



Plants  
and  
People

(M)PIMP Future Food  
Challenges for Global  
Food Security

September 3-4, 2019

Organized by PhD students



<https://plants-and-people.mpg.de>



IMPRS  
Primary Metabolism  
and Plant Growth



Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany

## **WELCOME to Plants and People 2019**

It is with both great pleasure and pride to welcome you all to the 5<sup>th</sup> Plants and People conference. Held biennially, the Plants and People conference is organized by PhD students at the Max Planck Institute of Molecular Plant Physiology. These conferences have always been unique in that they bring together experts from both the natural/physical sciences and the social sciences to give their talks and perspectives centered around a specific theme. In a manner of speaking, this is our way of getting a panoptic view on the chosen theme. We gather a panoply of speakers around the world with highly diverse expertise and exposures with the aim to blur knowledge divides and hopefully inspire new solutions.

This year's theme is **(M)PIMP Future Foods - Challenges for Global Food Security**. Without question, the efforts made by the plant scientists have played a crucial role in curbing world hunger as exemplified by Norman Borlaug's work that led to the green revolution. This year's conference will highlight what plant science has done to impact global food security in recent years; what is being done to address future food needs; what is going on beyond the walls of academia; and most importantly, will food generated using advanced science like recombinant DNA technology and gene-editing ever reach general acceptance.

We encourage you to listen critically, ask probing question, and start discussions so that perhaps one day, challenges for global food security will be a thing of the fossilized past.

Have a wonderful and informative time at the 5<sup>th</sup> Plants and People conference.

Additionally, we want to thank all the people who made the Plants and People conference possible:

Dr. Ina Talke from IMPRS 'Primary Metabolism and Plant Growth for the guidance and her great experience;

Juliane Vosswinkel from Administration for internal organization;

Stefan Heinrich from Max Planck Campus Golm who build the website;

the P&P team from 2011 who made Plants and People such a success worth to continue and who designed the logo;

our sponsors for providing refreshments for the breaks and gimmicks for the sessions;

and last but not least YOU for joining our conference, asking questions and enjoying the talks.

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**Tuesday, 3 September**

08:30 – 10:00	<b>Registration</b>
10:15 – 12:30	<b>Session 1</b>
10:15 – 10:20	Welcome
10:20 – 11:00	Mark Tester (KAUST, SA)
11:00 – 11:40	Björn Niere (BMZ, DE)
11:40 – 11:50	Student talk: Daniela Ríos Rodríguez (KIT, DE)
11:50 – 12:30	Christine Foyer (University of Birmingham, UK)
12:30 – 13:20	<b>Lunch break</b>
13:20 – 16:00	<b>Session 2</b>
13:20 – 14:00	Alison Smith (University of Cambridge, UK)
14:00 – 14:40	Kirsi-Marja Oksman-Caldentey (VTT, FI)
14:40 – 14:50	Student talk: Matthijs Hölscher (MPI-MP, DE)
14:50 – 15:30	Shanshan Luo (MPI-TM, DE)
15:30 – 16:00	<b>Coffee break</b>
16:00 – 17:30	<b>Session 3</b>
16:00 – 16:40	Fernando Geu-Flores (University of Copenhagen, DK)
16:40 – 16:50	Student talk: David Schröter (IGZ/DIfE, DE)
16:50 – 17:30	Joachim Schiemann (JKI, DE)
17:30 – 18:45	<b>Meet and Greet session with Tuesday's speakers (with refreshments)</b>

**Wednesday, 4 September**

09:15 – 10:45	<b>Session 4</b>
09:15 – 09:55	Rachel Wells (JIC, UK)
09:55 – 10:05	Student talk: Philipp Rink (IPK, DE)
10:05 – 10:45	Nick Saik (Know Ideas Media, CA)
10:45 – 11:15	<b>Coffee break</b>
11:15 – 12:45	<b>Session 5</b>
11:15 – 11:55	Matt Clark (NHM, UK)
11:55 – 12:05	Student talk: Maria Krantz (HU, DE)
12:05 – 12:45	Eva Gietl (KWS, DE)
12:45 – 13:00	<b>Conference group picture</b>
13:00 – 14:00	<b>Lunch break</b>
14:00 – 16:10	<b>Session 6</b>
14:00 – 14:40	Natalie Laibach (University of Bonn, DE)
14:40 – 15:20	Wendy Harwood (JIC, UK)
15:20 – 15:30	Student talk: Dora Pinczinger (JKI, DE)
15:30 – 16:10	Jessica Eise (Purdue University, USA)
16:15 – 17:30	<b>Meet and Greet session with Wednesday's speakers (with refreshments)</b>
From 18:00	<b>BBQ</b>

# GENETIC CHARACTERIZATION OF SALINITY TOLERANCE TRAITS TO INCREASE SALINITY TOLERANCE IN CROPS

**Mark Tester**

*King Abdullah University of Science & Technology, Thuwal, 23955-6900, Saudi Arabia*

One-third of the world's food is produced under irrigation. This is challenged by over-exploitation of water resources and global environmental change. This talk will focus on the use of forward genetics to discover genes affecting salinity tolerance in barley, rice, and tomatoes, along with some recent genomics in quinoa, a partially domesticated crop with high salinity tolerance. Rather than studying salinity tolerance as a trait in itself, we dissect salinity tolerance into a series of components that are hypothesized to contribute to overall salinity tolerance.

For tomatoes, the focus is on association genetics of tolerance in wild tomatoes. Tomatoes have been phenotyped in The Plant Accelerator® and in the field for three years, and analyses are currently in progress. For quinoa, the genome has been sequenced to high quality, and now about 1,000 lines have been re-sequenced. Up to 1,300 lines are being phenotyped in The Plant Accelerator and 10 field trial sites to identify natural variation in a range of domestication and tolerance traits. The application of this approach provides opportunities to significantly increase abiotic stress tolerance in crops and thus contribute to increasing agricultural production in many regions.

To deliver our research, we have now established a company, Red Sea Farms LLC, where we combine engineering and plant science to develop and use saltwater-based agricultural systems, to reduce the water and carbon footprint of modern agriculture, and to do this environmentally sustainably and economically viably.

# **SUSTAINABLE AGRICULTURE IN GERMAN DEVELOPMENT CO-OPERATION**

**Björn Niere**

*German Ministry for Economic Cooperation and Development (BMZ), Berlin, 10963, Germany*

The world's population is set to grow from roughly 7.5 billion people in 2017 to an expected 9.7 billion people in 2050. But even now, more than 800 million people suffer from hunger, two billion people are malnourished and another two billion are overweight or obese. The FAO estimates that in order to meet the needs of a growing population – mostly in developing countries and emerging economies - global food production will have to be 50 per cent higher than in 2012. However, it is unlikely that only an increased agricultural production will solve the already eminent problems. Food loss and waste needs to be addressed at different levels while changes in diets are also necessary in many parts of the world. At the same time, further increases of land used for agricultural production need to be halted. Past achievements in reducing hunger have also come at a heavy cost to the environment. Unsustainable agricultural practices are a main driver for deforestation, land degradation, biodiversity loss, and anthropogenic greenhouse gas emissions. Agriculture is, at the same time, a prime victim of the effects of climate change. Long term climatic changes particularly in Sub-Sahara Africa and Southeast Asia and the impact of extreme weather events negatively affect crop and livestock production.

There are severe global challenges to agriculture and food systems and it is unlikely that a single approach will solve these. It is also important to acknowledge that in developing countries the majority of food is produced by smallholder farmers. Industrialized farming systems are unlikely to serve as a blueprint for, e.g., Sub-Sahara Africa farming systems. More often than not industrial farming systems also do not adequately respect the environmental and social aspects of sustainability. The preservation of healthy ecosystems, natural resources and reducing greenhouse gas emissions while adapting agriculture to climate change is vital for sustainable food systems.

Agroecology is one approach to address all dimensions of sustainability. German development co-operation is actively engaged - in close cooperation with local, national and international institutions- in combating poverty, securing food, establishing peace, freedom, democracy and human rights, and preserving the environment and natural resources. The 17 Sustainable Development Goals (SDG) of the 2030 Agenda are the guiding principles for the German Federal Ministry of Economic Cooperation and Development (BMZ). The One World – No Hunger initiative of the BMZ contributes to achieve SDG 2 (End hunger) through several projects mostly in Africa. Currently the BMZ strives to promote, throughout its agriculture portfolio, agricultural practices that are ecologically responsible, socially just, economically efficient and regionally anchored. Such transformation may be realized at different levels: starting from simple input reductions to holistic food systems.

## DISSECTING DNA BARCODING AS A PLANT IDENTIFICATION TOOL: THE HOLY BASIL CASE

Daniela Ríos Rodríguez , Sahi V.P., Nick P.

*Molecular Cell Biology, Botanical Institute, Karlsruhe Institute of Technology, Karlsruhe, 76135,  
Germany*

DNA barcoding is a procedure used for species' identification through the amplification of short-length DNA sequences. It has been recognized as a modern technique for traceability that can be used as a tool for food security by ensuring plant identity. Holy basil - *Ocimum tenuiflorum* - is one of the new super foods in trend, and it has been surrogated by other *Ocimum* species with a quite different chemical profile, potentially harmful for the health of consumers. Our project aimed to identify *Ocimum tenuiflorum* by fast low-cost DNA barcoding: amplification of a known region of the DNA and then its verification by gel electrophoresis. We found that the genes commonly used for barcoding can be highly similar among *Ocimum* species. Therefore, we coupled DNA barcoding with other techniques and selected less common DNA regions for identification. We also found that food and beverages, such as tea infusions or powders, both sold in mixtures, obstruct a proper analysis. In our study, we were able to develop a method which identifies *Ocimum tenuiflorum* from other *Ocimum* sp. with a fast, low-cost procedure, with one exception where sequencing a segment of the DNA is still necessary for identification.



# THE ROLE OF LEGUMES IN SUSTAINABLE AGRICULTURE AND FOOD SECURITY

**Christine H. Foyer**

*Centre for Plant Sciences, Faculty of Biology, University of Leeds, Leeds, LS2 9JT, UK*

The United Nations Sustainable Development Goals present an urgent and formidable challenge to scientists and society alike, highlighting the urgent requirement to transform agriculture and the food sector to achieve food and nutrition security, ecosystem sustainability, economic growth and social equity over the coming decades. The intensification of legume-based agriculture must form a central pillar in the international commitment towards, food security, health, economic development and poverty alleviation. However, legumes are currently underutilized in comparison to cereals. Grain legume production is static or declining in developing countries, despite increasing global demand. This talk will describe our studies seeking to understand the physiological and molecular basis for stress tolerance in soybean (*Glycine max*) and other legumes.

# **ALGAE FOR FOOD – ENHANCING NUTRITIONAL VALUE AND REDUCING WASTE**

**Alison G. Smith**

*Department of Plant Sciences, University of Cambridge, Cambridge, CB2 1TN, UK*

There is increasing recognition of the need to reduce our reliance on fossil carbon for fuels and materials, whilst at the same time mitigating the consequences of the waste generated as a result of domestic, agricultural and industrial activities. Plants and algae, as photosynthetic organisms, offer considerable potential as means to generate everything from bulk feedstocks to platform chemicals and high value products, using solar energy as the main input. Microalgae in particular are an underexploited resource for sustainable production of a range of novel products. In addition, incorporation of microalgal cultivation into different processes in a modular fashion enables valorisation of waste streams – a concept that we have termed Circular Photosynthesis. I will discuss the reasons why microalgae are a rich source of vitamin B12, an essential organic micronutrient synthesised only by bacteria, and how it is possible for algae to obtain B12 in mutualistic co-culture with bacteria. We are exploiting this in efforts to produce food and feed with enhanced nutritional profiles. In addition, I will illustrate how we have been working with colleagues in developing countries to introduce Circular Photosynthesis approaches so that they can be deployed widely at local scale, supporting innovation and enterprise, and reducing waste.

## BIOTECHNOLOGY OF BERRY-BASED INGREDIENTS FOR COSMETIC, PHARMA AND FOOD APPLICATIONS

**Kirsi-Marja Oksman-Caldentey, Nohynek L., Alakomi H-L., Rischer H., Puupponen-Pimiä R.**

*VTT Technical Research Centre of Finland Ltd., Espoo, FI-02044, Finland*

Cosmetics are moving towards pharma and cosmeceuticals are entering the market. Modern biotechnology offers many advantages to develop new type of ingredients for industrial applications in an environmental friendly and sustainable way. We have developed industrial scale biotechnological production systems for wild and rare Nordic berry species including cell cultures with consistent quality and defined chemical composition. Moreover, through our novel bioprocessing technologies, such as seed sanning, fermentation and biotransformation, the berries and their side streams can be modified to obtain ingredients with new or improved activities, colours and flavours.

Due to the arctic growth conditions, Nordic berries are rich sources of natural biomolecules with multifunctional effects to the skin. We have shown that phenolic compounds in berries very efficiently inhibit the growth of many human pathogens including skin pathogens, such as *Staphylococcus aureus*, *S. epidermis* and *Pseudomonas aeruginosa* without effecting the growth of beneficial bacteria. Several mechanisms of action, including the weakening of the outer membrane of Gram- negative bacteria, are involved in the growth inhibition. More interestingly, various berry phenolics are shown to specifically block cell-to-cell signalling (quorum sensing) in a bacterial community. Thus these phytochemicals can act in cosmetic preparations in dual way, as natural preservatives to prevent spoilage of the product, and as stabilizers of healthy skin microbiota by inhibiting the growth of harmful skin microbes, and by supporting the growth of beneficial microbes. Our recent findings have shown that some of our berry extracts are also very effective against MRSA (Methicillin resistant *Staphylococcus aureus*) thus opening entirely new avenues in fighting against severe worldwide problem of antibiotic resistance.

Using plant cell and tissue culture technology whole biosynthetic capacity of the plant can be advantaged and even totally new beneficial compounds can be produced. The unusual phenolic profile of our cultured berry cells, as well as their fatty acid composition with a high proportion of  $\alpha$ -linolenic acid and high protein content makes them a unique and interesting alternative for food applications. Some examples and future perspectives of cellular agriculture including edible plant cells will be discussed.

## PRODUCTION OF POTENT SMALL-POLYPEPTIDE MICROBICIDES IN TRANSPLASTOMIC PLANTS

**Matthijs Hölscher, Forner J., Bock R.**

*Max-Planck-Institut für Molekulare Pflanzenphysiologie, Potsdam, 14476, Germany*

Multicellular organisms defend themselves against pathogens and pests with an arsenal of molecules, including small-polypeptide microbicides. These defense compounds provide a rich source of bioactive molecules that can be used for pharmaceutical purposes and in plant protection. Unfortunately, the chemical synthesis of polypeptide microbicides is usually not possible, and their production in microbial hosts is costly and often inefficient. Chloroplasts have a high capacity to accumulate foreign proteins and, therefore, represent an attractive platform for polypeptide production 1. We have explored the potential of transplastomic tobacco plants to serve as an inexpensive production platform for small-polypeptide microbicides. We recently demonstrated that the highly potent microbicide griffithsin that inhibits entry of HIV into human cells can be produced to very high levels in transplastomic tobacco plants. Chloroplast-produced griffithsin is fully active against HIV and retains high biological activity even in dried tobacco biomass 2. In ongoing studies, we are exploring diverse experimental strategies for the production of various small antimicrobial peptides (AMPs) that are active against pathogenic bacteria and fungi. These molecules are of great interest, because they (i) represent candidate next-generation antibiotics that can help to overcome microbial resistances against conventional antibiotics, and (ii) can potentially provide plant protection from bacterial and fungal pathogens. Progress with optimizing the production of AMPs in transplastomic plants will be reported.

# DESIGN AND CONSTRUCTION OF A SYNTHETIC CO<sub>2</sub> FIXATION CYCLE *IN VITRO*

Shanshan Luo

*Max Planck Institute for Terrestrial Microbiology, Marburg, D-35043, Germany*

Converting CO<sub>2</sub> into useful chemicals can be an ideal solution for a sustainable future. However, due to its high thermodynamic stability and kinetic inertness, the chemical transformation of CO<sub>2</sub> into organic compounds usually requires quite harsh conditions. In contrast, nature has evolved several CO<sub>2</sub> fixation pathways for synthesizing longer carbon chain compounds from CO<sub>2</sub> under ambient conditions. To date, six natural CO<sub>2</sub> fixation pathways have been reported. However, they all contain key carboxylases with intrinsic properties such as oxygen sensitivity and structural complexity that hinder their further engineering and applications. To circumvent these problems, we designed a synthetic CO<sub>2</sub> fixation cycle composed of all efficient, simple and oxygen tolerant enzymes and demonstrated its function *in vitro*. This pathway utilizes the two most active and oxygen-insensitive carboxylases, crotonyl-CoA carboxylase/reductase (Ccr) and phosphoenolpyruvate carboxylase (Ppc) to realize the fixation of two CO<sub>2</sub> equivalents to one acetyl-CoA in one cycle. This synthetic cycle produces key metabolites for cell growth, and is expected to be compatible with cellular metabolism and evolvable *in vivo*. In this talk, I will present how we designed this pathway using a modular approach and how we established and optimized this pathway *in vitro*.

# BIOSYNTHESIS AND TRANSLOCATION OF TOXIC ALKALOIDS IN LUPINS

**Fernando Geu-Flores**

*Department of Plant and Environmental Sciences, University of Copenhagen, Copenhagen, 1871,  
Denmark*

Lupins are nitrogen-fixing protein crops with great potential to curb the EU's dependency on imported soybean. However, lupins accumulate toxic alkaloids in most tissues, including the protein-rich seeds. Low-alkaloid varieties exist ("sweet varieties"), but they are more susceptible to herbivores. In addition, the alkaloid content of sweet varieties varies greatly from year to year, often surpassing the threshold imposed by the food and feed industries.

Our group investigates how the lupin alkaloids are synthesized in lupins. Using a high-alkaloid variety ("bitter variety") of narrow-leafed lupin, we have generated a high-quality transcriptome representing 8 tissues with contrasting alkaloid content. Through a combination of guilt-by-association and enzyme assays, we have initiated the discovery of new enzymes in the lupin alkaloid pathway. At the same time, we have addressed the question of whether the alkaloids are made in the seeds or transported to them. Using gene expression studies across seed development as well as studies on maternal determination, we have shown that the lupin alkaloids are mostly, if not exclusively transported to the seeds.

Our work establishes a solid basis for the full elucidation of the lupin alkaloid pathway and opens the possibility of using transport engineering to obtain herbivore-resistant bitter varieties that produce alkaloid-free seeds.

# CONSUMED BY MILLIONS, YET UNEXPLORED – A FUNTIONAL CHARACTERIZATION OF THE SECONDARY METABOLITE PROFILE OF AMARANTH LEAVES

**David Schröter**<sup>a b c</sup>, Ott, C.<sup>b</sup>, Grune, T.<sup>b</sup>, Schreiner, M.<sup>a</sup>, Neugart, S.<sup>a</sup>, Rohn, S.<sup>c</sup>

<sup>a</sup>*Plant Quality and Food Security, LeibnizInstitute of Vegetable and Ornamental Crops (IGZ),  
Grossbeeren, 14979, Germany*

<sup>b</sup>*Molecular Toxicology, German Institute of Human Nutrition Potsdam-Rehbruecke,  
Nuthetal, 14558, Germany*

<sup>c</sup>*Hamburg School Of Food Science, University of Hamburg, Hamburg, 20146, Germany*

*Amaranth* ssp. are globally grown food crops. In sub-Saharan Africa, they are traditional constituents of the daily diet. However, the chemical structure of their secondary metabolites is still insufficiently described, and their respective bioactivity is not yet studied in-depth. Nevertheless, detailed information on the concentrations and the exact chemical structures of the secondary metabolites is needed in order to elucidate the potential effects on consumers' health.

The scientific goal of this work was to quantify the phenolic compounds and carotenoids in 14 different amaranth genotypes from six species. To the best of our knowledge, this was the first time that caffeic acid esters of isocitric acid and several aldaric acids were isolated and quantified in a food-relevant matrix. Altogether, high concentrations of hydroxycinnamic acids and moderate amounts of flavonoids and carotenoids were detected. The quantitative data were then combined with data from molecular biological approaches (RAPD-PCR) to sort the amaranth genotypes in distinct groups, depending on the composition of the plant secondary metabolite profiles. To evaluate how amaranth-derived preparations facilitate anti-inflammatory effects on a molecular basis, RAW 264.7 macrophages were incubated with amaranth's 2-caffeoylisocitric acid as well as chlorogenic acid (C-QA) and caffeic acid (CA) as reference substances. It was shown that the different caffeic acid derivatives applied in physiological concentrations exhibited an anti-inflammatory effect regarding the reduction of inducible nitric oxide synthase, tumor necrosis factor  $\alpha$  and interleukin 6.

Thus, this work provides the basis (I) to establish an authentication method for unknown amaranth genotypes, (II) to select genotypes with high concentrations of novel hydroxycinnamic acids for future crop-breeding strategies, and (III) to increase the attractiveness of amaranth production for the diversification of western-style diets. Moreover, this work consolidates the knowledge on the effect mechanisms of plant-derived remedies and grants the opportunity to unveil bioactive compounds with nutraceutical potential.

# PLANT GENOME EDITING – POLICIES AND GOVERNANCE

**Joachim Schiemann**

*Julius Kühn Institut, Federal Research Center for Crops, Quedlinburg, 06484, Germany*

Genome editing is a transformative technology with general applicability providing a very wide range of potential uses to tackle societal challenges. The increased precision now possible in plant breeding using genome-editing techniques represents a big change from conventional breeding approaches, which in large part relied on random, uncontrolled chemical- or radiation-induced mutagenesis, and from genetic engineering that relies on unpredictable insertions of isolated genes into the plant genome. If conducive regulatory and social conditions are in place, genome editing could substantially increase the positive impacts of plant breeding on human welfare and sustainability.

The development and use of modern bio-techniques are regulated by different countries and communities of states according to their national laws and governance structures. The legal frameworks require submission of comprehensive scientific evidence about the biology of the organism and its safety with regard to human and animal health and the environment into which it will be released.

The decision of whether to classify plants with new traits as genetically modified organisms (GMOs) / living modified organisms (LMOs) has dramatic consequences for research and development in different jurisdictions, especially in the European Union. In the implementation of the EU biotechnology regulatory framework there is a disproportionate focus on the genetic improvement technique used. Whether or not the resulting organism is a GMO should depend on the fact if a novel combination of genetic material has been produced beyond the natural barriers of mating and recombination. The legal interpretations of biotechnology regulations by several other countries tend to exclude most or all genome-edited plants from GMO regulation. Looking over the edge of the European plate, regulatory triggers, the regulatory status of genome edited crops, and biotechnology oversight efforts in Argentina, Australia, Canada, China, Japan, and the USA will be discussed.

The assessment of safety can only realistically be made on a case-by-case basis and depends on features of the end product; genetically and phenotypically similar plants deriving from the use of different techniques are not expected to present significantly different risks. Plants modified by modern biotechniques should be excluded from specific regulations if their genetic changes are similar to or indistinguishable from those of conventionally bred plants and if no novel, product-based risk can be identified.



# OPTIMISING BRASSICA GENETICS TO MEET OUR GROWING CHALLENGES

Rachel Wells

*John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK*

During their lifecycle plants undergo several, environmentally sensitive developmental transitions which influence key yield traits such as flowering time, inflorescence architecture, fertility, seed number, seed size, germination and vigour. These transitions are controlled by an overlapping network of genes, many of which were originally identified in *Arabidopsis* for their role in the control of the floral transition. Targeting one transition may therefore have unintended consequences on others, causing difficulties when 'optimizing' for multiple traits during crop breeding. Bringing together UK plant scientists and representatives of the horticultural and oilseed Brassica industries, the BBSRC Brassica Rapeseed and Vegetable Optimization (BRAVO) project aims to understand the seasonal and environmental effects on developmental transitions in Brassica crops, and to use this information to improve reliability, yield and quality.

Trait optimization requires an integrated view of gene network function in different tissues across developmental time and knowledge of how these networks are affected by environmental cues. By generating a developmental transcriptome time series in both diploid and polyploid Brassicas with different life history strategies, BRAVO aims to discover where and when different genes are expressed. Constructing gene networks will identify key genes for each developmental transition. We will explore the potential sub-functionalisation of the multiple *Arabidopsis* gene homologues within Brassica, supporting trait optimization without 'trade-offs'. Exploiting the wealth of natural variation present within Brassica species, extensive detailed phenotyping (including the use of the National Plant Phenotyping Capability (NPPC) Lemnatec platform) will allow the association of genetic variation and gene expression with key traits. Determining relationships between genes, traits and the environment will aid targeted crop improvement to secure future yields.

## GENERATION OF A GENOME-WIDE VIRULENCE MAP OF *U. MAYDIS*

**Philipp Rink**<sup>a</sup>, **Uhse S.**<sup>b</sup>, **Djamei A.**<sup>a, b</sup>

<sup>a</sup>*Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Seeland, D-06466, Germany*

<sup>b</sup>*Gregor Mendel Institute of Molecular Plant Biology (GMI), Vienna, 1030, Austria*

Insertional mutagenesis screens are powerful tools to identify virulence genes of pathogens. Limiting for identification of mutants with reduced virulence by next-generation sequencing (NGS) is the underrepresented genetic material of the pathogen in comparison to host material. In a previous study of our laboratory, insertional Pool-Sequencing (iPool-Seq) was established, enabling the identification of genes involved in virulence of *Ustilago maydis* infecting maize. iPool-Seq utilizes NGS and unique molecular barcodes. In the next step we will use this method to identify virulence factors in a whole genome screen. To this end, a transposon mutagenesis will be performed and the generated *U. maydis* mutant library will be used to infect maize seedlings. For the identification of virulence reducing mutations, the iPool-Seq pipeline will be applied. The results of this screen will enable the generation of a virulence map of the *U. maydis* genome. Further, the generated mutant library and downstream processing can be used for different complex questions and deep phenotyping of the basidiomycetic model system *U. maydis*.

## **GMO: THE STATUS QUO**

**Nicholas Saik**

*Know IDEAS Media Inc.*

We are all familiar with biotechnology's role in our globalized food system, and the conflicts and turmoil that arise due to a seemingly unbridgeable gap between the suppliers of food, and the consumers of food. The question of biotechnology in food can be difficult to address, because an individual's relationship with food varies depending on region, culture, and a multitude of other factors. In other words, we're all looking at food from a different frame of reference.

GMO: The Status Quo will begin by addressing this perspective differential. We will not focus on biotechnology from a North American or European vantage point, as these perspectives are defined by a relative abundance of food, and a lack of involvement in the food supply chain. Abundance and apathy filter out the relative priority of these perspectives. We will frame this discussion by focusing on regions where innovations through biotechnology could have huge positive impacts on overall food security. We will put ourselves in the shoes of subsistence farmers in Kenya and Uganda, and contemplate various issues surrounding biotechnology from their frame of reference, such as the precautionary principle, multinational profit motivations, foreign NGO and activist pressure, export market anxiety, and crop protection product availability.

Lastly, we will expand our frame of reference slightly, and talk about our globalized food system's status quo. Why have we been unable to bring understanding to consumers? Why does the urban rural gap grow ever wider? Who profits from our food system remaining divided?

## **UNLOCKING BREAD WHEAT GENOME DIVERSITY WITH NEW SEQUENCING AND ASSEMBLY APPROACHES**

**Matt Clark**

*Life Sciences Algae, Fungi and Plants Division, Natural History Museum, London, SW7 5BD, United Kingdom*

Wheat, a plant species originating in the fertile crescent approximately 10,000 years ago is now the most widely grown crop across the world, spanning from Canada to Argentina in the Americas and from Portugal to China in Eurasia. This ability to thrive in such a variety of environments may be enabled by its genetic complexity – the largest and most complex of all major crop genomes. A complete wheat genome sequence would empower the breeding of improved wheat varieties and starts to reveal man's selection over thousands of years to the crop we now see. Yet to date wheat's large (~15Gbp) hexaploid and highly repetitive (>80%) genome had only been partially assembled and just to short sequences. The genome is now virtually complete, and furthermore we are now able to sequence and assemble multiple wheat genomes. Using comparative genomics combined with resequencing of modern cultivars, historical landraces in seed banks or even museum samples we can now gain key insights into wheat genetic variation overtime.

## MOONLIGHTING PROTEINS - A SYSTEMATIZATION

**Maria Krantz , Klipp E.**

*Theoretical Biophysics, Humboldt-Universität zu Berlin, Berlin, 10317, Germany*

Food Security will involve adapting plants to our needs, not only through selective breeding, but also through targeted changes in the genome. To be able to achieve this, we need to understand molecular mechanisms and the effect they have on the organisms, be it a unicellular algae or a complex, multicellular plant. One complicating phenomenon in the molecular organization of signaling and metabolism are moonlighting proteins. Moonlighting is a term used to describe proteins which perform two distinct tasks using the same domain of the protein. Several proteins performing moonlighting functions in the chloroplast of *Chlamydomonas reinhardtii* have been discovered.

Understanding their double functions and the effects they are having on metabolism and signaling in the chloroplast is important for our general understanding of the chloroplast behavior in response to signals from the nucleus. However, Moonlighting as a term is used to describe a variety of proteins and processes. Here, we propose a systematization of this concept. Based on a simple two pathway model we describe possible moonlighting cases and we simulate the effect these have on the output of these two pathways. The simulations show four different classes of possible behaviors of the pathways caused by the moonlighting protein.

# MODERN PLANT BREEDING FROM A COMPANY PERSPECTIVE

Eva Gietl

*KWS SAAT SE & Co KGaA, Einbeck, 37574, Germany*

KWS is a family-owned company that has been breeding plants successfully for more than 160 years. Today, KWS is active worldwide with its major crops sugarbeet, corn and cereals.

Plant breeding started more than 12,000 years ago, but was revolutionized when Mendel discovered the laws of inheritance in 1866. Since then, one breeding method after the other was developed until a veritable toolbox of plant breeding methods had emerged, including hybrid breeding, mutagenesis, tissue culture, genetic modification and marker technology among others. Lately, genome editing has added huge advantages to this toolbox by allowing for very precise changes to the DNA. Many of the changes cannot be distinguished from naturally occurring mutations or from mutations introduced by conventional breeding methods.

The European Court of Justice ruled in July 2018 that genome editing is not exempted from the genetic engineering regulation like conventional mutagenesis methods and needs to go through a costly and lengthy deregulation process. Because of the high costs and the acceptance problems of GMO, genome editing will not be available on the European market. Innovation will take place in other parts of the world. However, other countries, such as the United States, consider at least some applications of genome editing as equivalent to conventional breeding methods.

Sustainable agriculture has to meet a variety of challenges such as climate change, pre-harvest losses due to insect infestations and plant diseases, population growth and loss of arable land. Plant breeders support the farmers by supplying the plant varieties to meet these challenges. They strive to increase yield and resistance of the plants to a variety of stressors, to improve quality and to reduce the need for resources, such as water and fertilizers. To this end, they apply the complete toolbox of plant breeding methods.

# **TACKLING FOOD SECURITY FROM A TECHNOLOGY AND INNOVATION MANAGEMENT PERSPECTIVE – WHAT CAN WE LEARN FROM TECHNOLOGY, COMPANY AND INDIVIDUAL DATA?**

**Natalie Laibach**

*Institute for Food and Resource Economics, University of Bonn, Bonn, 53115, Germany*

As new technologies based on renewable raw materials and biological principles are becoming available, bioeconomic transformation could help to achieve the United Nations' Sustainable Development Goals (SDGs). SDG no. 2, Zero Hunger, is directly addressing food security and among those to which the bioeconomy can contribute to but also one that holds a high potential for conflicts about biomass and ecosystem trade-offs. To stay within the SDG triangle of ecologic, social and economic sustainability, emerging technologies in agriculture need not only to increase the harvest and value but have to meet nutritional and ecological criteria. Therefore, new technological development is needed in a very knowledge intensive field, cross-cutting many areas from plant biotechnology to app-based satellite solutions.

One of the major questions addressed by us is: which actors and technologies manage the path from science to market and why? To address these questions, we analyze the networks of science to technology using publication, patent and company data for instance in the field of genome editing or draw mechanisms of convergence between agriculture and digitalization. Investigating global diversity and needs concerning bio-based transformation, we found out that primary sector based economies are aware of their own problems, thus demanding a technological advance in agriculture to improve their social situation, while high tech economies are more focused on process optimization and economic profit. Moreover, we try to find out factors involved in the acceptance of technologies like GMOs, technology transfer issues and micro-foundations leading to the adoption of new, convergence of technologies.

Finally, we look into life cycle assessment and model data to prospect on the sustainability of new technologies, especially concerning land use change and greenhouse gas emissions. Looking from those different angles onto a complex challenge as food security we can raise awareness towards potential challenges involved in the technological realization and provide advice for companies and policy makers.

# CROP GENOME EDITING: OPPORTUNITIES AND CHALLENGES

**Wendy Harwood**

*John Innes Centre, Norwich, NR4 7UH, United Kingdom*

We face serious future challenges in providing the food required for a growing population, while coping with climate uncertainty and the need to farm in a sustainable way. Meeting these challenges is going to require a range of tools and approaches; genome editing technologies offer exciting opportunities and could make an important contribution.

CRISPR / Cas9 based genome editing is revolutionizing crop research and already providing the first commercial products. The beauty of this technology is its simplicity, requiring only two components, the Cas9 nuclease and the 'guide' RNA. CRISPR/Cas9 or RNA-guided Cas9 nuclease is, for the first time, providing a method for precise targeted mutagenesis leading to the 'knock-out' of target genes. Examples will be described in cereal and Brassica crops. Crops such as wheat with complex genomes present additional challenges, however, with careful design we have shown that it is possible to obtain the precise outcomes required. The CRISPR/Cas9 system can now be used for applications beyond the simple knock-out of single genes. The possibilities offered by gene targeting or 'knock-in' technologies are generating huge excitement but there are still technical challenges. Progress with gene targeting in barley will be described.

These new technologies still require methods for delivery of the genome editing components. Delivery is often via a genetic modification or transformation process followed by regeneration of plants containing the editing components. Plants with active editing can then be identified and, in the next generation, the editing components (transgenes) can be segregated away leaving a plant with a precise edit only. For many crops the transformation and regeneration processes are still a bottleneck to large scale application of genome editing technologies. Some approaches to overcome these limitations will be discussed. In addition, the regulation of plants produced using new genome editing techniques presents challenges, especially considering that these plants may be indistinguishable from plants containing natural mutations.



## NATURALLY OCCURRING FLOWER MUTATION IN OFFSPRING OF A LARGE FRUITED RASPBERRY CHANCE SEEDLING

**Dora Pinczinger, Hanke M-V., von Reth M., Flachowsky H.**

*Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Institute for Breeding Research on Fruit Crops, Dresden, 01326, Germany*

A raspberry population was established from an open pollinated, large fruited chance seedling. Three different floral phenotypes were identified in this population. Type 1 is a wild-type raspberry flower with five sepals and petals, with stamens and carpels present. Type 2 has six to eight sepals and petals, with stamens and carpels present. Type 3 has sepaloid and carpeloid structures, but lacks petals and stamens. Floral phenotype, fruit weight, length and drupelet number was evaluated for this population. Type 2 fruits are significantly larger and have more drupelets than the other types. In other Rosaceae, similar phenotypes are caused by mutation of the *PISTILLATA (PI)* gene, as *APETALA3* has several homologs and is thus more robust against impairment. We defined MADS- and K-box containing genes from *Rubus occidentalis* by Hidden Markov Model search. A neighbor joining tree was produced through amino acid sequence homology. Sequencing of PCR products of types 1 and 3 revealed two different nucleic acid sequences (*PI.1* and *PI.2*) present in both. RT-PCR using type 1 and type 3 whole flowers and individual whorls revealed substantial reduction of PI-levels in type 3. As there is no difference in *PI* itself on the genomic level between phenotypes, a mutation in a gene regulating *PI* like *LEAFY (LFY)* could be responsible for this difference. *LFY* specific primers revealed a size difference between genomic DNA samples, type 1 is about 2.500 bp, while type 3 about 6.000 bp long. Thus, the floral mutation could be caused by a disruption of the *LFY* gene by a transposon. *LFY* is currently being sequenced, with plans of complementation in *A. thaliana*. This project should lead to the development of molecular markers for fruit size, which might benefit current raspberry breeding programs.

# **THE HUMAN VARIABLE: HOW COMMUNICATION DETERMINES SCIENCE ADOPTION**

**Jessica Eise**

*Brian Lamb School of Communication, Purdue University, West Lafayette, IN 47907, United States*

Whether science will advance is not merely contingent upon research discoveries, but also the public's willingness to accept them. Critical food security decisions related to plant science, climate change and technological innovation, amongst others, are dependent upon society's perceptions of what is acceptable or unacceptable. Through policy, purchases and personal behaviors, the broader public wields vast power over scientific adoption; however the right social course of action is not predetermined. It is predicated upon an unceasing flow of information and messaging that shapes outlook and action. This powerful information flow – communication – informs how the public chooses to act and wield their power as consumers and members of a broader society. Ensuring that there is a reliable and trusted flow of information around the challenges we face to feed the world is, in fact, a challenge in itself.

In this talk, Jessica Eise discusses the practical obstacles researchers face when communicating around critical food security topics, including competing pressures, little training and a lack of incentive. She discusses how we can overcome this by working toward strategic, broader communication efforts built on alliances with diverse partners, shifting priorities and making a concerted effort to place sound, objective educational and actionable knowledge on critical food security issues, such as plant science, into our classrooms.

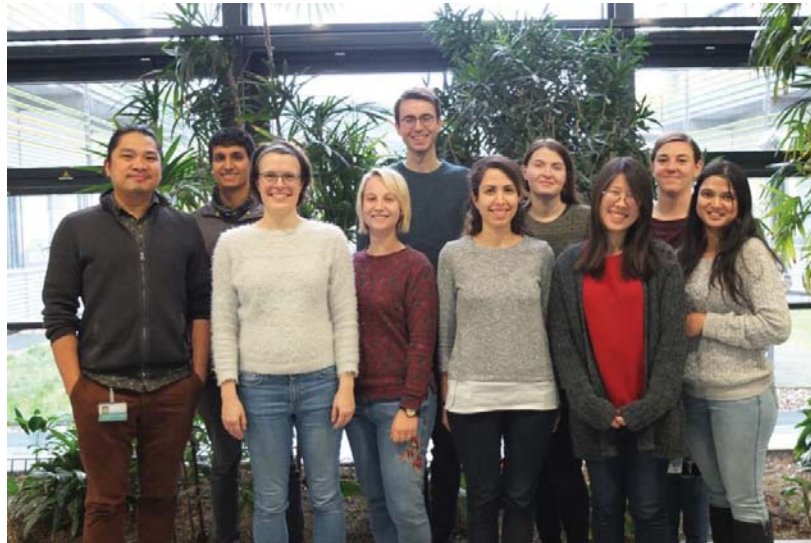
Eise concludes with a brief synthesis of best practices drawn from leading risk communication research for audience members interested in improving communication around their particular field.

We hope you enjoyed this year's P&P conference  
***(M)PIMP Future Foods –  
Challenges for Global Food Security***

Our next meeting will be in 2021.

We hope to see you then!

The 2019 organising team



Kora Vyse  
Liliana Calzadiaz Ramirez  
Maja Schuster  
Maryna Molochko  
Micha Wijesingha Ahchige  
Mitchell Rey Toleco  
Orarat Ginsawaeng  
Ritika Kulshreshtha  
Sara Omranian  
Stephanie Schaarschmidt  
Thomas Naake