Global Engage

6TH PLANT GENOMICS & GENE EDITING CONGRESS: EUROPE

PARTNERSHIPS IN BIOCONTROL, BIOSTIMULANTS & MICROBIOME: EUROPE

ROTTERDAM, THE NETHERLANDS

— 14-15 May 2018 —

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Global Engage

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

ANA ATANASSOVA
Global Regulatory Manager, Seeds, Bayer Crop Science

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

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

- Genomic Selection
- Climate Change
- Integrated Omics
- Sequencing Workflow
- Gene Editing
- Genome Design and the Future of New 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
- Product Formulation, Storage, and Delivery
- Cross-discipline/industry collaboration
- Biostimulants and Biopesticides Regulation
- Metagenomics methods

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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

SENIOR REPRESENTATIVE
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

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BLANCA SAN SEGUNDO
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Professor, Norwegian University of Life Science, Norway

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Associate Professor, Wageningen University & Research, The Netherlands

MAIKE STAM
Assistant Professor, University of Amsterdam, The Netherlands

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

NATHANIEL BUTLER
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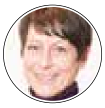


INGER AHMAN
Professor of Plant Breeding, Swedish University of Agricultural Sciences, Sweden

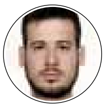
CLAUDIA JONAK
Principal Scientist, AIT Austrian Institute of Technology, Austria

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

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

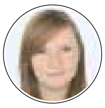
KIM HAMMOND-KOSACK
Professor and PI, Rothamsted Research, UK

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



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John Innes Centre, UK

BRANDE WULFF
Project Leader, John Innes Centre, UK

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

ANA ATANASSOVA
Global Regulatory Manager, Seeds, Bayer Crop Science

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 OSBORN
(Roundtable Host)
Director of New Breeding Technologies, Monsanto

KRISTINA GRUDEN
(Roundtable Host)
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

AGNES RICROCH
Associate Professor, AgroParisTech, France

MICHAEL PALMGREN
Professor, University of Copenhagen, Denmark

STEVE 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

CONFIRMED SPEAKERS

BIOCONTROL, BIOSTIMULANTS & MICROBIOME

BARRY GOLDMAN
VP and Head of Discovery, Indigo Agriculture

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

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

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

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

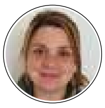
ANNA MARTENSSON
Professor, Swedish University of Agricultural Sciences, Sweden

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

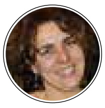
ANGELA SESSITSCH
Head of Bioresources, AIT Austrian Institute of Technology, Austria

STIG U ANDERSEN
Associate Professor, University of Aarhus, Denmark

CLAIRE STANLEY
Independent Team Leader, Agroscope, Switzerland



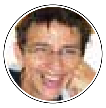
ANGELA FEECHAN
Assistant Professor and Lecturer, School of Agriculutre and Food Science, University of College Dublin, Ireland



MARIA J POZO
Tenured Scientist, CSIC, Spain

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

SIMON FLEISCHLI
Area and Product Manager, Andermatt Biocontrol, Switzerland



CLAIRE NEEMA (Chair)
Head of Biology and Genetics of Plant-Pathogen Interactions Group, CIRAD, INRA, and SupAgro, France

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

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

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

PETER JENS
CEO, AND Biopharma

08:00-09:00 Registration & Refreshments

PLANT GENOMICS & GENE EDITING CONGRESS

Global Engage Welcome Address and Track Chair's Opening Remarks:

09:00-09:40

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.

09:40-10:10

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NRGene

Title – TBC

PARTNERSHIPS IN BIOCONTROL, BIOSTIMULANTS & MICROBIOME

Global Engage Welcome Address and Track Chair's Opening Remarks: Claire Neema, Head of Biology and Genetics of Plant-Pathogen Interactions Group, CIRAD, INRA, and SupAgro, France

09:35-10:00

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.

09:40-10:10

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PLANT GENOME ENGINEERING: STRATEGIES & DEVELOPMENT

10:10-10:35

IAN GODWIN

Professor of Plant Molecular Genetics, The University of Queensland, Australia

Genomics-informed 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. 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.

PLANT GENOMICS CASE STUDIES

10:10-10:35

BEAT KELLER

Professor, University of Zurich, Switzerland

Genomics-based improvement of fungal pathogen resistance in wheat and other cereal crops

- The newly available reference genome of wheat allows for novel strategies in the isolation of wheat disease resistance genes.
- MutChromSeq: A novel method to rapidly identify genes in the wheat gene pool
- The vast genetic diversity of cereals stored in the global genebanks now becomes accessible to molecular characterization.

PARTNERSHIPS IN BIOCONTROL, BIOSTIMULANTS & MICROBIOME

10:10-10:35

BARRY GOLDMAN

VP and Head of Discovery, Indigo Agriculture

Plant-Microbiome Engineering to Improve Agriculture

Microbes have evolved in conjunction with plants over millions of years. The development of microbial products to achieve long-term agricultural sustainability is a growing industry. Indigo Ag, Inc. (www.indigoag.com) is focused on products that use microbial endophytes, and has developed a large and sophisticated pipeline to discover microbes that enhance plant performance. The pipeline starts when microbes isolated from row crops, sequenced and then enter a high throughput lab-testing pipeline. We currently collect and test thousands of microbes in these assays. The best of these are then tested under field conditions to identify our products. Indigo released its first product in 2016. Indigo CottonTM demonstrated a yield improvement of 11% in target fields, demonstrating the effectiveness of our discovery and development model.

10:35-11:45 Morning Refreshments / Even Poster Presentations

11:45-12:10

JOCHEN KUMLEHN

Head of Plant Reproductive Biology, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany

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

12:10-12:35

INGER AHMAN

Professor of Plant Breeding, Swedish University of Agricultural Sciences, Sweden

Site-directed mutagenesis of candidate susceptibility genes to achieve aphid and disease resistance in barley

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, 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.

11:45-12:10

TINA KYNDT

Professor of Molecular Biotechnology, University of Ghent, Belgium

Epigenomic and transcriptomic analyses of the interaction between rice and parasitic nematodes

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, 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.

12:10-12:35

HERIBERT HIRT

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

From signaling to chromatin: new insights into the role of MAP kinases in epigenetic regulation

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.

11:45-12:10

GREGORY SWORD

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

Cotton fungal endophytes: From discovery to commercial application

Beneficial fungal endophytes can confer protection to plants against a variety of stressors and improve yields in major agricultural crops. We have characterized fungal endophytes originally isolated from cultivated cotton (Gossypium hirsutum) by genomic studies, experiments in the laboratory, glasshouse, and other pre-commercial trials prior to launching them as commercial products. Using seed treatment protocols, individual plants can be inoculated with natively occurring fungi to deliver useful agronomic phenotypes throughout the growing season. We show that the targeted addition of selected fungal endophytes to cotton and other plants can mediate plant tolerance to multiple stressors such as drought, pests, and nematodes, with significant positive impacts on plant performance and yield under field conditions.

12:10-12:35

METTE NICOLAISEN

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

The Microbiomes of Fungal Biofertilizers – A Source of Fungal Helper Bacteria?

In nature, fungal hyphae are colonized by bacteria forming biofilms, and fungi are known to affect the size and composition of bacterial communities in their surroundings. Hyphae-associated bacteria can assist mycorrhiza formation and promote the function of the mycorrhizal symbiosis e.g. by improved spore germination, enhanced hyphal growth, and increased mycorrhizal root colonization. At present the helper bacteria concept is not established for relationships between non-mycorrhizal saprophytic fungi and their associated hyphal microbiome. We have investigated the composition of P-solubilizing Penicillium microbiomes, and isolated fungal growth promoting bacteria, which could be the key to stabilize and improve the performance of these fungal inoculants for increased efficiency and improved nutrient use efficiency across fertilizer form and environmental conditions.

12:35-13:05

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SENIOR REPRESENTATIVE

Novogene

Title - TBC

12:35-13:05

KEVIN FENGLER

Research Scientist, DuPont Pioneer, 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.

12:35-13:05

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13:05-14:05 Lunch

14:05-14:30

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.

14:05-14:30

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.

14:05-14:30

MARIA J POZO

Tenured Scientist, CSIC, Spain

Context dependency of microbe induced resistance: The challenge for biotechnological applications

14:30-14:55

ANTONIO GRANELL (Reserved)

Professor, Plant Genomics and Biotechnology Laboratory, CSIC, Spain

Gene Editing methods in tomato – Title TBC

We have

14:55-15:10

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 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 tRNAs, has been successfully designed. The construct was used to transform T. aestivum cv. Cadenza leaf protoplasts and isolated embryos.

14:30-14:55

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 asymmetrically 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.

14:55-15:25

MAIKE STAM

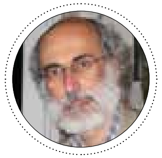
Assistant Professor, University of Amsterdam, The Netherlands

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.

14:30-14:55

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 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.

14:55-15:25

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.

15:10-15:25

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.

14:55-15:25

Continued

14:55-15:25

Continued

15:25-15:55

SOLUTION PROVIDER PRESENTATION: SENIOR REPRESENTATIVE

Cergentis

Title - TBC

15:25-15:55

SOLUTION PROVIDER PRESENTATION

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15:25-15:55

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15:55-16:45 Afternoon Refreshments / Poster Presentations

16:45-17:10

STEVE 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.

16:45-17:10

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.

16:45-17:35

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

Product Formulation, Storage, and Delivery

TABLE 4: **JOSEPH SCHMIDT**

SVP, Business Development & Strategy, BioConsortia, Inc.

Cross-discipline Collaboration

17:10-18:05

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

AGNES RICROCH
Associate Professor, AgroParisTech, France

17:10-17:35

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.

17:35-17:50

EARLY CAREER RESEARCHER: CORINNE 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 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.

16:45-17:35

TABLE 5: **MARIOS-NEKTARIOS MARKAKIS** (Reserved)
Programme Manager, European Commission

Biostimulants and Biopesticides Regulation

TABLE 6: Speaker TBC

Metagenomics Methods

*Full details of the Roundtables can be found at the end of Day 1

17:35-18:05

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

17:10-18:05

Continued

17:50-18:05

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 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.

17:35-18:05

Continued

18:05	Chair's Closing Remarks / End of Day 1
18:05-19:05	Networking Drinks Reception

If you would like to sponsor the drinks reception please contact Faizel Ismail at: faizel@globalengage.co.uk

ROUNDTABLE DISCUSSIONS:

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

Product Formulation, Storage, and Delivery

- Strategies for formulating biocontrol and biostimulant products to provide a stable substance for the farmer
- Delivery methods for biological products
- Overcoming storage challenges for mass-produced products

TABLE 4:

MARIOS-NEKTARIOS MARKAKIS (Reserved)

Programme Manager, European Commission

Biostimulants and Biopesticides Regulation

- Current country, FDA, EPA, and EU based policies for biopesticides and biostimulants regulation
- Future regulatory changes and how they might affect businesses
- Advice on how to meet regulation in your products

TABLE 5:

Speaker TBC

Metagenomics Methods

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

TABLE 6:

Speaker TBC

Cross-discipline Collaboration

- Bringing together academia and industry to drive biostimulant, biocontrol, and microbiome research and product development – challenges and benefits
- Utilising expertise from various backgrounds including engineers and data analyst to derive novel biological solutions for agricultural issues

08:30-08:55 Refreshments

PLANT GENOMICS & GENE EDITING CONGRESS

08:55-09:00 **Track Chair:**

09:00-09:40

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

SOLUTION PROVIDER PRESENTATION:
SENIOR REPRESENTATIVE

PerkinElmer

Title – TBC

PARTNERSHIPS IN BIOCONTROL, BIOSTIMULANTS & MICROBIOME

08:55-09:00 **Track Chair:** **Christophe Clement**, Scientific Director, CNRS and Professor, University of Reims Champagne Ardenne, France

09:00-09:40

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.

09:40-10:10

SOLUTION PROVIDER PRESENTATION

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DEVELOPMENTS IN NGS, RNA-SEQ, AND OMIC TECHNOLOGIES

10:10-10:35

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 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

BIOINFORMATICS AND DATA ANALYSIS

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 data content provided comes from >2300 manually curated references and reports information on 4775 genes from 264 pathogens tested on 173 hosts (plant, animal, others) in 8610 interactions. Direct targets of pathogen effector proteins are 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.

PARTNERSHIPS IN BIOCONTROL, BIOSTIMULANTS & MICROBIOME

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

10:10-10:35 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.

10:10-10:35 Continued

10:10-10:35 Continued

10:35-11:45 Morning Refreshments

SOLUTION PROVIDER PRESENTATION

11:45-12:15 For sponsorship opportunities please contact Faizel Ismail at:
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12:15-12:55

ROUNDTABLE DISCUSSIONS:

ROUNDTABLE 1:

Genomic Selection

RODOMIRO ORTIZ

Professor and Chair of Genetics and Plant Breeding, Swedish University of Agricultural Sciences, Sweden

ROUNDTABLE 2:

Integrated Omics

KRISTINA GRUDEN

Professor and Leader of the Omics Approaches Group, National Institute of Biology, Slovenia

ROUNDTABLE 3:

Genome Design and the Future of New Breeding Technologies

TOM OSBORN

Director of New Breeding Technologies, Monsanto

ROUNDTABLE 4:

Climate Change

Speaker TBC

ROUNDTABLE 5:

Gene Editing

Speaker TBC

SOLUTION PROVIDER PRESENTATION

11:45-12:15 For sponsorship opportunities please contact Faizel Ismail at:
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12:15-12:40

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.

12:40-12:55

EARLY CAREER RESEARCHER: STAVROS MAKRODIMITRIS

Delft University of Technology, The Netherlands

Combining Protein Sequence Similarities and GO-term Semantic Similarities Improves Protein Function Prediction in Arabidopsis

- 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.

SOLUTION PROVIDER PRESENTATION

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12:15-12:40

STIG U ANDERSEN

Associate Professor, University of Aarhus, Denmark

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 accessions, 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.

12:40-13:05

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.

12:55-14:05 Lunch

DEVELOPMENTS IN NGS, RNA-SEQ, AND OMIC TECHNOLOGIES

14:05-14:30

HONGBIN ZHANG (Reserved)
Professor of Plant Genomics and Systems Biology, Texas A&M University, USA

Genome-Wide High-Throughput Gene Cloning – Title TBC

14:30-14:55

BRANDE WULFF
Project Leader, John Innes Centre, UK

Understanding and exploiting immune receptor diversity in wild wheats

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 and cloning of resistance genes from crop wild relatives using mutant and natural populations and their rapid deployment in domesticated crop varieties.

INDUSTRY SHOWCASE

14:05-14:30

TOM GREENE
Senior Research Director, 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.

14:30-14:55

ERIK JONGEDIJK
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.

PARTNERSHIPS IN BIOCONTROL, BIOSTIMULANTS & MICROBIOME

10:10-10:35

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.

14:30-15:20

PANEL DISCUSSION:

The Current Status and Future of Investment in Agricultural Biologicals

Covering topics including:

- Government and business led programmes to support commercialisation of agricultural biologicals
- Business-academia collaboration to advance biologicals research and product development
- What companies are looking for in a business investment
- Current market opportunities and funding climate in Europe

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

PETER JENS
CEO, AND Biopharma

14:55-15:10

EARLY CAREER RESEARCHER: AMBIKA DUDHATE

University of Tokyo, Japan

Elucidating relative drought stress responsiveness in 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 situation. Present study focused on Pearl millet [Pennisetum glaucum (L.) R.Br] a drought tolerant cereal crop. 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.

15:10-15:35

JOHN DOONAN

Director and Professor of Genetics, National Plant Phenomics Centre, Aberystwyth University, UK

Phenomics method development – Title TBC

14:55-15:20

ANA ATANASSOVA

Global Regulatory Manager, Seeds, Bayer Crop Science

Regulatory developments from genome editing in plant breeding

- Review of biotech regulatory trends applicable to genome editing tools globally
- Realistic regulatory outcome scenarios and potential challenges

15:20-15:45

LAKSHMI SASTRY-DENT

External Technology Leader, R&D, Dow AgroSciences

Engineering biology applications in plant biotechnology

14:30-15:20

Continued

15:20-15:45

JAKE MALONE

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

One ligand, two regulators and three binding sites: how KDPG controls primary carbon metabolism in Pseudomonas fluorescens

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.

15:35-16:15 Afternoon Refreshments

16:15-16:40

HANS DE JONG

Emeritus Professor of Cytogenetics, Wageningen University & Research, The Netherlands

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 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.

16:15-16:40

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.

16:15-16:40

ANGELA FEECHAN

Assistant Professor and Lecturer, School of Agriculutre 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.

16:40-17:05

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.

17:05	Conference Close

ROUNDTABLE DISCUSSIONS:

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

- How to bring different omics methods and data sets together to form a coherent picture of crop development
- The benefits of using a multi-omic approach to plant research
- The challenges in combining different omic techniques

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?

TABLE 4:

Speaker TBC

Climate Change

- Best methods to analysing how plants adapt to environmental changes
- Evaluation of how climate change will affect crop production worldwide
- Breeding crops to withstand climate change

TABLE 5:

Speaker TBC

Gene Editing

- Improved process and workflow systems
- Future applications of the technology
- Troubleshooting and problem solving

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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Global Engage

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