageningen University & Research, The Netherlands
- **BEAT KELLER** 
  Professor, University of Zurich, Switzerland
- **GEORGE COUPLAND** 
  Professor and Director of Plant Developmental Biology, Max Planck Institute for Plant Breeding, Germany
- **TINA KYNDT** 
  Professor of Molecular Biotechnology, University of Ghent, Belgium
- **ANGELA SESSITSCH** 
  Head of Bioresources, AIT Austrian Institute of Technology, Austria
- **AMIT VASAVADA** 
  Senior VP of R&D and Chief Technology Officer, Marrone Bio Innovations
- **DAN FUNCK JENSEN** 
  Professor, Swedish University of Agricultural Sciences, Sweden
- **PETER JENS** 
  CEO, AND Biopharma
PLANT GENOMICS & GENE EDITING CONGRESS

DAY 1 TRACK 1 – PLANT GENOME ENGINEERING: STRATEGIES AND DEVELOPMENTS

• Synthetic biology/Genome editing applications using techniques including TALENs, CRISPRs, and ZFNs
• Improving gene editing technology, enzymes, and methods
• Regulating genome editing and the latest on country/EU policies
• Site-directed mutagenesis
• Metabolic engineering
  > Genome / DNA assembly for editing
• Case Studies
• Panel: Plant Gene Editing for the Consumer

DAY 1 TRACK 2 – PLANT GENOMIC CASE STUDIES

Applications of NGS, omic, and gene editing technologies for:
• Epigenetics and DNA methylation studies
• Molecular marker development / Marker assisted selection
• Disease and stress resistance
• miRNA and RNA analysis
• Plant breeding methods
• Pathogen detection and analysis
• Nutrient uptake

DAY 2 TRACK 1 – DEVELOPMENTS IN NGS, RNA-SEQ, AND OMIC TECHNOLOGIES

• Sample preparation technology
• NGS platform comparison / Best practice guidelines / Future uses
• Genotyping by sequencing
• Phenomics and high throughput phenotyping technology
• Metabolomic and proteomic method development
• Integrated and multi-omic strategies and applications
• Improving qPCR and digital PCR methods for plant genetic analysis
• High resolution scanning
• Single-cell analysis methods
• SNP discovery, QTL mapping, alternative splicing & marker-assisted selection

DAY 2 TRACK 2 – A) BIOINFORMATICS AND DATA ANALYSIS; B) INDUSTRY SHOWCASE

A)
• Bioinformatics analysis and challenges
• Use of genomic data for candidate genes
• Identifying novel functional genes /networks / knowledge from complex data sets
• Application of bioinformatics software for DNA / RNA analysis
• Sequencing pipelines and assembly
• Computational systems for modelling and visualisation of information
• Cloud computing and storage solutions

B) Industry applications of the latest genomic technologies
• Collaborations and how they can drive plant research
• Insight into regulatory challenges

ROUNDTABLE DISCUSSIONS

• Roundtable 1: Genomic Selection
• Roundtable 2: Integrated Omics
• Roundtable 3: Genome Design and The Future of Breeding Technologies
PARTNERSHIPS IN BIOCONTROL, BIOSTIMULANTS & MICROBIOME CONGRESS

TOPICS FOR RESEARCH PRESENTATIONS: PLANT AND SOIL MICROBES

- Microbial biopesticides & biostimulants development
- Fungi / bacteria / protozoa / viruses
- Metagenomics
- Ecology research for crop improvement
- Plant microbiome systems analysis for disease resistance
- Soil microbiome & root assembly
- Host-pathogen interactions
- Structure and specificity of plant microbiomes
- Rhizosphere biology and soil health
- Nitrogen fixation and nutrient uptake
- Strategies for integrated pest management
- Cross-discipline collaborations for improved microbial research

NON-LIVING INPUTS AND LIVING ORGANISMS FOR CROP IMPROVEMENT

- Natural predators / entomopathogenic nematodes / parasitoids
- Plant extracts
- Fungal extracts
- Humic / fulvic acids
- Protein hydrolysates
- Seaweed extracts
- Applications and case studies
- Challenges and solutions

PANEL & ROUNDTABLE DISCUSSIONS

PANEL:
- The Current Status and Future of Investment in Agricultural Biologicals

ROUNDTABLES:
- Commercialization, Product Launch, and Business Development
- Successful application strategies in biological plant disease control – single microbial strains, consortia or synthetic microbiome applications
- Formulating Biologicals: Strategies and Challenges
- Cross-discipline/industry collaboration
<table>
<thead>
<tr>
<th>Confirmed Speakers</th>
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<tr>
<td><strong>RICHARD VISSER</strong></td>
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<td>Professor, Chair, and Head of Plant Breeding, Dean of Research, Wageningen University &amp; Research, The Netherlands</td>
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| **SARAH RAFFAN**  |
| Rothamsted Research and University of Bristol, UK |

| **GIL RONEN**  |
| CEO, NRGene |

| **IAN GODWIN**  |
| Professor of Plant Molecular Genetics, The University of Queensland, Australia |

| **BEAT KELLER**  |
| Professor, University of Zurich, Switzerland |

| **JOCHEN KUMLEHN**  |
| Group Leader, Plant Reproductive Biology, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany |

| **AMBika DUDHATE**  |
| PhD Student, University of Tokyo, Japan |

| **TINGTING ZHOU**  |
| General Manager, Novogene Europe |

| **BLANCA SAN SEGUNDO**  |
| Research Professor, Spanish Research Council (CRAG-CSIC), Spain |

| **CHRIS MALIEPAARD**  |
| Associate Professor, Wageningen University & Research, The Netherlands |

| **MAIKE STAM**  |
| Assistant Professor, University of Amsterdam, The Netherlands |

| **GEORGE COUPLAND**  |
| Professor and Director of Plant Developmental Biology, Max Planck Institute for Plant Breeding, Germany |

| **NATHANIEL BUTLER**  |
| University of Wisconsin-Madison, USA |

| **INGER AHMAN**  |
| Professor of Plant Breeding, Swedish University of Agricultural Sciences, Sweden |

| **CLAUDIA JONAK**  |
| Principal Scientist, AIT Austrian Institute of Technology, Austria |

| **HOLGER SCHULTHEISS**  |
| Research Manager, Fungal Resistance Projects, BASF Plant Science Research Management |

| **ALAN SCHULMAN**  |
| Professor of Plant Biotechnology, LUKE and University of Helsinki, Finland |

| **KIM HAMMOND-KOSACK**  |
| Professor and PI, Rothamsted Research, UK |

| **RODOMIRO ORTIZ**  |
| (Roundtable Host) Professor and Chair of Genetics and Plant Breeding, Swedish University of Agricultural Sciences, Sweden |

| **STAVROS MAKRODIMITRIS**  |
| Delft University of Technology, The Netherlands |

| **LAKSHMI SASTRY-DENT**  |
| External Technology Leader, R&D, Dow AgroSciences |

| **CORINNE ARNOLD**  |
| John Innes Centre, UK |

| **BRANDE WULFF**  |
| Project Leader, John Innes Centre, UK |

| **TINA KYNDT**  |
| Professor of Molecular Biotechnology, University of Ghent, Belgium |

| **HANS DE JONG**  |
| Emeritus Professor of Cytogenetics, Wageningen University & Research, The Netherlands |

| **TOM GREENE**  |
| Senior Research Director, Trait Discovery Organization: DuPont Pioneer |

| **NEHA VAID**  |
| Post-doctoral Researcher, Max Planck Institute of Plant Physiology, Germany |

| **GREG GOCAL**  |
| Chief Scientific Officer and Executive VP, Cibus |

| **TOM OSBORNE**  |
| (Roundtable Host) Director of New Breeding Technologies, Monsanto |

| **KRISTINA GRUDEN**  |
| Professor and Leader of the Omics Approaches Group, National Institute of Biology, Slovenia |

| **JOHN DOONAN**  |
| Director and Professor of Genetics, National Plant Phenomics Centre, Aberystwyth University, UK |

| **ERIK JONGEDIJK**  |
| Head of Business Development Technology, KWS SAAT SG |

| **JIM DUNWELL**  |
| Professor, University of Reading, UK |

| **HERIBERT HIRT**  |
| Professor Director, Center for Desert Agriculture, URGV and King Abdullah University of Science and Technology (KAUST), Saudi Arabia and France |

| **AGNÉS RICOCH**  |
| Associate Professor in Evolutionary Genetics and Plant Breeding, AgroParis Tech, and Adjunct Professor, Pennsylvania State University, Secretary of Life Sciences Section of the French Academy of Agriculture |

| **MICHaEL PALMGREN**  |
| Professor, University of Copenhagen, Denmark |

| **STEVEN KELLY**  |
| Associate Professor, University of Oxford, UK |

| **JULIEN ROUZADE**  |
| NGS Field Application Specialist, PerkinElmer |

| **INGO HEIN**  |
| Principal Investigator, James Hutton Institute and the University of Dundee, UK |

| **KEVIN FENGLER**  |
| Research Scientist, Corteva Agriscience, Data Science and Informatics |

| **TOMASZ GOLAS (Chair)**  |
| Lead Research Laboratory, Deliflor Chrysanten |

| **SARAH SCHMIDT (Chair)**  |
| Project Coordinator, Heinrich-Heine-University Düsseldorf |

| **JUDITH BERGOEER**  |
| Scientific Account Manager, Cergentis, The Netherlands |

<p>| <strong>MAGDALENA ZUK (Chair)</strong>  |
| Assistant Professor, University of Wroclaw |</p>
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<tr>
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<tr>
<td>GUIDO F. SMITS</td>
<td>CSO, DataStories International BV</td>
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<td>ROEL VAN DEN BERGH</td>
<td>Vice President of Commercial Operations, DataStories International BV</td>
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<td>GREGORY SWORD</td>
<td>Professor and Chair of Cotton Entomology, Texas A&amp;M University, USA</td>
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<td>Assistant Professor and Lecturer, School of Agriculture and Food Science, University of College Dublin, Ireland</td>
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<td>DONALD R. MARVIN</td>
<td>President and CEO, Inocucor Corporation (U.S.) and Inocucor Technologies (Canada)</td>
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<td>SIMON FLEISCHLI</td>
<td>Area and Product Manager, Andermatt Biocontrol, Switzerland</td>
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<td>METTE NICOLAISEN</td>
<td>Associate Professor, Head of Section for Microbial Ecology and Biotechnology, University of Copenhagen</td>
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<td>NICK MOON</td>
<td>Global Regulatory Manager, Plant Impact</td>
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Keynote Address: Richard Visser
Professor, Chair, and Head of Plant Breeding, Dean of Research, Wageningen University & Research, The Netherlands

The use of novel editing techniques in practical breeding: possibilities and challenges

With the availability of novel breeding techniques the speed and efficiency by which new varieties can be generated is changing rapidly. Using novel editing techniques requires to know not only which genes and alleles of genes are responsible for the desired trait but also which parts of the gene are linked to the biological function of the trait. This is important in order to prevent pleiotropic negative effects. Without a doubt this is possible for single copy genes responsible for a trait but for genes belonging to gene families (resistance genes belonging to NBS LLR families, peroxidases or transcription factors) this is still a challenge. Although the scientific advantages of using these editing techniques are clear the legal status of these techniques is still undecided.

Keynote Address: Angela Sessitsch
Head of Bioresources, AIT Austrian Institute of Technology, Austria

Ecology understanding to advance plant microbiome applications

Current microbial applications are mostly selected based on lab-based functional screens, which do not consider complex interactions in the environment. As a consequence many inoculants do not show the expected effects in the field or do not persist in the target environment. Considering that the holobiont plant is associated with a huge diversity of organisms it can be expected that functioning as well as persistence and colonization greatly depend on the abiotic and biotic environment and ongoing complex interactions. A few aspects of microbiome ecology will be addressed and discussed in relation to the development of microbial applications.

Solution Provider Presentation:
Gil Ronen, CEO, NRGene

Improving genetic research and breeding of the most complex genomes with denovo assembly and pan genome analysis

The efficient assembly of large and polyploid genomes was, until recently, an unmet challenge, leading to limited use of genomic tools in breeding. The availability of a reference genome significantly advanced the genetic research of a given species. In addition, for crop plants, a reference is used to develop and employ DNA marker sets for breeding applications. Still, the genetic diversity within a given species is only partially represented by one reference genome, due to the broad intra-species genomic variability, including SNPs, InDels, translocations, and inversions. To capture the genomic diversity of a given plant species, one needs to create and compare multiple full genomes de-novo, representing genetically distinguished lines, ultimately creating a pan-genomic structure. Here we present the successful de novo assembly and all-to-all comparison of several maize and bread wheat genomes, revealing significant genomic and intragenic sequence additions to the first available reference genome. Gene presence/absence, copy number, and expression profile variations are all revealed by comparing genomes with mRNA and expression data. This functional diversity database could be used to correlate phenotypic and genomic variation, expanding our genetic understanding towards breeding more productive plants. A global effort will be described aiming to create pan-genome databases of additional major crop plants during 2018. These databases will enable overcoming the future threat of food shortages.
Sorghum is a major staple cereal with over 500 million people worldwide dependent on it every day. It has worldwide importance for animal feed, bio-industrial end uses, and for human consumption in the form of beer and spirits. We have used genetic engineering and genomics approaches in parallel to improve the key quality parameters of sorghum: starch, protein and sugars. We have manipulated the kafirin seed storage proteins and enzymes involved in packaging the endosperm protein-starch matrix. This has led to altered grain size, digestibility and processing qualities. We have also manipulated plant architecture genes that have a major effect on plant architecture, with altered leaf size, tiller number, root angle and number. We are now using CRISPR/Cas9 gene editing to improve sorghum grain quality.

**Site-directed genome modification in barley and wheat**

- A modular vector system for simultaneous expression of multiple target-specific guide RNAs and various Cas derivatives
- Prevalidation tests for specified endonucleases
- Examples for site-directed mutagenesis and precise genome editing

**Genome-specific GM and gene edited sorghum for improved grain quality and plant architecture**

Sorghum is a major staple cereal with over 500 million people worldwide dependent on it every day. It has worldwide importance for animal feed, bio-industrial end uses, and for human consumption in the form of beer and spirits.
the gene editing technique CRISPR/Cas9. Certain barley genes are upregulated more in susceptible than in resistant breeding lines when attacked by the bird cherry - oat aphid, suggesting they might make the host more favourable for the aphid. Two genes from the same gene family are now mutated in cv Golden Promise by using Agrobacterium-based transformation of CRISPR-Cas9 constructs. In the net-blotch/barley pathosystem the necrotrophic pathogen manipulates its host to trigger cell death. We have two candidate susceptibility genes in barley, one in cv Kombar and another in cv Rika. We use gene gun bombardment with CRISPR/Cas9-constructs in order to mutate these candidate S-genes.

In response to extracellular stimuli, numerous protein kinases transmit signals to the nucleus. In the nucleus, regulation of gene transcription ultimately determines the fate of cells, forming the basis of biological diversity. The regulation of gene expression is closely coupled to chromatin structure and its modifications, which determine the accessibility of many regulatory proteins and non-coding RNAs to the DNA, adding a further layer of complexity to the genetic information encoded by the DNA sequence. The identification of MAPK signaling cascades that signal to plants an attack by pathogens allows to monitor the in vivo epigenetic effects of a pathogen on host plant cells in real-time. I will discuss our latest findings on the use of this experimental system to identify novel components of plant defense and develop a global vision of how plant innate immunity is linked to epigenetic regulation.

The genome sequencing of crops is critical to improve crop genetic discovery, gene-editing, and product development. Reference genomes for crop plants serve as a platform for genetic discovery, gene-editing, and product development. During last decade, the rapid development of next generation sequencing technologies enabled the sequencing of many new genomes. In recent years, the availability of SMRT sequencing and several long-range mapping technologies enabled the producing of highly accurate and contiguous genomes, while techniques like 10X Genomics Linked-Read techniques enabled fast and cost-effective large-scale pan-genome studies. We will introduce our recent progress on the study of complex plant genomes and pan-genomes using these cutting edge new techniques.

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A new scenario for natural biocontrol: controlling harmful species by their extracellular self-DNA. The research for new products against pathogens, parasites, and infesting species implies huge scientific and economic efforts. Traditional approaches are based on random screening procedures searching for bioactive compounds from different sources. However, the development of new products, in most cases, has been limited by side effects on biological systems other than the target, environmental contamination, and by the induction of resistance in the organisms to be controlled. Consequently, despite the major and increasing efforts on research of new products in both agriculture and medicine, the rate of approval is significantly decreased in recent years. The recent discovery of the inhibitory effect of extracellular self-DNA has opened new perspectives for highly species-specific inhibitory product for biological control, with relevant economic and environmental advantages.

SOLUTION PROVIDER

TINGTING ZHOU

General Manager, Novogene Europe

Unveiling complex plant genome and pan-genome using cutting edge sequencing techniques

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BioNano genome mapping can produce complements of genomes that are the least amount of time? How can the traditional choke points of resolving chimeric-assemblies, gap filling and ordering scaffolds be overcome? PacBio long reads, paired with 10X Chromium linked reads, and BioNano genome mapping can produce uninterrupted, chromosome-length reference genomes in a high-throughput process.

KEVIN FENGLER

Research Scientist, Corteva AgriScience, Data Science and Informatics

Going “beyond platinum” with continuous, chromosome-spanning crop genome assemblies

Reference genomes for crop plants serve as a platform for genetic discovery, gene-editing, and product development. However, to effectively mine the high-levels of diversity in many plant genomes, a single reference genome is not enough. For a robust pan-genome view, a method for rapidly generating platinum-grade reference genomes is needed. A combination of complementary genomics technologies can now be used to achieve this goal. What is the optimal recipe to achieve the most complete and accurate assemblies created to date in the least amount of time? How can the traditional choke points of resolving chimeric-assemblies, gap filling and ordering scaffolds be overcome? PacBio long reads, paired with 10X Chromium linked reads, and BioNano genome mapping can produce uninterrupted, chromosome-length reference genomes in a high-throughput process.

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STEFANO MAZZOLENI

Professor of Applied Ecology and Modelling, University of Naples “Federico II”

A New Scenario for Natural Biocontrol: Controlling Harmful Species By Their Extracellular Self-DNA

A new scenario for natural biocontrol: controlling harmful species by their extracellular self-DNA. The research for new products against pathogens, parasites, and infesting species implies huge scientific and economic efforts. Traditional approaches are based on random screening procedures searching for bioactive compounds from different sources. However, the development of new products, in most cases, has been limited by side effects on biological systems other than the target, environmental contamination, and by the induction of resistance in the organisms to be controlled. Consequently, despite the major and increasing efforts on research of new products in both agriculture and medicine, the rate of approval is significantly decreased in recent years. The recent discovery of the inhibitory effect of extracellular self-DNA has opened new perspectives for highly species-specific inhibitory product for biological control, with relevant economic and environmental advantages.

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CONGRESS SCHEDULE

JIM DUNWELL
Professor, University of Reading, UK
Regulatory aspects of gene-edited crops
An important issue relating to the products of gene-editing, and their potential commercialization in the future, is whether they will considered as GM organisms (regulated) or products of mutagenesis (usually non-regulated), and many discussions are underway around the world to consider this matter. I will provide a summary of these various debates.

EARLY CAREER RESEARCHER: SARAH RAFFAN
Rothamsted Research and University of Bristol, UK
Genome editing for low-acrylamide wheat
Acrylamide is a processing contaminant and a Group 2a human carcinogen which was recently found in many foods. Wheat represents one of the major sources of dietary acrylamide intake.

BLANCA SAN SEGUNDO
Research Professor, Spanish Research Council (CRAG-CSIC), Spain
The role of microRNAs (miRNAs) in rice innate immunity
MicroRNAs (miRNAs) are short regulatory non-coding RNAs that guide gene silencing in eukaryotes by sequence-specific cleavage or translational repression of target transcripts. During the last years, the adoption of high-throughput sequencing technologies has significantly contributed to decipher the miRNA transcriptome of different plant species, including rice. However, although a substantial fraction of the rice miRNAome has been shown to be responsive to pathogen infection, the exact role of most of these pathogen-regulated miRNAs in rice immunity remains elusive. The major focus of our lab is to study miRNA-mediated gene regulation in the response of rice plants to pathogen infection. Towards this end, we use deep sequencing of small RNA libraries in combination with gain-of-function and loss-of-function (CRISPR/Cas9) approaches. Our findings support that miRNAs represent an integral part of the rice immune system.

CHRISTOPHE CLEMENT
Scientific Director, CNRS and Professor, University of Reims Champagne Ardenne, France
How some beneficial microorganisms may help grapevine to face both biotic and abiotic stresses
Grapevine (Vitis vinifera L.) culture is consuming huge amounts of phytochemicals among which fungicides are the most represented. In parallel, viticulture is confronted to the global warming, inducing hot periods and, as a paradox, cold/freezing night during early flowering. The bacterium Paraburkholderia phytofirmans strain PsJN is able to colonize the whole plant as an endophyte, entering the vascular system through the roots and diffusing in all plant organs. As soon as installed, it confers to the host plant some protection against severe diseases such as Botrytis and some efficient acclimation to cold/freeze stresses, mainly acting as stimulating plant metabolism and priming plant immunity.

MAIKE STAM
Assistant Professor, University of Amsterdam, The Netherlands
Genome-wide identification of regulatory sequences in Zea mays using DNA and chromatin features
While most cells in multicellular organisms carry the same genetic information, in each cell-type only a subset of genes is being transcribed. Such differentiation in gene expression depends, for a large part, on the activation and repression of regulatory sequences, including transcriptional enhancers. Transcriptional enhancers can be located tens of kilobases from their target genes, but display characteristic chromatin and DNA features, allowing their identification by genome-wide profiling. We have shown that integration of genome-wide DNA methylation, histone acetylation and chromatin accessibility data sets can be applied to predict tissue-specific distal enhancer candidates in Zea mays, thereby providing a basis for a better understanding of gene regulation in this important crop plant. The presentation will elaborate on the identification, but also characterization of identified enhancer candidates.

DAN FUNCK JENSEN
Professor, Swedish University of Agricultural Sciences, Sweden
Biocontrol interactions important for plant disease control with the fungus Clonostachys rosea
The fungus Clonostachys rosea has shown significant biocontrol of a range of plant diseases including Fusarium head blight and Septoria leaf blotch in wheat, grey mould in strawberry and, several seed- and soil-borne diseases. It is, however, crucial for successful biocontrol, to understand the disease cycle and the biology or lifestyle of the biocontrol agent (BCA) for predicting the right time for application and understand to what niche(s) on the plant to apply the BCA. It must also be addressed how it interacts with target pathogens and the natural plant/soil microbiome. The environment and cultural practises at application and during biocontrol interaction are also important. These aspects are discussed based on our molecular approaches for studying biocontrol interactions and our results from field experiments.

EARLY CAREER RESEARCHER: NATHANIEL BUTLER
University of Wisconsin-Madison, USA
First generation genome editing in potato using hairy root transformation
Genetic transformation has become a bottle-
**CONGRESS SCHEDULE**

**DAY 1 MONDAY 14TH MAY 2018**

**14:00-14:30**

**14:00-14:25**

**STEVEN KELLY**
Associate Professor, University of Oxford, UK

**The impact of photosynthetic efficiency on the evolution of plant genes and genomes**

I will discuss how the photosynthetic efficiency of a plant can directly influence the composition of its genes and genomes. I will further reveal how photosynthetic efficiency modulates gene evolutionary rate. Finally I will discuss how this interaction between photosynthesis and evolution can explain differences in patterns of species diversification rates, both through geological time and geographical space.

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**14:30-15:00**

**CLAUDIA JONAK**
Principal Scientist, AIT Austrian Institute of Technology, Austria

**Signaling towards abiotic and biotic stress resistance**

Unfavorable environmental conditions and pathogen infections limit plant growth and development. Plants have evolved complex cellular and physiological mechanisms to prevent damage and enable growth under stress conditions. These responses are controlled by stress-type specific but also common and interacting signaling pathways, which may inhibit each other explaining the trade-off between biotic and abiotic stress responses. In this talk, an evolutionary conserved signaling module that links protein phosphorylation cascades to metabolic adjustment under both abiotic and biotic stress conditions will be discussed.

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**15:00-15:25**

**PETER JENS**
CEO, AND Biopharma

**Regulations: From product- to systems thinking**

Many new biological products enter the market; novel technologies blur the lines between biologicals and chemicals; new actors grow rapidly, old ones consolidate. Consumers and citizens become more vocal on the product-quality, retailers demand safe and clean products, way above any legal requirement. Novel technologies enable to see more and more microbial interactions. New discoveries will end, at times rabiate- public stalemated discussions. What is actually a genetically modified organism nowadays? What is a risk? How to measure, how to judge, how to regulate the new agspace? I argue that the current dialogue, discussion, lobby, positioning and regulatory approach is fated. Different thinking is required and I will give some examples on how more ecological thinking may help unravel the regulatory quagmire of agrochemicals and agrobiologics.

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**15:25-15:55**

**15:25-15:55**

**SOLUTION PROVIDER PRESENTATION:**

**JUDITH BERGBOER**
Scientific Account Manager, Cergentis, The Netherlands

**TLA technology for targeted complete Next Generation Sequencing of (trans)genes and gene editing events in plants**

- Introduction into the TLA technology for targeted complete Next Generation Sequencing
- TLA-based analysis of transgenes, integration sites and gene editing events
- TLA-based complete gene sequencing and haplotyping

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**14:45-15:00**

**NEHA VAID**
Post-doctoral Researcher, Max Planck Institute of Plant Physiology, Germany

**Identification of molecular mechanism of hybrid breakdown in Arabidopsis thaliana**

We are studying a case of hybrid chlorosis among two Arabidopsis

---

**16:00-16:25**

**EARLY CAREER RESEARCHER:**

**NEHA VAID**
Post-doctoral Researcher, Max Planck Institute of Plant Physiology, Germany

**Identification of molecular mechanism of hybrid breakdown in Arabidopsis thaliana**

We are studying a case of hybrid chlorosis among two Arabidopsis

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**14:45-15:00**

**EARLY CAREER RESEARCHER:**

**CLAUDE ARNOLD**
PhD Student, John Innes Centre, UK

**Powdery Mildew: A Tale of Two Fungicides**

Blumeria graminis is a powdery mildew pathogen which infects many cereals across the world. It is mainly controlled by the application of fungicides
thaliana accessions, Shahdara (Sha, Tajikistan) and Lövvik-5 (Lov-5, Sweden) that has been mapped to interaction between two recessive alleles, one of which has been identified as a conserved RNA helicase (RH18) gene from Lov-5. This gene is quite common to Lövvik area, indicating its possible role in local adaptation. I will present our recent findings regarding the molecular mechanism that drives the incompatibility phenotype in hybrid between Sha and Lov accessions. Hybrid incompatibility cases are often traced to conflicts among rapidly evolving alleles associated with rapidly evolving defence responses. Our study establishes that incompatible molecular interactions with relatively conserved loci can also lead to hybrid breakdown.

but only a few are still available. I have characterised isolates from an outbreak of B. graminis f.sp. tritici (Bgt) on wheat where two of the major fungicides used against Bgt were ineffective: Cyflamid and Corbel. All Bgt isolates from the study site were completely resistant to Cyflamid sprayed at the recommended field rate. However, over the following two years, the Bgt population recovered sensitivity to Cyflamid. Additionally, following two sprays of Corbel, these Bgt isolates had significantly lower sensitivity to Corbel than field isolates. Genetic and genomic analysis is in progress, with the aim of identifying candidate genes for resistance to Cyflamid and to Corbel.

### TABLE 2: DAN FUNCK JENSEN

Professor, Swedish University of Agricultural Sciences, Sweden

Successful application strategies in biological plant disease control – single microbial strains, consortia or synthetic microbiome applications

### TABLE 3: JOSEPH SCHMIDT

SVP, Business Development & Strategy, BioConsortia, Inc.

Cross-discipline Collaboration

### TABLE 4: AMIT VASAVADA

Senior VP of R&D and Chief Technology Officer, Marrone Bio Innovations

Formulating Biologicals: Strategies and Challenges

### TABLE 5: NICK MOON

Global Regulatory Manager, Plant Impact Biostimulant Regulation

*Full details of the Roundtables can be found at the end of Day 1*
### TABLE 1:
**DONALD R. MARVIN**  
President and CEO, Inocucor, USA and Canada  
Commercialisation, Product Launch, and Business Development

- Companies operating in the agri-tech space must manage limited working capital to navigate the post R&D, pre-investment period.
- Steps to successful commercialization include: secure the IP; run trials to validate the science; build an achievable product strategy; attract the brightest scientists and build a strong Board of Directors.
- To attract high-caliber investors, a company’s leadership team needs to be able to convey the company’s story in a compelling, convincing and honest fashion.
- When it comes to investors, what is the difference between smart money and easy money?

### TABLE 2:
**DAN FUNCK JENSEN**  
Professor, Swedish University of Agricultural Sciences, Sweden  
Successful application strategies in biological plant disease control – single microbial strains, consortia or synthetic microbiome applications.

We will address the importance of understanding the biology of the biocontrol agents (BCAs), the target pathogen and its disease cycle and, the role of the plant microorganisms for successful inoculation biocontrol.
- What constraints or possibilities do you see for inoculation biocontrol using BCAs based on 1) a single strain 2) consortia of BCAs?
- What biological knowledge is required about the plant, the disease(s)/pathogen(s) and the biocontrol agent(s)?
- What role do the right timing and placement of BCAs play for successful biocontrol?
- Do the function of the plant microbiome play an important role for successful BCA applications?
- What impact do crop management including IPM strategies have?
- Are synthetic microbiome applications a realistic approach (focussing on biology not on legislative aspects)?

### TABLE 3:
**JOSEPH SCHMIDT**  
SVP, Business Development & Strategy, BioConsortia, Inc.  
Cross-discipline Collaboration

Cross-disciplinary collaborations have become an increasingly important part of science and technology. The synergistic and skillful combining of different disciplines can achieve insight beyond current borders and thereby generate novel solutions to complex problems. The combination of methods and data from different fields can achieve more than the sum of the individual parts could do alone. The biological crop input segment is segment that is ripe for improvement through cross-disciplinary collaborations. To kick off the discussion, participants' opinions will be sought on the best opportunities in this area. In addition to this discussion, we will discuss keys to success.

### TABLE 4:
**AMIT VASAVADA**  
Senior VP of R&D and Chief Technology Officer, Marrone Bio Innovations  
Formulating Biologicals: Strategies and Challenges

Novel biological solutions for Agriculture are being advanced to the next stage as innovative approaches are employed to find and develop biopesticides and biostimulants. Complex nature of bioactives coupled with formulation technologies need a special attention due to inherent stability, delivery and economic considerations. Ranging from single molecule for biochemical products in premixes and tank mixes to single or multiple biologicals pose a variety of challenges compared to conventional chemicals. This round table discussion is designed to stimulate an interactive dialog to share thoughts, experiences and challenges for this exciting industry.

### TABLE 5:
**NICK MOON**  
Global Regulatory Manager, Plant Impact  
Biostimulant Regulation

Europe is advancing with legislation which will regulate plant biostimulants and lead to a Single Market opportunity for the products. With the initiation of the trilogue involving the European Commission, European Council and European Parliament, the institutions are in the process of reaching an agreement on the text of the draft fertilising products regulation which includes plant biostimulants in its scope. This regulation will amend the current EC Regulations No. 1069/2009 and No. 1107/2009. This discussion will focus on:
- Diversity of biostimulants and the draft definition.
- Current situation of the Regulation and the path moving forward.
- Global perspective on biostimulant regulation.
- Positive aspects of the Regulation for industry.
- Obstacles and challenges which need to be overcome prior to the Regulation entering into force.
- The support of the biostimulants industry by the European Biostimulants Industry Council (EBIC).
**Track 1: Exchange Hall**

**PLANT GENOMICS & GENE EDITING CONGRESS**

**08:00-08:25**

**Room: The Shipping Hall**

**Refreshments**

**08:25-08:30**

**Track Chair:** Magdalena Zuk, Assistant Professor, University of Wroclaw

**KEYNOTE ADDRESS:**

**GEORGE COUPLAND**

Professor and Director of Plant Developmental Biology, Max Planck Institute for Plant Breeding, Germany

Genomic and molecular-genetic analysis of divergence of annual and perennial life history in the Brassicaceae

- Comparison of the genomes of annual and perennial species within a phylogenetic framework.
- Description of specific reproductive traits that have diverged during the separation of annual and perennial species.
- Use of CRISPR-cas9 reverse genetics to analyse the function of genes in the perennial species.

**09:40-10:05**

**Track Chair: Christophe Clement, Scientific Director, CNRS and Professor, University of Reims Champagne Ardenne, France**

**KEYNOTE ADDRESS:**

**AMIT VASAVADA**

Senior VP of R&D and Chief Technology Officer, Marrone Bio Innovations

Developing Customer-friendly Formulations to deliver Biopesticides and Plant Health Products

Marrone Bio Innovations is an industry leader biopesticide company that discovers, develops and delivers solutions for Integrated Pest Management. MBI has harnessed a unique library of natural microbes and their metabolites to develop EPA-approved bio-based insecticides, fungicides, herbicides and nematicides in addition to plant health products. Presentation of biological activity in the final product has been achieved with the development of novel formulation strategies customized for foliar, aerial, and soil applications. The presentation will address the development of various formulations.

**SOLUTION PROVIDER PRESENTATION:**

**JULIEN ROUZADE**

NGS Field Application Specialist, PerkinElmer

From Extraction To Analysis, PerkinElmer’s Solutions For The Whole Plant Genomic Workflow

With applications expertise spanning the Genomic workflow from extraction to analysis, we enable automated workflows for next generation sequencing (NGS) library prep chemistries to produce accurate, reproducible sequencing results. PerkinElmer’s NGS offerings include nucleic acid extraction solutions, instrumentation, and assays to simplify nucleic acid and library analysis, workstations to automate library preparation, library preparation kits, and software for the analysis of complex sequencing data. PerkinElmer’s NGS workflow solutions are designed to solve the researcher’s problems. From improving nucleic acid yields, to increasing throughput, to reducing bias, we have the solution you need.
CHRIS MALIEPAARD  
Associate Professor, Wageningen University & Research, The Netherlands  
Genetic mapping and QTL analysis in polyploids  
Construction of genetic linkage maps and QTL mapping in polyploids is challenging: instead of dealing with presence/absence of only two parental alleles of markers and QTLs, we have to account for more possible dosages of alleles and more than one type of heterozygote. Different modes of inheritance have to be considered as well. Moreover, many polyploids lack the availability of a genome sequence and are often outbred with no homozygous parental lines. In our research, we develop advanced quantitative methods and tools for genetic mapping and QTL analysis in polyploid crosses of different crops, such as potato, rose and chrysanthemum.

STIG UGGERHØJ ANDERSEN  
Associate Professor, Plant Molecular Biology, Aarhus University  
The effects of host and microbe natural variation on symbiotic nitrogen fixation in white clover  
• The NCHAIN project aims to optimize the symbiotic interaction between white clover and rhizobium to increase nitrogen fixation efficiency in low-input agricultural systems in temperate regions.  
• We have collected and genotyped 200 white clover and rhizobium accesses, which we are testing in pairwise combinations both in the greenhouse and in the field to understand the genetic interactions underpinning nitrogen fixation efficiency.  
• Natural variation in rhizobium and clover populations and its impact on nitrogen fixation will be discussed.

PacBio sequencing, EMS-mutagenesis, transformation, transient expression, and allele mining allowed us to verify and characterize the gene and the resistance it confers. A functional copy of Yr15 was found only in the B genome of wild emmer wheat, while non-functional copies were found in any of the genomes of modern pasta durum and common wheat. These results indicate that Yr15 has the potential to improve stripe rust resistance in a wide range of wheat varieties and emphasize the role of wild emmer wheat germplasm as a reservoir of resistance genes for wheat.

Also included. The different use types and the future directions of PHI-base, including the development of an online author curation tool, will be discussed.

How AI/Machine Learning can even help non-data scientist to find the dominant SNPs over a coffee?  
• Through technological breakthroughs, now even domain experts can apply AI and Machine Learning and augment their intelligence of the studied topic.  
• Learn how our proprietary technology is crushing eg. PCA accuracy and is able to determine the dominant variables out of even thousands and thousands of variables, like needed within genomics.  
• Learn how in-silico design optimizes conflicting targets (eg. Yield and Resistance) boosting the performance of plant innovation.  
• Specific examples will be shared.
13:00-14:00
Room: The Shipping Hall
Lunch

TOM GREENE
Senior Research Director, Trait Discovery Organization: DuPont Pioneer
Targeted Breeding Applications with CRISPR-Cas

Plant breeders have created new plant hybrids and varieties through plant breeding methods for thousands of years. CRISPR-Cas represents the next generation of modern breeding tools that enables a more targeted way to discover and develop valuable traits within the crop of interest. Our success to date builds on our growing knowledge of the crop’s genome, our ability to resolve or associate key phenotypic responses down to a validated candidate gene and our development of a suite of enabling technologies that allow us to create the specified variations within the crop. In this presentation, I will share how we are using CRISPR-Cas to deliver new trait opportunities across our core crops and enable product development in our most elite genetics.

ERIK JONGEĐIJK
Head of Business Development Technology, KWS SAAT SG

Genome editing in agriculture ... an industry perspective on requirements for robust outcomes beyond low-hanging fruits

Robust Genome Editing technologies in plants promises to revolutionize biological research and to facilitate faster and cheaper development of commercial crops with enhanced traits. To date the technology is at the peak of its hype curve expectations are sky-high but significant breakthrough developments in a number of adjacent biologic research fields will be required for Genome Editing to achieve its full potential in plant breeding and agriculture. This talk will focus on opportunities and limitations for Genome Editing technology in plant breeding programmes and focus on key developments in plant biology required to overcome current technical, regulatory and intellectual property hurdles limiting the achievement of its full potential.

CLAIRE STANLEY
Independent Team Leader, Agroscope, Switzerland

Microbiome-on-a-Chip: New frontiers in plant-microbiota research

• Recently, it has been demonstrated that microfluidic technology offers several new opportunities to study whole organisms and their interactions. Microfluidics has a great potential to provide a unique view of biological events at the level of single organisms and cells (i.e. microbe–microbe interactions), allowing precise environmental control, high-resolution imaging and the simulation of environmental complexity.
• In this talk a variety of case studies will be highlighted, demonstrating how this technology has been used to study bacterial-fungal interactions, the dynamic response of a fungal mycelium toward nutrients and predators and the local adaptation of plant roots to environmental asymmetry.
• We are now developing new tools to enhance our understanding of interactions in the plant microbiome by using microfluidic technology to zoom into the microscale.

DONALD R. MARVIN
President and CEO, Inocucor, USA and Canada

Catalyzing Continuous Improvement Through Customer Trials

We will report about Inocucor’s methodology and philosophy related to its more than 150 field trials currently underway with high-value produce and row crops in varied geographies including:
• Two strawberry trials in California: One in an organic field in 2016, the other in potted strawberries, just completed in Summer 2017.
• A California lettuce trial for which Inocucor just received data with impressive results. Given the potential for nitrogen regulation in California, this trial was set up using reduced rates of nitrogen with the addition of Inocucor IN-M1.
• Results of recent trials with corn, soybean, wheat, canola, potatoes and cotton.
Pearl millet is a cereal crop known for its high tolerance to drought, heat and salinity stresses as well as for its nutritional quality. The molecular mechanism of drought tolerance in pearl millet is unknown. Here we attempted to unravel the molecular basis of drought tolerance in two pearl millet inbred lines, ICMB 843 and ICMB 863 using RNA sequencing. Under greenhouse condition, ICMB 843 was found to be more tolerant to drought than ICMB 863. We sequenced the root transcriptome from both lines under control and drought conditions using an Illumina Hi-Seq platform, generating 139.1 million reads. Mapping of sequenced reads against the foxtail millet genome, which has been relatively well-annotated, led to the identification of several differentially expressed genes under drought stress. Total of 6799 and 1253 differentially expressed genes were found in ICMB 843 and ICMB 863, respectively. Pathway and gene function analysis by KEGG online tool revealed that the drought response in pearl millet is mainly regulated by pathways related to photosynthesis, plant hormone signal transduction and mitogen-activated protein kinase signalling. The changes in expression of drought-responsive genes determined by RNA sequencing were confirmed by reverse-transcription PCR for 7 genes. These results are a first step to understanding the molecular mechanisms of drought tolerance in pearl millet and lay a foundation for its genetic improvement.

The benefits of molecular cytogenetics in modern genomics of crops
Recent innovations in microscopy, genomics and bioinformatics have contributed enormously to modern plant cytogenetics. Such technologies have generated an unprecedented knowledge in how chromosomes are organised, how they recombine at meiosis and how they are transmitted to the next generations. Spectacular achievements of chromosome painting

Recent advancements in microscopy, genomics and bioinformatics have contributed enormously to modern plant cytogenetics. Such technologies have generated an unprecedented knowledge in how chromosomes are organised, how they recombine at meiosis and how they are transmitted to the next generations. Spectacular achievements of chromosome painting

The Design-Build-Test-Learn (DBTL) concept, enabled by effective testing of ideas to accelerate product development. Biology integrates advances in chemistry, biology, computer science and engineering to enable rapid, precise and cost effective testing of ideas to accelerate product development. The Design-Build-Test-Learn (DBTL) concept, enabled by

Effective regulation of primary metabolism is critical for bacteria to adapt to different environments. I will discuss how plant-associated pseudomonads control carbon metabolism by sensing the Entner-Doudoroff pathway intermediate KDPG. KDPG bonds to two highly similar transcription factors; the ED regulator HexR, and the previously uncharacterised regulator RccR. RccR inversely controls the glyoxylate shunt, gluconeogenesis and pyruvate metabolism, suppressing the first two pathways as pyruvate metabolism genes are expressed, and vice versa. This complex regulation is enabled by two distinct consensus sequences in the RccR regulon promoters. KDPG binding simultaneously increases RccR affinity for the glyoxylate shunt/gluconeogenesis promoters, and releases repression of pyruvate metabolism. This elegant two-regulator circuit allows Pseudomonas to rapidly respond to carbon availability in the rhizosphere by sensing a single key intermediate.
now bridge the gaps between genetic and physical mapping by positioning genetic markers and contigs on the chromosomes; in addition, it helps us to understand how chromosomes are molecularly organized. FISH technology also supports genomics and bioinformatics in positioning annotated contigs and establishes the size of gaps in between them. In comparative genomics, we are able to elucidate chromosome rearrangements, repeat dynamics, centromere and heterochromatin locations and are able to interpret linkage drag and other problems in breeding programs.

14:15-14:40

advances in high throughput DNA assembly, genome editing, rapid testing systems and analytical platforms, is critical for genome and organism level interrogation/engineering for applications of interest. Current examples of engineering biology in plant biotechnology and focus areas for future growth to meet customer needs will be described.

14:00-14:40

Continued

14:40-15:05

JOHN DOONAN
Director and Professor of Genetics, National Plant Phenomics Centre, Aberystwyth University, UK
Phenomics method development

14:40-15:05

HOLGER SCHULTHEISS
Research Manager, Fungal Resistance Projects, BASF Plant Science Research Management
Input and output traits – examples for sustainable solutions in agriculture
Fungal diseases cause major economic losses in many important crops all over the world. One of the strategic pillars of BASF Plant Science Company is the development of disease resistant crops. Our recent project focuses on fungal disease resistance in the major row crop soybean, targeting Asian Soybean Rust. Eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) are polyunsaturated fatty acids with health benefits. The current sources of EPA and DHA are primarily wild caught fish and microbial fermentation. Supply is constrained by sustainability limits on the wild fish harvest and the higher cost of fermentation. We envision an affordable supply of EPA and DHA that is scalable and highly sustainable. Our breakthrough was achieved by introducing all genes to make EPA and DHA into canola.

14:40-15:05

ANGELA FEECHAN
Assistant Professor and Lecturer, School of Agriculture and Food Science, University of College Dublin, Ireland
Field isolates of Z. tritici differentially express small secreted proteins
Ireland’s wheat yields are on average the highest in the world but these yields are under threat from Septoria Tritici Blotch (STB) caused by Zymoseptoria tritici. Irish field isolates of Z. tritici have been reported to be particularly virulent in the field. Increased pycnidia formation was observed at 21 days post infection (dpi) with an Irish field isolate compared to the Dutch reference isolate IPO323. In order to investigate genes that might be responsible for increased virulence, RNAseq was carried out. Analysis revealed a small number of genes (58) that were significantly differentially expressed between the three isolates including a subset of small secreted proteins (SSPs). Functional assays will be required to confirm a role for these genes in virulence.

15:05-15:30

GREG GOCAL
Chief Scientific Officer and Executive VP, Cibus
Cibus' trait machine is accelerating plant breeding using the Rapid Trait Development System (RTDS™) to benefit consumers, farmers and processors
- Over thousands of years, breeders have relied on random variation for crop improvement.
- Cibus has developed a process called the Rapid Trait Development System (RTDS) that combines advanced cell culture and a range of modern mutagenesis tools to accelerate plant breeding by precisely specifying beneficial typographical changes in crop genomes much like a word processor on your computer.
- What used to be a random process taking many years can now be accomplished in months with outcomes indistinguishable from those that can occur in nature.

15:30

Conference Close
### MAKING A POSTER PRESENTATION

Poster presentation sessions will take place in breaks and alongside the other breakout sessions of the conference. Your presentation will be displayed in a dedicated area, with the other accepted posters from industry and academic presenters. We also issue a poster eBook to all attendees with your full abstract in and can share your poster as a PDF after the meeting if you desire (optional). Whether looking for funding, employment opportunities or simply wanting to share your work with a like-minded and focused group, these are an excellent way to join the heart of this congress.

In order to present a poster at the congress you need to be registered as a delegate. Please note that there is limited space available and poster space is assigned on a first come first served basis (subject to checks and successful registration). We charge an admin fee of £100 to industry delegates to present, that goes towards the shared cost of providing the poster presentation area and display boards, guides etc. This fee is waived for those representing academic institutions and not for profit organisations.

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<tr>
<th>POSTER PRESENTATION TITLE</th>
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<th>AFFILIATION</th>
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<td>Application of molecular data to construct common bean core collection (Central and South Eastern European germplasm example)</td>
<td>Barbara Pican, Peter Dolničar, Aleš Sedlar, Jelka Šuštar-Vozlič, Lovro Sinkovič, Vladimir Meglič</td>
<td>Agricultural Institute of Slovenia</td>
</tr>
<tr>
<td>The effects of Ascophyllum nodosum extract and its possible oligosaccharides on the soybean gene expression.</td>
<td>Chao Wang, Zhongmin Dong</td>
<td>Saint Mary’s University</td>
</tr>
<tr>
<td>Combining Protein Sequence Similarities and GO-term Semantic Similarities Improves Protein Function Prediction in Arabidopsis</td>
<td>Stavros Makrodimitris1, Roel and C.H.J. van Ham11, Marcel J.T. Reinders1</td>
<td>Delft Bioinformatics Lab, Delft University of Technology, Mekelweg 4, 2628CD, Delft, the Netherlands and 2Keygene N.V., Agro Business Park 90, 6708PW, Wageningen, the Netherlands.</td>
</tr>
<tr>
<td>RNA-Seq analysis of Orobanche resistance in tobacco: development of molecular markers for breeding recessive resistance from Wika tobacco variety.</td>
<td>Cotutcheau, J.; Julio E.; Malpica, A.; Bachet, S.; Volpatti, R.; Decors, C.</td>
<td>Imperial Tobacco Limited, Leaf research, La Tour, 24100 Bergerac, France 1Bergere Seed and Breeding, La Tour, 24100 Bergerac, France.</td>
</tr>
<tr>
<td>In situ mapping in the whole-genome sequencing era</td>
<td>Ludmila Khristaleva, Dmitry Romanov, Ilya Kirov, Natalia Kudryavtseva, Sergey Odintsov, Alexey Ermolaev</td>
<td>Russian State Agrarian University-Moscow Timiryazev Agricultural Academy</td>
</tr>
<tr>
<td>Plant repeatome: bridging the gap between linear DNA sequence and genome structure</td>
<td>Ilya Kirov, Dmitry Romanov, Natalia Kudryavtseva, Sergey Odintsov, Alexey Ermolaev, Ludmila Khristaleva</td>
<td>Russian State Agrarian University-Moscow Timiryazev Agricultural Academy</td>
</tr>
<tr>
<td>DRAWID: user-friendly java software for chromosome measurements and idiogram drawing</td>
<td>Dmitry Romanov, Ludmila Khristaleva, Natalia Kudryavtseva, Sergey Odintsov, Alexey Ermolaev, Ilya Kirov</td>
<td>Russian State Agrarian University-Moscow Timiryazev Agricultural Academy</td>
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<tr>
<td>Candidate genes for resistance to Fusarium oxysporum f.sp. cubense Race 1 in the wild diploid banana species Musa acuminate var. malaccensis</td>
<td>Fajarudin Ahmad, Vuuy S. Poerba, Hugo A. Volkart, Harold JG Meijer, Hans de Jong, Henk J Schouten, Gert HJ Kema</td>
<td>Wageningen University &amp; Research, Laboratory of Plant Breeding, Wageningen, the Netherlands.</td>
</tr>
<tr>
<td>Identification of novel priming agents by monitoring the expression of defence genes in rice cell suspension cultures</td>
<td>J. De Kesel, R. Gonzalez-Gutierrez, E. Pauwels, S. Siddique, T. Kyndt</td>
<td>Ghent University, Faculty of Bioscience Engineering, Department of Biotechnology</td>
</tr>
<tr>
<td>Study of the physiological importance of rice EUL lectins in root development and drought stress response using CRISPR technology.</td>
<td>Jeroen Lambin, Kondeti Subramanyam, Isabel Verbeke, Elis J.M. Van Damme</td>
<td>University Ghent</td>
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<td>SES: Synthetic expression system for plants</td>
<td>Anssi Rantasalo, Jussi Joensuu, Heiko Rischer, and Dominik Mojzita</td>
<td>VTT Technical Research Centre of Finland Ltd</td>
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<tr>
<td>Comparative de novo transcriptomic profiling of salinity stress responsiveness in contrasting pearl millet lines</td>
<td>Harshraj Shinde, K. Keisuke Tanaka, Ambika Dudhate, Daisuke Tsugama, Shinkui Liu, and Tetsuo Takanod</td>
<td>The University of Tokyo, Japan</td>
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<tr>
<td>Towards the pBC‘4 in accelerated introgression breeding for fire blight resistance using a “Fast Track” approach in apple</td>
<td>1Simonne Schuetz, Laura Dallenhach, Luzia Lussi, Iisable Baumgartner and Markus Kellerhals</td>
<td>Institute for Plant Production Sciences IPS, Agroscope, Switzerland -Online master student in plant breeding at Wageningen University</td>
</tr>
<tr>
<td>GFP-based transient gene editing marker system to support selection of agronomic traits: A case study of targeting elevated tryptophan content in maize</td>
<td>Bettina Nagy, Györgyi Ferenc, Katalin Török, István Nagy, Dénes Dudits and Ferhan Ayaydın</td>
<td>Biological Research Centre of Hungarian Academy of Sciences</td>
</tr>
<tr>
<td>Comparison of two different genome-editing technologies (OTNE and CRISPR/Cas9) in maize (Zea mays L.) and rice (Oryza sativa L.) cells</td>
<td>Zoltán Zombori, Szabolcs Péter Török, Bettina Nagy, Györgyi Ferenc, Katalin Török, Dénes Dudits and Ferhan Ayaydın</td>
<td>Biological Research Centre of Hungarian Academy of Sciences</td>
</tr>
</tbody>
</table>
17. Chemical modification of template ssDNAs and gRNAs for increasing the efficiency of plant gene editing

Györgyi Ferenc, Zoltán Kupínhár, Elfrieda Fodor, Tamás Kukli, Ákos Szamosvölgyi, Bettina Nagy, Zoltán Zombori, Ayşegül Öktem, István Nagy, Dénéts Dudit and Ferhan Ayaydın

Hungarian Academy of Sciences, Biological Research Centre, Szeged

18. Identification of genes differentially expressed in resistance reaction to Didymella pinodes in Pismum sativum L. field experiment

Magdalena Gawlowaska, Anna Durska, Wojciech Święcicki, Lech Boros

Institute of Plant Genetics, Polish Academy of Sciences, Strezyszyk 34, 60-479 Poznań

19. Impact of Colorado potato beetle gut microbiome in the adaptation of plants to drought and heat stresses associated to climate change

Carolina Rausell, Inmaculada García-Robles, M. José López-Galliano, M. Dolores Real

Department of Genetics, University of Valencia

20. Reliably detecting copy number variation in plant genomes

Raul Y. Wijfjes, René Boesten, Sandra Smit, Mark G.M. Aarts, Dick de Riddler

Bioinformatics Group, Wageningen University & Research

21. A fast and reliable method for detecting single base editing

Cornelia Hampe1, Montse Morell2, Tatiana Garachtenko3, Patrick Martin1, Baz Smith1, Michael Haugwitz1, and Andrew Farmer1

Takara Bio Europe SAS, 78100 Saint-Germain-en-Laye, France; Takara Bio USA, Inc., Mountain View, CA 94043, USA

22. Enhancing Soil Fertility in Northern Mountainous Areas of Vietnam by Developing Rhizobial Inoculants for Cowpea Vigna Unguiculata (var. Cylindrica) in Intercropping Systems

Trung Thanh Nguyen1,2,3, Mithoöthe Herviait1, Hai Thi Thanh Nguyen1, Vinh Le Bui1, Mary Otieno1, Olivier Couillert2, Hang Le Thuy1, Tuan Anh Nguyen4 and Didier Lescuer5,6,7

1Vietnam National University of Agriculture, Hanoi, Vietnam; 2CIAT-Asia, Hanoi, Vietnam; 3Kasetsart University, Bangkok, Thailand; 4AgroParisTech, Paris, France; 5NOMAFIS, Phu Tho, Vietnam; 6CIRAD, Montpellier, France; 7Deakin University, Melbourne, Australia

23. The EU official control system for GM food and feed

W. Broothaerts, M. Mazzara, H. Emons

Joint Research Centre, European Commission

24. CRISPR/Cas9 GoldenBraid toolkit application to generate tomato chlorophyll-retaining gfi mutants

Gianoglio S1, Comino C1, Acquaro A1, Moglia A1, Blasio F2, Lanteri S1, Orzaez D1, and Granell A1

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25. Knock-out of Polyphenol Oxidase Genes in Eggplant using the CRISPR/Cas9 GoldenBraid toolkit

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Mariette Andersson, Helle Turesson, Niklas Olsson, Ann-Sofie Fält, Pia Olsson, Mathias Samuelsson and Per Hofvander

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Nigel G. Halford and Sarah Raffan

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Magdalena Dziazo, Agata Hnitecka, Jan Szopa, Magdalena Zuk

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Magdalena Zuk, Magdalena Dziazo, Jan Szopa

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Špela Baebler1, Anna Coli2, Živa Ramšak2, Tjaša Star2, Oren Tzfadia2, Yves Van de Peer1, Kristina Gruden2

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Ayşegül Öktem, Györgyi Ferenc, Áladska Kalic, Elfrieda Fodor, Dénéts Dudit and Ferhan Ayaydın; Elfreda Fodor, Dénéts Dudit and Ferhan Ayaydın

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36. Transcription factor STZP1 participates in the reproductive development of Solanum tuberosum

Jagoda Czarnecka, Agnieszka Kiełbowicz-Matuk, Tadeusz Rorat

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Agnieszka Kiełbowicz-Matuk, Urszula Talar, Tadeusz Rorat

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