7TH PLANT GENOMICS & GENE EDITING CONGRESS: EUROPE

EXPLORING NGS, OMIC TECHNOLOGIES, BIOINFORMATICS, PHENOTYPING, & MICROBIOME STUDIES FOR THE ADVANCEMENT OF PLANT RESEARCH

ROTTERDAM, THE NETHERLANDS
— 21 - 22 May 2019 —

#PlantGenomicsGE

www.global-engage.com
Global Engage is pleased to announce the 7th Plant Genomics & Gene Editing Congress: Europe, taking place 21st-22nd May 2019, in Rotterdam, The Netherlands. This event is part of our widely-regarded Plant Genomics Series which includes an Asian and US meeting each year.

Attracting over 300 experts working in all areas of plant science, this event will examine the latest in gene editing methods for plant genomics research. CRISPR/Cas9 case studies and the very best strategies for plant genome engineering will be presented by industry leaders, experts and pioneering academics at the forefront of plant research. Developments in gene editing, NGS, and omic technologies will all be explored for crop trait development, disease resistance, plant breeding, and more.

This year, a key focus of the event will be the latest ECJ ruling on GMOs, and what this means for the future of gene editing research. Experts in policy and regulatory affairs will present and join our in-depth panel discussion and will consider pertinent issues such as the impact of the ruling on existing and future research, and what alternative strategies & technologies there might be for progressing plant genomics as a whole.

Elsewhere, tracks dedicated to plant & soil microbiomes, and the importance of plant phenotyping in the context of bioinformatics challenges, will encourage a holistic approach to plant research; the former will focus on identifying microbes to enhance crop productivity & disease resistance, while the latter will showcase the best tools for overcoming bioinformatics bottlenecks, applicable to plant research across the board.

There will also be opportunities for early career researchers to present their work, as well as an afternoon of roundtable discussions, encouraging debate and interaction with your peers on the hot topics in plant genomics research today.

EXPERT SPEAKERS INCLUDE:

JOHNATHAN NAPIER
Professor, Flagship Leader and Science Director, Rothamsted Research, UK

ANA ATANASSOVA
Global Regulatory Policy Manager, BASF Agricultural Solutions, Belgium

IAN BANCROFT
CNAP Chair of Plant Genomics, University of York, UK

HENRIK BRINCH-PEDERSEN
Professor, Aarhus University, Denmark

CLaire STANLEY
Independent Team Leader, Agroscope, Switzerland
PLANT GENOME ENGINEERING: STRATEGIES AND DEVELOPMENTS

- Genome editing methods and applications
- Improving gene editing technology
- CRISPR/Cas9 case studies
- Site-directed mutagenesis
- Regulating genome editing and the latest on country/EU policies
- Alternatives to gene editing - other technologies & developments exempt from the latest ECJ ruling
- Panel Discussion: The Future of Plant Genomics: Navigating the latest ECJ court ruling on GM crops

PLANT PHENOTYPING & BIOINFORMATICS

- Plant phenomics
- High-throughput plant phenotyping technology
- Bioinformatics analysis and challenges
- Sequencing pipelines and assembly
- Computational systems for modelling and visualisation of information
- Application of bioinformatics software for plant phenotyping research

PLANT & SOIL MICROBIOMES

- Identifying microbes to enhance crop productivity & disease resistance
- Plant microbe systems analysis for disease resistance
- Soil microbiome and root assembly
- Host-pathogen interactions
- Structure and specificity of plant microbiomes
- Technologies and techniques for microbiome research

PLANT GENOMICS CASE STUDIES

- Crop trait development
- Disease and stress resistance
- Pathogen detection and analysis
- Plant breeding methods
- DNA methylation studies

Case studies using the following methods and technologies

- NGS platform comparison
- Genotyping by sequencing
- Metabolic 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
- Molecular marker development/ marker assisted selection

ROUNDTABLES

- Table 1 – The Future of Breeding Technologies
- Table 2 – Genome Editing Regulation
- Table 3 – Genomic Selection
- Table 4 – Bioinformatics
- Table 5 – Plant Gene Editing & the Consumer

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).
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SPONSORSHIP & EXHIBITION OPPORTUNITIES AVAILABLE
For more details contact Faizel Ismail: faizel@globalengage.co.uk or call +44 (0) 1865 849841
CONFIRMED SPEAKERS

JOHNATHAN NAPIER
Professor, Flagship Leader and Science Director, Rothamsted Research, UK

ANA ATANASSOVA
Global Regulatory Policy Manager, BASF Agricultural Solutions, Belgium

JIM DUNWELL
Professor, University of Reading, UK

AALT-JAN VAN DIJK
Assistant Professor, Plant Systems Biology, Wageningen University, The Netherlands

DAVIDE BULGARELLI
Principal Investigator, University of Dundee, UK

PIET VAN DER MEER
Professor, Ghent University, Vrije Universiteit Brussels, Belgium

BJÖRN USADEL
Professor RWTH Aachen University & Director Forschungszentrum Jülich, Germany

TIM MAUCHLINE
Project Leader, Sustainable Agriculture Sciences, Rothamsted Research, UK

GIL RONEN
President, NRGene

TERESA BABUSCIO
Director, Agricultural & Cross Division Affairs, Belgium

KIM HAMMOND-KOSACK
Professor & Principal Investigator, Rothamsted Research, UK

NICOLA HOLDEN
Principal Investigator, Molecular Bacteriologist, James Hutton Institute, UK

DENNIS ERIKSSON
Researcher, Genetics & Plant Breeding, SLU (Swedish University of Agricultural Sciences, Sweden

KAI PURNHAGEN
Associate Professor of Law, Wageningen University, & Distinguished International Visitor Erasmus, University of Rotterdam, The Netherlands

ALEXANDER WITTENBERG
Scientist, Next Generation Sequencing, KeyGene

JOACHIM SCHIEMANN
Professor & Director of the Institute for Biosafety in Plant Biotechnology, Germany

RENÉ CUSTERS
Regulatory & Responsible Research Manager, VIB, Belgium

ERIK BONGCAM-RUDLOFF
Professor of Bioinformatics, SLU (Swedish University for Agricultural Sciences), Sweden

ALEXANDRE JOUSSET
Assistant Professor, Utrecht University, The Netherlands

SENIOR REPRESENTATIVE
Novogene

STAVROS MAKRODIMITRIS
PhD Candidate, Delft University of Technology, Germany

MARCOS EGEA-CORTINES
Professor of Genetics, Director of the Plant Biotechnology Institute, University of Cartagena, Spain

CLAIRE STANLEY
Independent Team Leader, Agroscope, Switzerland

UMA PRIYA KUPUSAMY
Scientific Officer at Department of Chemistry, Malaysia; PhD student, Newcastle University, UK

EGEM OZBUDAK
PhD Student, Plant Pathology Department, University of Florida, USA

VLADIMIR NEKRASOV
Project Leader, Rothamsted Research, UK

SELIM LOUAFI
Senior Research Fellow, Cirad, Joint Research Unit Genetic Improvement and Adaptation of Mediterranean and Tropical Plants (AGAP), Montpellier, France

MARCEL VAN VERK
Team Leader Crop Data Science, KeyGene, The Netherlands

RAQUEL CARVALHO
Postdoctoral Research Associate, University of York, UK

IAN BANCROFT
Professor, CNAP Chair of Plant Genomics, University of York, UK

LEE HICKEY
Senior Research Fellow, The University of Queensland, Australia

HENRIK BRINCH-PEDERSEN
Professor, Aarhus University, Denmark

ANNA COLL RUJ
Scientific Associate, NIB (National Institute of Biology), Slovenia

WENDY HARWOOD
Professor, John Innes Institute, UK

AARON HUMMEL
Head of Genome Editing Technology, Pairwise, USA

GUENTER WELZ
Strategic Alliance Manager, Breeding & Biologics, Bayer CropScience, Germany

THORBEN SPRINK
Group Leader & Senior Scientist, Julius Kuehn Institute, Germany

GIOVANNI GIULIANO
Research Director, ENEA, Tecan Trading AG

JURRIAN TON
Professor, University of Sheffield, UK

NICK JORDAN
Field Applications Specialist, Fluidigm

SEKHAR BODDUPALLI
President, AgBio Division, Intrexon, USA

SYLVIA DE PATER
Assistant Professor, Leiden University, The Netherlands

RICK VAN DE ZEDDE
Senior Scientist, Wageningen University

NIGEL HALFORD (Chair)
Senior Research Scientist, Rothamsted University, UK

MATTIONE MILNER
Senior Scientist, NIAB (National Institute of Agricultural Botany), UK

PETER VAN DER TOORN
Head of Government & Industry Relations, Syngenta, The Netherlands

ANINDYA BANDYOPADHYAY
Genome Editing Program Lead, Syngenta, China

7TH PLANT GENOMICS & GENE EDITING CONGRESS: EUROPE 2019
### Keynote Address:
#### Johnathan Napier
Professor, Flagship Leader and Science Director, Rothamsted Research, UK
**Thoughts on the UK’s first and last field trial of gene-edited plants**
- Rationale and focus for carrying out field trials of CRISPR-Cas9 gene-edited plants
- Impact of the ECJ ruling on such trials
- The way forward, under GM regulations, and the importance of field trials to validate potentially useful traits.

### Registration & Refreshments
08:00-08:50

### Global Engage Welcome Address and Track Chair’s Opening Remarks:
**Wendy Harwood**, Professor, John Innes Institute, UK

### 7th Plant Genomics & Gene Editing Congress: Europe 2019

### Room: Rotterdam Hall

#### Room: Mercurius Hall

#### Room: Van Oldenbarnevelt

#### Room: Leeuwen Room I&II

#### Room: Van Oldenbarnevelt

#### Room: Leeuwen Room I&II

#### Room: Leeuwen Room I&II

### Keynote Address:
#### Ana Atanassova
Global Regulatory Policy Manager, BASF Agricultural Solutions, Belgium

**Developments in biotechnology regulations – a global perspective**
- Regulatory approaches adopted by governments in different countries to regulation of gene editing
- Regulation that enables innovation
- The need for scientific evidence in support of regulatory policy in the area of gene editing

### Morning Refreshments / One-to-One Meetings / Even-Numbered Poster Presentations

### Room: Rotterdam Hall

### PLANT GENOME ENGINEERING: STRATEGIES & DEVELOPMENTS

**Chair:** Wendy Harwood, Professor, John Innes Institute, UK

#### Jim Dunwell
Professor, University of Reading, UK

**Prospects for Regulation of Gene-Edited Crops Post-Brexit**
Following the European Court of Justice decision that geneedited crops must be considered as GM and regulated as such, the UK government has various options. It can either accept this judgement, with which it disagrees, or it could decide to develop its own policy in this area. The UK government minister responsible for this subject has recently discussed the procedures necessary for developing an independent approach. However, any decision to move away from the EU system must wait until the UK finally leaves the EU; during any transition period the status quo will

### Room: Mercurius Hall

### PLANT PHENOTYPING & BIOINFORMATICS

**Chair:** Nicola Holden, Principal Investigator, James Hutton Institute, UK

#### Aalt-Jan van Dijk
Assistant Professor, Plant Systems Biology, Wageningen University, The Netherlands

**Machine learning based prediction and analysis of meiotic crossovers**
- Crossover occurrence within various plant genomes can be predicted by DNA sequence and shape features.
- Some features related to genome content and to genomic accessibility are consistently related to crossovers in various species; other features are found as predictive only in specific species.
- Integrative analysis of crossovers, genomic synteny and structural variation is provided.

### Room: Leeuwen Room I&II

#### Davide Bulgarelli
Principal Investigator, University of Dundee, UK

**Defining the host genetic control of the rhizosphere microbiota**
- Plants wear their gut on the outside: the rhizosphere microbiota as an untapped resource of plant probiotic functions;
- The plant genome is a determinant of the microbiota;
- Linking microbial diversity with plant genetic diversity

### Room: Leeuwen Room I&II

### Room: Leeuwen Room I&II

### Room: Leeuwen Room I&II
Giovanni Giuliano
Research Director, ENEA, Tecan Trading AG

Single Primer Enrichment genotyping highlights the worldwide population structure of tomato and eggplant genebank holdings

G2P-SOL (www.g2p-sol.eu) is an EU-funded project, bringing together the main European and international genebanks hosting germplasm of the four major Solanaceous crops: potato, tomato, pepper and eggplant. 23,900 tomato and 5,900 eggplant accessions, including wild relatives of both crops, have been inventoried within the project. To gain information about the population structure of the collections, the novel Single Primer Enrichment Technology (SPET, US Patent 9,650,628) developed by NuGEN was used for genotyping of tomato and eggplant materials. An SNP/indel panel was developed by assaying 14k probes for tomato and 11k for eggplant, evenly distributed in the gene-rich regions, and selecting the 5k best performing probes for each species. DNA samples were prepared by the genebanks using pre-tested protocols, subjected to QC and sample normalization, genotyped and sequenced. Reads were aligned to the eggplant and tomato reference genomes using BWA-MEM and SNP calling was performed. Several tens of thousands of high-quality SNPs were determined across 15,000 tomato and 3,600 eggplant accessions. The data were used to assess the genetic relationships in the tomato and eggplant genepools, as well as the extent of duplications within and between different genebanks.
PANEL DISCUSSION:
The Future of Plant Genomics: Navigating the latest ECJ court ruling on GM crops

- Impact of the latest ECJ ruling on plant gene editing research – now & in the future.
- Industry, academic, & global perspectives, from both outside and inside the EU
- Understanding the new regulations and how to continue gene editing research within the law
- Alternatives to gene editing – other technologies & developments exempt from the GMO laws

CONGRESS SCHEDULE
DAY 1 TUESDAY 21ST MAY 2019

13:00-14:00 Room: Mercurius Hall Lunch / One-to-One Meetings
Room: Rotterdam Hall
Chair: Nigel Halford, Senior Research Scientist, Rothamsted University, UK

TERESA BABUSCIO
Director, Agricultural & Cross Division Affairs, Belgium
Genome Editing Regulation

KIM HAMMOND-KOSACK
Professor & Principal Investigator, 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.

NICOLA HOLDEN
Principal Investigator, Molecular Bacteriologist, James Hutton Institute, UK
Microbial community composition and function associated with arable agricultural production in Scotland

The rapid advances in analysis of the community structures associated with arable crop production has produced a wealth of data and vastly expanded our knowledge of plant- & soilmicrobe interactions. Here, I will describe how the James Hutton institute has built on historic datasets and are applying state-of-the-art technology to go beyond community composition to functional analysis. This has exciting implications for agricultural management with the potential to impact on multiple benefits such as yield, biodiversity and disease control.

ERIK BONGCAM-RUDLOFF
Professor of Bioinformatics, SLU (Swedish University for Agricultural Sciences), Sweden
Presentation on bioinformatics applications, analysis, and challenges

JURRIAAN TON
Professor, University of Sheffield, UK
Long-term adaptation to biotic stress: involvement of epigenetic mechanisms and microbiomes
- Plants employ short- and long-term strategies to resist pests and diseases. This presentation will focus on long-term strategies, involving internal epigenetic mechanisms and external mechanisms that rely on the root-associated microbiome.
- Plants can acquire long-term resistance upon biotic stress exposure. This acquired resistance often relies on priming of inducible defences, enabling a faster and/or stronger defence induction following secondary attack. In some cases, priming can be transmitted to following generations. Current research
Today's agricultural scientists need to respond to demands on yield and quality from a growing global population, while also adapting to environmental changes. This means having a quick, robust, and cost-effective way to monitor genetic and phenotypic traits of the plants and animals we rely on to feed the world. With our Biomark HD and Juno systems, Fluidigm offers flexible and scalable solutions for the robust processing of samples in nanoscale reactions. Our products enable quick and reliable SNP genotyping by PCR, amplicon library preparation for genotyping by sequencing (GBS), digital PCR, and gene expression analysis. The platform allows flexibility in assay design, supporting a multitude of applications from marker assisted breeding to pathogen detection and resistance.

For sponsorship opportunities contact Faizel Ismail: faizel@globalengage.co.uk / +44 (0) 1865 849841
Knockdown of S1 gene in rice using RNA interference confers resistance to rice brown planthopper

Brown planthopper (BPH) is one of the most serious rice pests in rice production, causing significant yield loss globally. Developing BPH resistant rice varieties is one of the most effective and environmentally friendly strategies for protecting the rice crop. This study demonstrated that knockdown of S1 gene in a susceptible rice cultivar, TN1 enhanced resistance to BPH. RNAi rice genotypes using a constitutive promoter was generated, as were their respective empty vector controls. RNAi lines significantly (p<0.05) decreased BPH survival and significantly (p<0.05) decreased the rate of development. Survival of insects on the RNAi lines decreased approximately to 50% as compared to their respective transformed empty vector lines and TN1, which were used as control.

Automatic identification of experimental conditions relevant to specific traits

- Co-expression of two genes across different conditions is indicative of them being involved in the same pathway/trait
- In large datasets with many experimental conditions, only a minority of them are expected to be carry meaningful co-expression signal about a specific pathway.
- We developed a fast algorithm to automatically select the relevant RNA-Seq samples for a specific pathway/trait from the vast set of available samples in public databases.

Phenomics is an enhancer of Genetics
- The advent of automatic data acquisition or phenomics has allowed high throughput studies of single traits. Moreover, phenomics data allow the refinement, and sometimes finer dissection of genetic traits.
- We have used in-house phenomic facilities to study growth and flower development in Petunia and Antirrhinum in a variety of genes silenced by RNAi.
- We found that the detailed analysis of images allowed the dissection of growth rate and timing in different organs suggesting organ-specific gene functions of ZEITLUPE in Petunia. Furthermore, we found an undescribed kinetic of flower opening that appears to be under control of EARLY FLOWERING 4.

Microfluidic technology can offer new opportunities to study whole living organisms and their interactions and 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).
- In this talk a variety of case studies will be highlighted, demonstrating how this technology has been used to study bacterial-fungal and fungal-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 microfluidic tools to investigate microbial interactions in the rhizosphere, specifically to probe the cell biology and physiology of microbe association and colonisation of arbuscular mycorrhizal fungi at the cellular level.
Table 2: Genome Editing Regulation
SELIM LOUAFI
Senior Research Fellow, Cirad, Joint Research Unit Genetic Improvement and Adaptation of Mediterranean and Tropical Plants (AGAP), Montpellier, France

Table 3: Bioinformatics
MARCEL VAN VERK
Team Leader Crop Data Science, KeyGene, The Netherlands

Table 4: Plant Phenotyping
RICK VAN DE ZEDDE
Senior Scientist, Wageningen University

Table 5: How to Acquire the Social License for Gene Editing in Plant Breeding
PETER VAN DER TOORN
Head of Government & Industry Relations, Syngenta, The Netherlands

Full details shown on next page.

7TH PLANT GENOMICS & GENE EDITING CONGRESS: EUROPE 2019
### TABLE 1: VLADIMIR NEKRASOV
**Project Leader, Rothamsted Research, UK**

**The Future of Breeding Technologies**

- 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: SELIM LOUAFI
**Senior Research Fellow, Cirad, Joint Research Unit Genetic Improvement and Adaptation of Mediterranean and Tropical Plants (AGAP), Montpellier, France**

**Regulating Genome-Editing: Alternatives to the Classical Risk-Based Management Approach**

Regulation of emerging technology has mainly focused on responding to the consequences of innovation. Relying on such model for genome editing bears the risk of reproducing the same confrontational situation that occurred with GMOs. By contrast, alternative models recognize the diversity of innovation trajectories that offer the possibility to better anticipate obstacles and to adequately modulate the innovation process in real time. These models target softer interventions that modulate ongoing socio-technological developments interventions at policy, organizational and individual (i.e. scientist) levels. As consumers of complexity, scientists should be engaged in designing initiatives that counteract the current polarized trend in genome editing as well as other fields. New initiatives that move beyond the regulatory approach and embed scientists in the development of solutions will be discussed.

### TABLE 3: MARCEL VAN VERK
**Team Leader Crop Data Science, KeyGene, The Netherlands**

**New kids on the block, upcoming developments in bioinformatics**

- Affordable large scale RNA-seq studies
- Single cell sequencing
- Wide variety commercial / open source tools
- Virtual- and augmented reality

### TABLE 4: RICK VAN DE ZEDDE
**Senior Scientist, Wageningen University**

**Plant Phenotyping**

### TABLE 5: PETER VAN DER TOORN
**Head of Government & Industry Relations, Syngenta, The Netherlands**

**How to Acquire the Social License for Gene Editing in Plant Breeding**

This round table will discuss the need to acquire a social license for gene editing, next to regulatory FTO. Typical questions include:

- How do we show the societal value of gene editing in plants?
- To what extend should we be transparent on breeding innovations used?
- How can we step up as a scientific community and industry to reach out to the wider public?
- How can we present gene editing in the framework of the public concerns about the agricultural production system?
KEYNOTE ADDRESS:
IAN BANCROFT
Professor, CNAP Chair of Plant Genomics, University of York, UK

Genomics-led “traditional” approaches to crop genome engineering
Chemical and radiation mutagenesis, along with Doubled Haploid production and alien introgression, are classed as traditional approaches for crop improvement and are not considered by the European Court of Justice to result in plants classed as GMOs. I will describe recent advances in genomics that can accelerate genome engineering by these methods, illustrating their impacts on genome structure.

SOLUTION PROVIDER PRESENTATION:
ALEXANDER WITTENBERG
Scientist, Next Generation Sequencing, KeyGene
Crop genome insight through long read nanopore sequencing
KeyGene was announced as the first PromethION service provider by Oxford Nanopore Technologies in May 2018. Combining our unique expertise in HMW nuclear DNA isolation with the ultra-long reads from the PromethION platform and our bioinformatics capabilities has allowed KeyGene to now routinely produce contiguous, high-quality assemblies of large and repetitive crop genomes. The genome insight that is generated enables unraveling of traits at an unprecedented speed therefore accelerating the development of new varieties. Some of KeyGene’s latest results on completed high-quality reference genomes will be presented. In addition we will present results on our CRISPR-Cas-based targeted sequencing approach with high enrichment percentages in a number of crops.

SOLUTION PROVIDER PRESENTATION:
TINGTING ZHOU
General Manager, Novogene
Title TBC

AARON HUMMEL
Head of Genome Editing Technology, Pairwise, USA
Enhancing crop diversity with novel genome editing tools
- Pairwise is committed to developing healthy, convenient, sustainable and affordable food using gene editing technology to leverage native plant diversity.
- We will discuss development of base editing technology in crop systems and application in generating novel alleles of important genes

SEKHAR BODDUPALLI
President, AgBio Division, Intrexon, USA
Ag Innovations in precision genetics and precision biologicals
Innovation in Ag for enabling sustainable food production for a growing population, while maintaining the natural ecosystems is a challenging unmet need and opportunity. Over the past decade, several platforms ranging from biologicals to digital have emerged. At Intrexon, we are focused on precision genetics and precision biological solutions to improve the quality of food and feed while preserving our valuable natural ecosystems – Better World through Better DNA™. An overview of the current status and recent progress in products using our Florian™, Botticelli™, and ActoBiotics™ platforms would be discussed.
CONGRESS SCHEDULE

Day 2
Room: Van Oldenbarnevelt

12:35-13:00
- Sustainable long-term genetic gain.
  - Outline the opportunities & challenges associated with the fusion of these breeding tools to achieve substantially reduce the length of the breeding cycle and maximise genetic gain per unit time. We real wheat data sets we exemplify how a combination of genomic selection and speed breeding can breeding technologies, including genome editing and genomic selection. Using simulations based on

13:00-13:25

14:30-14:55

SYLVIA DE PATER
Assistant Professor, Leiden University, The Netherlands
CRISPR/Cas-induced genome engineering in Arabidopsis DNA repair mutants
Sequence-specific nucleases like CRISPR/Cas can be used for induction of double strand breaks (DSBs), which are repaired via homologous recombination (HR) or non-homologous end-joining (NHEJ). There are various NHEJ pathways, which can be subdivided into the KU-dependent classical NHEJ (c-NHEJ) pathway and one or more less well defined alternative pathways, involving the poly (ADP-ribose) polymerases (PARPs) and Polymerase theta (Polθ). Imperfect repair via NHEJ may result in mutations, which depend on the repair pathway used. Absence of functional Ku directs the outcome towards larger deletions with more templated insertions, which are hallmarks for Polθ-mediated end-joining (TMEJ). Repair via HR may result in precise changes of the target if a homologous donor template is provided, a technique known as gene-targeting.

LEE HICKEY
Senior Research Fellow, The University of Queensland, Australia
Fusing breeding technologies to supercharge our future crops
The slow rate of crop improvement is inadequate to meet future demands. In this presentation, we highlight innovative breeding strategies that integrate rapid generation advance technology called ‘speed breeding’ with other modern breeding technologies, including genome editing and genomic selection. Using simulations based on real wheat data sets we exemplify how a combination of genomic selection and speed breeding can substantially reduce the length of the breeding cycle and maximise genetic gain per unit time. We outline the opportunities & challenges associated with the fusion of these breeding tools to achieve sustainable long-term genetic gain.

THORBEN SPRINK
Group Leader & Senior Scientist, Julius Kuehn Institute, Germany
DNA free genome editing - applications and regulations
Genome Editing using engineered endonucleases has a great impact on many fields incl. science, breeding and medicine. In Plants Genome Editing has been done in more than 50 species addressing several targets ranging from basic research to field applications. In many cases the tools for Genome Editing are introduced into the genome of the target to achieve the aimed alteration with subsequent outcrossing but edits are also possible without stable introduction of the tools in the genome. The presentation will give an overview on DNA-free Genome Editing its applications and its potential advantages over conventional Genome Editing concerning GMO regulation in some countries.

OMID ANSARI
Head of Research, Ecofibre, USA
Marker-assisted selection in Cannabis
This presentation highlights research activities focused on development of Cannabis (Industrial hemp) varieties with improved characteristics suitable for food, fibre and medicinal applications using modern genetic improvement strategies, such as marker-assisted selection as well as genomic selection. Cannabis sativa is a high yielding biomass crop that is widely considered as a short-day plant and therefore highly dependent on photoperiod for the initiation of flowering. Cannabis is a prolific producer of a class of medically relevant secondary metabolites commonly identified as phytocannabinoids. Discovery and refinement of genomic and genetic tools may accelerate varietal development in Cannabis for a number of important agronomic characteristics. We report the preliminary findings from a novel approach to variant discovery referred to as extreme-phenotype genome-wide association study (XP-GWAS) and demonstrate proof of concept using the THCA synthase locus as an exemplar. More detailed analysis may expose diagnostically valuable markers for cannabinoid composition and facilitate the genetic metabolic engineering of Cannabis for different end-uses.

VLADIMIR NEKRASOV
Project Leader, Rothamsted Research, UK
Genome editing as a tool for enhancing disease resistance in crops
The presentation will give an overview of how the genome editing technology (CRISPR/Cas) can be applied for the purpose of improving disease resistance in crops in a way, which is faster and more precise as compared to conventional breeding. The gene editing approach will be compared to the transgenesis one, as well as conventional breeding, and a few examples will be given. The presentation will also address precision of CRISPR/Cas in plants and whether the off-targeting should be an issue of concern.
ANINDYA BANDYOPADHYAY
Genome Editing Program Lead, Syngenta, China
Presentation on a novel CRISPR mediated technique HI-Edit /SEDHI to produce advanced crops

JUANDE ALCHE
Scientific Researcher, Spanish National Research Council (CSIC), Spain
Transcriptomic approaches to the analysis of reproductive biology in the olive tree (Olea europaea L.) and applications in the development of alternative olive products, olive oil characterization and health improvement.

We have developed transcriptomic approaches focused in the analysis of the reproductive tissues (pollen, stigma, seed), of the olive tree (Olea europaea L.), a crop of paramount importance. These tissues have large implications in the yield, olive oil quality, and other aspects like pollen allergies. Also, new materials are arising from the alternative processing of the olives. This is the case of the olive seed, which is the source of a differential oil used in cosmetics, and biomolecules of alimentary and pharmaceutical interest like the olive seed flour, which has been demonstrated to have anti-inflammatory/anti-diabetic properties. Our data were obtained after using subtractive (SSH) libraries, then 454+ sequencing, and finally Illumina RNAseq, all of them combined with experimental, massive proteomic datasets. The sequences obtained were implemented in an olive reproductive database: ReprOlive (www.reprolive.eez.csic.es), built with newly developed bioinformatic tools like TransFlow. We use this knowledge database to develop new agro-food uses, and also to identify new pollen allergens, allowing the improvement of allergy diagnosis and therapy.

GUENTER WELZ
Strategic Alliance Manager, Breeding & Biologics, Bayer CropScience, Germany
Industry strategy for genome engineering

WENDY HARWOOD
Professor, John Innes Institute, UK
Cereal genome engineering using CRISPR/Cas9
- CRISPR/Cas9 based genome editing is revolutionizing progress in many crop research fields.
- In the key cereal crops, wheat and barley, production of targeted gene 'knock-outs' is now routine. Examples will be given.
- Attention now turns to expanding the CRISPR toolbox, in particular developing technologies for gene targeting or 'knock-ins'. Progress in this area will be described for barley and the opportunities arising from expanded genome engineering capabilities discussed.

MATTHEW MILNER
Senior Scientist, NIAB (National Institute of Agricultural Botany), UK
Gene Editing in Cereal Species
Our results show that in common with other groups, editing in rice is extremely efficient – with 80-90% of transformed plants having edits even when single guides are used to target the Cas9 nuclease. We have then used single guides in hexaploid wheat and find that efficiencies of up to 17% can be achieved with single genome targeted guides, but to achieve a knock-out in all six alleles in T0 plants, multiple guides are required. Six allele knock out efficiencies of up to 24% have been achieved using this strategy in wheat. To increase the relevance of this technology to agriculture, we have transformed over 40 bread wheat varieties, including winter and spring types, and durum wheats. This enables new technologies such as gene editing to be applied directly in the elite germplasm of choice, without the need for lengthy back-crossing into the germplasm of choice.

ANNA COLL RUIS
Scientific Associate, NIB (National Institute of Biology), Slovenia
Development of PLANT X-TENDER, a toolbox for the assembly, delivery and expression of multigene constructs in plants
Cloning multiple DNA fragments for delivery of several genes of interest into the plant genome is one of the main technological challenges in plant synthetic biology. Here I will present Plant X-tender, an extension of the highly efficient, scar-free and sequence-independent multigene assembly strategy AssemblX, based on overlap-dependent cloning methods and rare-cutting restriction enzymes. Plant X-tender consists of a set of plant expression vectors and the protocols for most efficient cloning into the novel vector set needed for plant expression and thus introduces advantages of AssemblX into plant synthetic biology. We have further validated the developed procedure for plant protein expression by cloning different cassettes into the newly developed vectors and subsequently transferred them to Nicotiana benthamiana in a transient expression setup. We expect our results will support faster introduction of synthetic biology into plant science.
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