6TH PLANT GENOMICS & GENE EDITING CONGRESS: EUROPE

PARTNERSHIPS IN BIOCONTROL, BIOSTIMULANTS & MICROBIOME: EUROPE


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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 VISSE
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

BARRY GOLDMAN
VP and Head of Discovery, Indigo Agriculture
CONGRESS SYNOPSIS

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: Future Potential of New Breeding Technologies
PARTNERSHIPS IN BIOCONTROL, BIORSTIMULANTS & 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
CONFIRMED SPEAKERS

RICHARD VISSER
Professor, Chair, and Head of Plant Breeding, Dean of Research, Wageningen University & Research, The Netherlands

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
University of Tokyo, Japan

WENKAI JIANG
Senior Technical Director, Novogene

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

ODD ARNE OLSEN
Professor, Norwegian University of Life Science, Norway

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, LUK and University of Helsinki, Finland

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

RODMIRO 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, DuPont Pioneer

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

GREG GOCAL
Chief Scientific Officer and Executive VP, Cibus

TOM OSBORNS
(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 JONGEDJUK
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

AGNÈS RICROCH
Associate Professor in Evolutionary Genetics and Plant Breeding, AgroParis Tech, and Adjunct Professor, Pennsylvania State University

MICHAEL PALMGREN
Professor, University of Copenhagen, Denmark

STEVEN KELLY
Associate Professor, University of Oxford, UK

SENIOR REPRESENTATIVE
PerkinElmer

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

KEVIN FENGLER
Research Scientist, DuPont Pioneer, Data Science and Informatics

TOMasz GOLAS (Chair)
Lead Research Laboratory, Deliflor Chrysanten

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

MAX VAN MIN
CEO & Founder, Cergentis, The Netherlands

Partners

6TH PLANT GENOMICS & GENE EDITING CONGRESS / PARTNERSHIPS IN BIOCONTROL, BIOSTIMULANTS & MICROBIOME EUROPE 2018
CONFIRMED SPEAKERS

BARRY GOLDMAN  
VP and Head of Discovery, Indigo Agriculture

ANGELA SESSITSCH  
Head of Bioresources, AIT Austrian Institute of Technology, Austria

METTE NICOLAISEN  
Associate Professor, Head of Section for Microbial Ecology and Biotechnology, University of Copenhagen

GREGORY SWORD  
Professor and Chair of Cotton Entomology, Texas A&M University, USA

STIG U ANDERSEN  
Associate Professor, University of Aarhus, Denmark

JOSEPH SCHMIDT  
SVP, Business Development & Strategy, BioConsortia, Inc.

CHRISTOPHE CLEMENT  
Scientific Director, CNRS and Professor, University of Reims Champagne Ardenne, France

CLAIRE STANLEY  
Independent Team Leader, Agroscope, Switzerland

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

JAKE MALONE  
Project Leader, John Innes Centre and Senior Lecturer, University of East Anglia, UK

ANGELA FEECHAN  
Assistant Professor and Lecturer, School of Agriculture and Food Science, University of College Dublin, Ireland

PETER JENS  
CEO, AND Biopharma

DAN FUNCK JENSEN  
Professor, Swedish University of Agricultural Sciences, Sweden

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

JOSEPH SCHMIDT  
SVP, Business Development & Strategy, BioConsortia, Inc.

ANNA MARTENSSON  
Professor, Swedish University of Agricultural Sciences, Sweden

SIMON FLEISCHLI  
Area and Product Manager, Andermatt Biocontrol, Switzerland

CLAIRE NEEMA  
Chair of Plant-Pathogen Interactions Group, CIRAD, INRA, and SupAgro, France

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

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

CLAIRE NEEMA  
Chair of Plant-Pathogen Interactions Group, CIRAD, INRA, and SupAgro, France
**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.

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**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.

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**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.

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faizel@globalengage.co.uk
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 starch, protein and sugars. We have 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.

The root knot nematode (RKN) Meloidogyne graminicola is an obligate, sedentary endoparasite, causing yield losses in tropical aerobic rice production. Our research group has generated in-depth transcriptomic data of rice upon infection with parasitic nematodes, revealing that RKN is a master in manipulation of the host’s metabolism. For a selection of metabolic pathways, nematodes, revealing that RKN is a master in manipulation of metabolic pathways of the host’s metabolism. For a selection of metabolic pathways, we have validated their physiological role in this plant-nematode interaction. Genes encoding epigenetic modification enzymes are upregulated in nematode-induced giant cells. Therefore, we are currently investigating epigenomic changes upon infection of rice with this RKN. Next to that, the transcriptional response of rice to nematodes has been compared with its response to other pathogens, identifying rice genes with a central role in the plant immune system.

THE ROOT KNOT NEMATODE (RKN) MELIODOGYNE GRAMINICOLA IS AN OBLIGATE, SEDENTARY ENDOPARASITE, CAUSING YIELD LOSSES IN TROPICAL AERobic RICE PRODUCTION. OUR RESEARCH GROUP HAS GENERATED IN-DEPTH TRANSCRIPTOMIC DATA OF RICE UPON INFECTION WITH PARASITIC NEMATODES, REVEALING THAT RKN IS A MASTER IN MANIPULATION OF THE HOST’S METABOLISM. FOR A SELECTION OF METABOLIC PATHWAYS, NEMATODES, REVEALING THAT RKN IS A MASTER IN MANIPULATION OF METABOLIC PATHWAYS OF THE HOST’S METABOLISM. FOR A SELECTION OF METABOLIC PATHWAYS, WE HAVE VALIDATED THEIR PHYSIOLOGICAL ROLE IN THIS PLANT-NEMATODE INTERACTION. GENES ENCODING EPIGENETIC MODIFICATION ENZYMES ARE UPREGULATED IN NEMATODE-INDUCED GIANT CELLS. THEREFORE, WE ARE CURRENTLY INVESTIGATING EPIGENOMIC CHANGES UPON INFECTION OF RICE WITH THIS RKN. NEXT TO THAT, THE TRANSCRIPTIONAL RESPONSE OF RICE TO NEMATODES HAS BEEN COMPARED WITH ITS RESPONSE TO OTHER PATHOGENS, IDENTIFYING RICE Genes WITH A CENTRAL ROLE IN THE PLANT IMMUNE SYSTEM.
Here we present a recent approach to develop resistant breeding lines, through mutations in plant susceptibility genes by using 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, 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.

The genome sequencing of crops is critical to improve crop production. 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.

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.
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.
• Within Europe there is an important legal case being considered by the European Court of Justice to determine the scope of the exemption provided in the EU GM regulations in relation to new mutagenesis techniques.
• I will review the progress of this case and its possible outcomes, in the context of European agricultural production and global trade post-Brexit.

ODD ARNE OLSEN
Professor, Norwegian University of Life Science, Norway

Improved resolution in bread wheat grain transcriptomics: using the IWGSC genome sequence to expression profile commercial wheat cultivars for quality genes and potential allergenicity epitopes
We have previously shown that the expression of genes from sub-genomes A, B and D in the endosperm are largely independent, with the exception of a sub-set of asymetrically genes form each sub-genome that may contribute to the unique properties of bread wheat (Pfeifer et al., Science 2014). Our current aim is to identify detailed expression profiles of commercial bread wheat cultivars in order to improve our understanding of the pattern of expression and the interaction of the genes involved in specifying quality traits as well as to identify selection criteria for bread wheat breeding. A second ongoing effort is to present a comprehensive map of known and potential sites that cause allergenicity reactions in consumers.

BLENANC ANGUEGUILO
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.

EARLY CAREER RESEARCHER:
SARAH RAFFAN
Roathsmeld 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 foodstuffs. Wheat represents one of the major sources of dietary acrylamide intake.

• Acrylamide forms from the reaction of free asparagine with reducing sugars during the Maillard reaction. Asparagine synthesis is catalysed by a family of enzymes called asparagine synthetases (TaASN1-4), with TaASN2 showing grain-specific expression.

• The CRISPR/Cas9 system has been applied for the targeted knockout of TaASN2 to generate wheat material with low acrylamide-forming potential. A multiplexed guide-RNA construct, containing four gRNAs designed to target the first exon of TaASN2, interspaced with i RNAs, has been successfully designed. The construct was used to transform T. aestivum cv. Cadenza leaf protoplasts and isolated embryos.

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

Ecology and evolution of microbial communities for stimulating plant growth and disease suppression – Title TBC
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 or 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.
CERGENTIS

SOLUTION PROVIDER PRESENTATION:
MAX VAN MIN
CEO & Founder, 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

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 bottleneck for genome editing and cis-gene breeding in crop species
• Hairy root transformation using Agrobacterium rhizogenes provides a rapid method to generate transgenic hairy root clones which express genome editing reagents, such as CRISPR/Cas and carry targeted mutations
• Regeneration protocols have been developed in potato which allow whole plants to be regenerated from individual transgenic hairy root clones that carry germline targeted mutations identified in the original hairy root clone and minimal effects of chimerism in a single generation.

SOLUTION PROVIDER PRESENTATION:
MAX VAN MIN
CEO & Founder, Cergentis, The Netherlands
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• TLA-based complete gene sequencing and haplotyping

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 geographical space and through geological time.

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.

ANNA MARTENSSON
Professor, Swedish University of Agricultural Sciences, Sweden
Biofumigation combined with plant growth promoting consortia is a promising alternative for disease suppression in organic tomato production
• Addition of mustard seed may decrease disease severity in organic greenhouse tomato production
• Incorporation of mustard seeds increases biomass of organically cultivated greenhouse tomatoes
• Combining biofumigation, that is mustard seed incorporation in soil, with plant-growth promoting consortia could be an alternative for organic greenhouse tomato growers having problems with ‘disease’ soils due to an intensive production
**ROUNDTABLE DISCUSSIONS:**

**TABLE 1: DONALD R. MARVIN**
President and CEO, Inocucor, USA and Canada
Commercialisation, Product Launch, and Business Development

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

**TABLE 4: JOSEPH SCHMIDT**
SVP, Business Development & Strategy, BioConsortia, Inc.
Cross-discipline Collaboration

*Full details of the Roundtables can be found at the end of Day 1*
### INGO HEIN
Principal Investigator, James Hutton Institute and the University of Dundee, UK

**The impact of modern genomics on potato disease resistance breeding**

Methods to track and verify the integrity of multiple disease resistance genes are needed for crop improvement. Diagnostic resistance gene enrichment sequencing (dRenSeq) enables the high-confidence identification and complete sequence validation of functional resistance genes in crops.

- We have shown that the technology can direct parental selection in breeding programs and confirms transgene integrity in GM crops.
- DRenSeq is more robust and cheaper in the detection of functional disease resistance genes than whole-genome sequencing and supersedes PCR-based tests as well as effector recognition studies.
- Our study reveals a very limited base of utilised resistances in major potato cultivars but has identified additional and currently very effective resistances in potato varieties that could now be combined with the help of the technology.

### PANEL DISCUSSION: Plant Gene Editing and the Consumer

Covering topics including:

- How gene editing can be focused on consumer needs
- The impact of public perception on advances in gene editing research and ways to overcome this
- Evaluating the market for gene edited foods
- How regulation and politics impacts gene editing progression in food markets

**IAN GODWIN** (Chair)
Professor of Plant Molecular Genetics, The University of Queensland, Australia

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

**MICHAEL PALMGREN**
Professor, University of Copenhagen, Denmark

**AGNÈS RICROCH**
Associate Professor in Evolutionary Genetics and Plant Breeding, AgroParis Tech, and Adjunct Professor, Pennsylvania State University

17:15-17:55

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If you would like to sponsor the drinks reception please contact Faizel Ismail at: faizel@globalengage.co.uk
- 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 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 microbiomes 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:**
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 4:**
JOSEPH SCHMIDT  
SVP, Business Development & Strategy, Bio Consortia, Inc.  
Cross-discipline Collaboration

- Challenges in metagenomics analysis and strategies to overcome this
- The latest technologies to improve metagenomic analysis
- Applications of metagenomics in agricultural biologicals development
08:30-08:55 Refreshments

PLANT GENOMICS & GENE EDITING CONGRESS

08:55-09:00 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.

09:00-09:40

09:00-09:40

SOLUTION PROVIDER PRESENTATION: SENIOR REPRESENTATIVE
PerkinElmer
Title – TBC

09:40-10:10 SOLUTION PROVIDER PRESENTATION:
SOLUTION PROVIDER PRESENTATION:

SENIOR REPRESENTATIVE

PerkinElmer

Title – TBC

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.

09:40-10:10

ALAN SCHULMAN
Professor of Plant Biotechnology, LUKE and University of Helsinki, Finland
Positional cloning and verification of Yr15, which confers broad-spectrum resistance to stripe rust, from wild emmer wheat by exploitation of NGS and -omics approaches

Stripe rust, caused by Puccinia striiformis f. sp. tritici (Pst), is a devastating fungal disease that threatens global wheat production. The wild emmer wheat (Triticum turgidum ssp. dicoccoides) gene Yr15 confers robust resistance to a broad spectrum of Pst races. We have positionally cloned Yr15 by exploiting saturation mapping with markers from collinear regions in syntenic genomes, minimal tiling path BAC clones for related reference genomes, and a non-gridded BAC library from the Yr15-bearing accession of wild emmer wheat. PacBio sequencing, EMS-mutagenesis, transformation, transient expression, and allel 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

10:10-10:35

KIM HAMMOND-KOSACK
Professor and PI, Rothamsted Research, UK
The Pathogen-Host Interactions database: PHI-base

PHI-base (www.phi-base.org) is a knowledge database accessed by researchers in over 125 countries. PHI-base contains expertly curated molecular and biological information on genes proven to affect the outcome of pathogen-host interactions reported in peer reviewed research articles. Genes not affecting the disease interaction phenotype are also curated. PHI-base data is linked to the genome browsers and advanced query tools in ENSEMBL and FungiDB.

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

10:10-10:35

SIMON FLEISCHLI
Area and Product Manager, Andermatt Biocontrol, Switzerland
Biostimulating bacterial inoculants to bridge imbalances of intensive agricultural production systems

• Practical considerations to use root associated plant-growth promoting bacteria
• Multiple action mechanisms for enhanced plant growth and vigor
• RhizoVital – demonstrated flexibility for field application
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.

Modern agriculture depends increasingly on large-scale, genetically uniform cropping systems requiring intensive use of chemicals to control pathogens. The wild ancestors of our domesticated crops, however, contain genetically diverse resistance genes. Deploying these genes in crops represents an underexploited and environmentally benign disease control option. I will describe a series of enabling technologies for the accelerated discovery 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.

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.

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.
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.

Population explosion and land exploitation leads to several extreme issues worldwide, like food insecurity and water scarcity (drought) causing global agricultural yield loss. Hence there is an immediate need to study the crops, which are naturally tolerant to drought situation. Present study focused on Pearl millet [Pennisetum glaucum (L.) R.Br] inbred lines through RNA sequencing. Population explosion and land exploitation leads to several extreme issues worldwide, like food insecurity and water scarcity (drought) causing global agricultural yield loss. Hence there is an immediate need to study the crops, which are naturally tolerant to drought. With the help of RNA-Seq technique an attempt was made to study the regulatory mechanism of drought tolerance in the crop. In our study different genes were found to have role in drought stress. Mapping shows the significant relation of these genes with different metabolic pathways. Study of these pathways in pearl millet can become a solution over the loss in agriculture due to effect of drought worldwide.

We use machine learning to automatically assign Gene Ontology (GO) terms to Arabidopsis Thaliana proteins. Our method creates a similarity profile of each protein based on its sequence similarity to a set of annotated proteins. GO terms are then assigned to unannotated proteins based on the annotations of proteins with the most similar profiles. We exploit the inherent redundancy of GO terms imposed by their hierarchical structure and transform them into a more compact function representation that is easier for machine learning methods. We propose two new such transformations: one based on the GO hierarchy and one based on semantic similarity of terms.
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 binds 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.
TABLE 1: RODOMIRO ORTIZ
Professor and Chair of Genetics and Plant Breeding, Swedish University of Agricultural Sciences, Sweden
Genomic Selection
Genomic estimated breeding values (GEBV) for selection in plant improvement: why, when and how?
- Advancing genetic gains by using GEBV: increasing accuracy, saving time and what else?
- GEBV for selection and genome editing: seeking new frontiers for plant breeding?

TABLE 2: KRISTINA GRUDEN
Professor and Leader of the Omics Approaches Group, National Institute of Biology, Slovenia
Integrated Omics
- Importance of Standards and FAIR data principles in complex datasets
- Approaches in data integration: molecular levels, scale in time and space
- From data integration to mathematical modeling

TABLE 3: TOM OSBORN
Director of New Breeding Technologies, Monsanto
Genome Design and the Future of New Breeding Technologies
- What do we mean by genome design?
- What are some near and long term approaches to designing genomes?
- What do we need to achieve these design capabilities?

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 Triticum 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.

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.

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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Beursplein 37,
3011 AA Rotterdam,
The Netherlands

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- Located in the city centre (surrounded by shops, architecture, museums, restaurants and the Port of Rotterdam)
- Walking distance from the international train station
- Rotterdam – The Hague airport with flights to at least 30 international destinations is a short taxi ride
- A large number of parking facilities can be found in the area
- A wide variety of hotels are within walking distance. (Details will be sent to you in your welcome letter when you register)