Conference on New Breeding Techniques - regulate or not to regulate
New Breeding Techniques - regulate or not to regulate

Date:
26 - 27 September 2016

Venue:
Hungarian Academy of Sciences
1051 Budapest, Széchenyi István sqr. 9.

Large auditorium / Nagyterem

(Cover source: Feng Zhang, MIT)
New Breeding Techniques
–
regulate or not to regulate

Organised:
Ervin Balázs & Dénes Dudits

Aims of the conference
The new precision genome editing (PGE) techniques are currently widely discussed as key elements in the new breeding methods serving the agricultural innovation also in Europe. Unfortunately among the EU member states, there is no consensus on the use of GM technology in agricultural practices. In this hostile climate our scientific community is particularly concerned and feels an utmost importance in emphasizing the significance and the potentials of the PGE techniques and to engage the European agricultural policy for a supportive attitude towards this new innovation, which stance should be represented at the Council meetings as well in shaping the associated EU regulation.

Lecturers
Joachim Schiemann (Germany), Holger Puchta (Germany), Agnes Ricroch (France), Eva Stoger (Austria), Dénes Dudits (Hungary), László Hiripi (Hungary), Attila Molnár (Scotland), Tom Lawrenson (UK), Bhanu Telugu (USA), Kristin M Whitworth (USA).

Round table discussion
Moderated by Jeremy Sweet (UK). Panel members: Ivo Frebort (Czech Republic), Tomasz Twardoswski (Poland), Elena Rakosy-Tican (Romania), Borut Bohanec (Slovenia).
## Programme

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<td><strong>Kristin Whitworth M.</strong> (USA)&lt;br&gt;„Gene Editing with CRISPR/Cas9 to Develop PRRS Resistant Pigs“</td>
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ABSTRACTS
DOUBLE-STRAND BREAK-INDUCED GENOME ENGINEERING IN PLANTS

HOLGER PUCHTA

Botanical Institute, Karlsruhe Institute of Technology, Karlsruhe GERMANY
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Sequence-specific nucleases can be used to induce site-specific double-strand breaks (DSBs) in plant genomes. In the past we could show that thus gene targeting (GT) by homologous recombination (HR) can be enhanced and targeted mutagenesis can be achieved by error-prone non-homologous end joining (NHEJ). Moreover, by inducing several DSBs sequences can be deleted out of the genome and chromosome arms exchanged. In the last years the CRISPR/Cas system became the major tool for targeted mutagenesis in plants. We were able to demonstrate Streptococcus pyogenes (Spy)Cas9 nuclease induced, NHEJ mediated, heritable targeted mutagenesis in Arabidopsis thaliana as well as homology dependent in planta GT. A major concern for biotechnological applications is the specificity of the Cas9 nuclease. Off-target effects might be avoided using two adjacent sgRNA target sequences to guide a Cas9 protein that was transformed from a nuclease to a nickase to each of the two DNA strands, resulting in the formation of adjacent single strand breaks (SSBs). We could show that this Cas9 paired nickase strategy has a mutagenic potential at the target site comparable to that of the nuclease. Interestingly, sequence duplications are a prominent outcome of this approach, hinting to the possibility that in general the repair of adjacent SSBs is a major cause of sequence duplications during genome evolution of plants. Recently, we applied the Cas9 orthologues from Streptococcus thermophilus (Sth1Cas9) and Staphylococcus aureus (SauCas9) for error-prone non-homologous end-joining (NHEJ)-mediated targeted mutagenesis in A. thaliana. We obtained efficiencies at least comparable to those of SpyCas9. Stable inheritance of the induced targeted mutations was demonstrated for both nucleases at high frequencies. We were also able to show that the SauCas9 and SpyCas9 proteins only work in the presence of their species-specific single guide (sg) RNAs. These proteins are not prone to inter-species interference with heterologous sgRNA expression constructs. Thus, the Cas9 proteins of S. pyogenes and S. aureus should be appropriate for simultaneously addressing different sequence motifs with different enzyme activities in the same plant cell. The simultaneous use of different Cas9 orthologues will offer the opportunity to control genetic information of plant cells on more complex levels than before and will lay the basis for future synthetic approaches in plant biology.

Plant virus infections pose a ubiquitous threat to crop production by hampering the growth and fertility of plants and rendering certain crops un-marketable. In our recent research (Pyott et al., 2016) we used a new genome editing technology called CRISPR/Cas9 (often referred to as molecular scissors) to delete a plant gene (eIF), which is needed by certain viruses to complete their lifecycle. We showed that deletion of this gene results in complete resistance to Turnip Mosaic Virus (TuMV) without negative effects on plant growth. Furthermore, we were able to demonstrate that this engineered resistance is heritable and, importantly, does not require the presence of a transgene. Therefore, we believe that a similar approach will be pivotal for generating virus resistant crops in the near future. Other technologies to generate transgene-free designer plants will also be discussed.

**GENERATING GENE KNOCKOUTS IN CROPS USING CRISPR/CAS9**

**TOM LAWRENSON**

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We have used RNA-guided Cas9 with the aim of making indel based mutants in various crop species and have found it to work in all cases to date. We saw variability in terms of how efficiently a target gene is hit and this appears to be largely a function of the specific guide RNA used. In the best scenarios primary transgenics are largely knocked out in the first generation leading to T0 phenotypes and easy recovery of germ-line events in the T1 generation where T-DNA segregation
has occurred. Even where enrichment of indel events is required for their detection in T0, germline events have still been obtained by T2 after screening a greater number of progenies. Of the 50 or so guides we have data for currently, 30-40% of these work well, enabling indel detection in T0 without enrichment in 10-90% of plant lines created. Many of the remaining guides probably work to some extent but by discarding these and selecting the most active we can achieve transgene free edits more quickly and by handling less material.

Currently we are streamlining the process further, simplifying construct assembly, developing a rapid transient test for guide RNA validation, reducing off-target effects, simultaneously knocking out more than one gene target and screening using multiplexed systems”.

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**APPLYING CRISPR/CAS TO BARLEY: OUR EXPERIENCE WITH THE TECHNOLOGY, ITS ACCEPTANCE AND THE NATIONAL REGULATORY LANDSCAPE**

**ESZTER KAPUSI, JULIA HILSCHER AND EVA STOGER**

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The development of gene targeting and gene editing techniques based on programmable site-directed nucleases (SDNs) has increased the precision of genome modification and made the outcomes more predictable and controllable. These approaches have achieved rapid advances in plant biotechnology, particularly the development of improved crop varieties.

In addition, the advent of the widely used CRISPR-Cas9-derived system provides a straightforward reverse genetics approach for functional annotation in model and non-model organisms, and thus facilitates applied and translational research by making it much easier to introduce precise genetic modifications.

We are using the CRISPR-Cas9-derived system in the context of pharmaceutical protein production, attempting to add specific properties to individual plant production platforms. Cereal seeds for example are favourable for recombinant protein production as they are naturally adapted for protein accumulation and possess specialized storage organelles that may be exploited to accumulate recombinant proteins, offering stability both in planta and after harvest. However, post-translational modifications, such as glycan removal by endoglycosidases in barley endosperm have
to be prevented for specific products. We have therefore used the CRISPR-Cas9-derived system to introduce one or two double strand breaks to knock out endoglycosidase function.

Genome editing is certain to have an enormous impact on plant biotechnology worldwide, but its practical impact on the fate of high-performance commercial crops in the EU is entirely dependent on the pending decision concerning its regulatory status. The rapid technological development has caught the regulatory authorities off guard and the regulatory status of crop varieties developed with this technology needs to be clarified urgently. In Austria, we have just completed a study on genome editing in plants commissioned by the Federal Ministry of Health and Women’s Affairs. In the course of this study we also interacted with stakeholders, the general public and national regulatory authorities, and I will summarize our general impressions and experiences in a country with a traditionally strong opposition against GM plants.

GENOME EDITING AS AN ESSENTIAL TOOL TO MEET GLOBAL FOOD SECURITY CHALLENGES

KI-EUN PARK¹², CHI-HUN PARK¹², ANNE POWELL², DAVID M. DONOVAN¹², BHANU P. TELUGU¹²,*

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² Animal Bioscience and Biotechnology Laboratory, USDA, ARS, Beltsville, MD, USA

Bhanu.Telugu@ars.usda.gov;

The breeding of domestic animals has a longstanding and successful history, starting with domestication several thousand years ago. Modern animal breeding strategies predominantly based on population genetics, artificial insemination (AI) and embryo transfer (ET) technologies have led to significant increases in the performance of domestic animals, and are the basis for regular supply of high quality animal derived food at acceptable prices. However, the current strategy of marker-assisted selection and breeding of animals to introduce novel traits over multiple generations is too pedestrian in responding to unprecedented challenges such as changing climate, global pandemics, and feeding an anticipated 33% increase in global population in the next three decades. Here, we propose site-specific genome editing technologies as a basis for “directed” or “rational selection” of agricultural traits. These genome editing tools are expected to facilitate targeted modification of
individual traits without affecting the overall genetic merit of the animal thereby ushering the animal biotechnology into the functional genomics era. The animal science community envisions these technologies as essential tools in addressing critical priorities for global food security and environmental sustainability, and strives to develop these technologies for maximum societal benefit.

GENOME EDITING IN RABBITS: AGRICULTURAL AND MEDICAL ASPECTS

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hiripi@abc.hu

The development of genome editing methods like Zinc-Finger Nucleases (ZFN), Transcriptional Activator-Like Effector Nucleases (TALEN) and RNA-Guided Nucleases (CRISPR/Cas9) has completely changed the potential of transgenic technology via opening new perspectives in livestock genetic modifications in the last 5 years.

The first gene targeted rabbits were reported in 2011 in which the immunoglobulin M locus was targeted in an attempt to produce humanized antibodies. This experiment represents the future of innovative agriculture where livestock animals used to produce special added value. Genome editing technologies are capable to alter traditional agricultural products. More than 1.2 billion rabbits are used for meat globally every year. Myostatin is a highly conserved negative regulator of skeletal muscle mass in mammals. Introducing precise disruption of this gene in rabbits can be achieved and safely used to improve meat productivity. We have produced myostatin targeted rabbits with different genetic background to analyze the quality of rabbit meats in animals harboring the new mutation.

Traditionally rabbit is an important model for studying human diseases. Genome editing in rabbits will provide novel means not only for the elucidation of molecular mechanisms but also for translational research. Genome programs in mammals revealed that more than 1000 genes are shared between rabbits and humans where murine counterparts are missing. Some potential promising gene targeted rabbit models will be presented. Application of genome engineering of rabbits and farm animals will open a new era in animal models for human diseases.
GENE EDITING WITH CRISPR/CAS9 TO DEVELOP PRRS RESISTANT PIGS

KRISTIN M. WHITWORTH PHD, KEVIN D. WELLS PHD, ALAN J. MILEHAM PHD AND RANDALL S. PRATHER PHD
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Genetic selection and breeding programs have resulted in remarkable improvements in almost every aspect of swine production including increased litter size and feed efficiency as well as improved carcass quality. New technologies have recently been introduced that permit quick and efficient editing of the genome by utilizing meganucleases such as CRISPR/Cas9. Creating pigs with a simple DNA edit resulting in disease resistance to porcine reproductive and respiratory syndrome virus (PRRSV), African Swine Fever virus (ASFV) or other diseases could prevent significant economic and emotional losses throughout the world. One project initiated at the University of Missouri in collaboration with Kansas State University and Genus plc created pigs with biallelic edits to the cluster of differentiation 163 (CD163) gene. Two different methods were used to create the pigs: editing of fetal fibroblast cell line with CRISPR/Cas9 followed by somatic cell nuclear transfer (SCNT), and directly injecting CRISPR guide RNA with Cas9 mRNA into embryos at the zygote stage. Although both methods were effective, direct injection of zygotes resulted in biallelic CD163 edits in 100% of the piglets that were born. Zygote injection also avoids any of the negative nuclear reprogramming effects associated with SCNT. The offspring of the resulting pigs were challenged with both Type 1 and Type 2 PRRSV isolates and remained healthy with no clinical signs of infection even after repeated exposure to the virus from the sick wild type pen mates. The lung histopathology from the PRRSV infected CD163−/− pigs was normal when compared to wild type control pigs that had clear edema and infiltration of mononuclear cells. Further analysis showed no PRRSV nucleic acid present as measured by PCR or anti-PRRSV antibody present as measured by ELISA in the serum of the CD163−/− infected pigs. In vitro experiments with additional PRRSV isolates have further confirmed PRRSV resistance in pulmonary alveolar macrophages (PAMs) with the CD163−/− genotype. PRRS has proven to be a challenging disease across the world as effective vaccine development and genetic selection for resistance has not been achieved. CD163 has been confirmed to be the viral gatekeeper for the PRRSV by the use of gene editing by CRISPR/Cas9. Using such genomic edited pigs in production agriculture could substantially reduce PRRS related economic losses and prevent this devastating disease.
USE OF SYNTHETIC OLIBONUCLLEOTIDES FOR GENE SPECIFIC MUTAGENESIS IN SEVERAL GENOME EDITING STRATEGIES

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Mutation events contribute to the genetic variability in both natural habitats and breeding materials in a great extent. The natural mutation rate can be increased to one alteration in a thousand nucleotides by radiation or chemical treatment. This random mutagenesis became as an integrated tool in practical plant breeding and resulted in at least three thousand crop varieties. Development of different precision genome editing techniques including the oligonucleotide-directed mutagenesis (ODM) has opened a new dimension for mutation breeding by increasing specificity in alteration of gene structure and function. The oligonucleotide-targeted nucleotide exchange (OTNE) at a specific site of plant genomic DNA can be achieved by using chemically synthesized short DNA molecules. Methodologies of oligonucleotide (SDO) delivery into plant cells were based either on PEG-mediated uptake, on electroporation into protoplasts, or bombardment of SDO molecules co-precipitated onto gold particles into cultured cells or tissues. According to the widely accepted general model, after invading the targeted site of the duplex DNA, SDOs are hybridized to the complementary strand through transient D-loop formation. Finally, the mutation is introduced into the DNA by cellular repair or replication machinery. Despite of positive results in using ODM for the production of plant mutants with improved agronomic traits (see review by Sauer et al. 2016) the low frequency of OTNE can limit the wider application. We established a test system based on transgenic maize cell lines expressing the non-functional, Green Fluorescent Protein (mGFP) gene carrying a TAG stop codon. These transgenic cells were bombarded with corrective oligonucleotides to recover GFP expression. Sequencing PCR fragments of the GFP gene from corrected cells indicated a nucleotide exchange in the stop codon (TAG) from T to G nucleotide that resulted in the restoration of GFP function. Using this system we showed that maize cells with more relaxed chromatin after histone deacetylase inhibitor treatment could serve as an improved recipient for targeted nucleotide exchange as indicated by a 2.7-3.6-fold increase in GFP-positive cells (Tricz et al. manuscript). SDO molecules can also be used as repair templates in combination with RNA-guided Cas9 endonuclease (Svitashev et al. 2015). In addition, the phosphorylated SDOs (~24 nucleotides) can function as guide DNA for Argonaute endonucleases in creation of site-specific DNA double-strand breaks (Gao et al. 2016). All the presented examples show a central role for synthetic oligonucleotides in various genome editing techniques.

In light of the ongoing discussion in the EU whether new plant varieties generated by the new precision genome editing (PGE) techniques are genetically modified organisms (GMOs) or not, we propose a novel approach for regulating plant breeding in general. Our proposal involves a flexible and scalable risk assessment that is capable of adapting to the rapid evolution of new technologies. It proposes an operational method that accounts for traditional and novel technologies, which focuses on the phenotype of a novel breed instead of the method used to generate it.

Any new plant events would have to be authorized for use and marketing in the EU. Anyone seeking authorization proposes a risk classification based on the biology of the crop species and on the phenotype: herbicide-tolerant, pest-resistant, drought-resistant, salt-tolerance, nutritional fortification, etc. The new trait will be subjected to the appropriate risk assessment, which will determine the potential threats and known vulnerabilities for human and animal health, and for the environment. All modern plant breeding techniques, including marker-assisted selection, should enter the risk assessment from the same starting line.

Our proposal also takes into account that any new risk paradigm must be understood and accepted by the public, suggests a greater role for farmers in ensuring the safe use of new PGE techniques. Autonomous monitoring systems and digital diagnostic tools could help farmers to identify potential or present pests or herbicide-resistant weeds or invasive plants in such precision agriculture. Satellite or drone-based surveillance systems would help optimize pest and weed control, irrigation, and use of fertilizers. This closer cooperation between plant scientists, agricultural scientists, and farmers could improve crop management and increase yields in a
sustainable manner. Biotechnology including the PGE techniques as agricultural tools could inspire more cooperation between farmers and researchers to improve existing technologies and develop new ones.

HOW WILL GENOME EDITED PLANTS BE REGULATED? THE CALM BEFORE THE STORM?

JOACHIM SCHIEMANN

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Novel plant genome editing techniques call for an updated legislation regulating the use of plants produced by genetic engineering or genome editing, especially in the European Union. Established more than 25 years ago and based on a clear distinction between transgenic and conventionally bred plants, the current EU Directives fail to accommodate the new continuum between genetic engineering and conventional breeding. Despite the fact that the Directive 2001/18/EC contains both process- and product-related terms, it is commonly interpreted as a strictly process-based legislation. In view of several new emerging techniques which are closer to the conventional breeding than common genetic engineering, it should be actually interpreted more in relation to the resulting product. A legal guidance on how to define plants produced by exploring novel genome editing techniques in relation to the decade-old legislation is urgently needed, as private companies and public researchers are waiting impatiently with products and projects in the pipeline. In a recently published paper we outlined the process in the EU to develop a legislation that properly matches the scientific progress. As the process is facing several hurdles, we also compared it with existing frameworks in other countries and discussed ideas for an alternative regulatory system.

Already in October 2007 the European Commission established an expert group with the mandate to examine New Plant Breeding Techniques (NPBTs) in the context of the GMO legislation. The final report was provided in February 2012 and distributed amongst the Member States’ Competent Authorities but not formally published. In its report the expert group suggested to exclude the following techniques from GMO legislation: ODM; ZFN-1 and -2 (without recombinant DNA) [according to present knowledge all sequence-directed nucleases (SDN)]; Offspring and fruits from grafting with non-GM scion; Offspring of plants subjected to Agro-infiltration “sensu stricto”;

[1]
RdDM subjected plants without heritable change of their DNA (methylation alone is not a heritable genetic change); Offspring from reverse breeding [analogous generally null-segregants?].

In a letter to the Member States’ Competent Authorities dated June 2015 the European Commission stated the following: „Being aware that the current legal uncertainty is unsatisfactory, the Commission’ services are committed to present their legal analysis to the Competent Authorities and stakeholders before final adoption by the Commission foreseen before the end of this year.“ In contrast to this promise the European Commission failed to provide a legal interpretation of the NPBTs including genome editing until today. According to a letter of the European Seed Association (ESA) to the European Commission dated April 2016, the Commission (DG SANTE) informed that the publication of its guidance document regarding the regulatory status of NPBTs is delayed again and will not be finalised before « the end of the year ». In this letter ESA reiterates its former advice: “Where new breeding techniques lead to products that may also be obtained by classical breeding or that may even develop naturally by spontaneous mutations, and where their products do not contain any foreign DNA of sexually incompatible species, there is neither base nor need for a classification as a GMO.”

In a recently updated Statement on Crop genetic improvement technologies for a sustainable and productive agriculture addressing food and nutritional security, climate change and human health the European Plant Science Organisation (EPSO) is calling the European Commission for urgent actions 2:

“The European plant science community is following the current debate on the legislative classification of NPBTs along the lines of European GMO legislation with great interest and concern. Over the years, the EU regulatory framework for GMOs has become increasingly dysfunctional in the sense that:

- decisions are often not taken within the legal time frames, and often not on the basis of scientific evidence and risk assessment;
- information requirements and risk assessments have not been differentiated based on gained knowledge, but instead increased and galvanized without scientific justification;
- uncertainty is created about the applicability of the regulatory framework on organisms developed through new crop genetic improvement techniques such as genome editing.

EPSO has highlighted in an earlier statement that one of the causes of this situation is that in the implementation of the regulatory framework there is a disproportionate focus on the genetic improvement technique used. This has led to the following misinterpretations:

- GMOs are merely defined by the use of certain techniques. This is incorrect. Whether or not the resulting organism is a GMO depends entirely on the fact if a novel combination of genetic material has been produced beyond the natural barriers of mating and recombination. This is for example not the case for point mutations obtained by genome editing.

In the present debate on the GMO legislation an increasing number of competent authorities, risk assessment bodies, and stakeholders interpret the EU GMO legislation as both process-
product-based. EPSO acknowledges this interpretation and considers that this could help to clarify
the legal status of the NPBTs.”


2 http://www.epsoweb.org/file/2147
LECTURERS, PANEL MEMBERS
AND ORGANISER
Lecturers

**Dudits, Dénes**

Dénes Dudits, professor emeritus has basic training in agricultural sciences. His research career started with mutation research and later he was active in studying cereal tissue culture, somatic hybridization by plant protoplast fusion. His laboratory initiated the use of recombinant DNA techniques in plant research in Hungary. In basic science his research has been focused on understanding molecular control of somatic embryogenesis and regulation of cell division cycle. His laboratory discovered and characterized several genes and protein complexes in alfalfa and rice. In collaborative project his group published a technology for regeneration of maize plants from embryogenic protoplasts used also for production of transgenic maize plants. They developed and published several transgenic strategies to generate abiotic stress resistance by using novel genes and metabolic pathways. He coordinated nationwide projects to improve drought-tolerance of cereals for application in local wheat breeding programs. Recently he published the production of autotetraploid energy willow genotypes with improved CO$_2$ fixation capability. His present activities are concentrated on projects using synthetic oligonucleotides as mutagenic agents in plants.

He is member of the Hungarian Academy of Sciences, Academia Europea and the European Molecular Biology Organization. He was elected to be the vice president of the Hungarian Academy of Sciences, responsible for Life Sciences (2008-2014). He also served as director general of the Biological Research Centre H.A.S in Szeged.

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**Hiripi, László**

László Hiripi studied Biology at the University of Szeged, followed by a PhD (2002) in Animal Husbandry at the Szent Istvan University of Godollo, in Hungary. He received a Marie Curie Fellowship to pursue postdoctoral studies in the School of Biomedical Sciences at the University of Ulster in the UK from 2003. In 2005 he returned to the Agricultural Biotechnology Center in Godollo where he was involved in projects aimed to produce transgenic rabbit models for human diseases. In 2011 he became the head of the Ruminant Genome Biology Group. His main interest is to study bovine regulatory SNPs in transgenic mice. Since 2014 he is the head of the Department for Animal Biotechnology in the NARIC-Agricultural Research Institute.

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**Lawrenson, Tom**

Tom Lawrenson has worked at JIC for the last 15 years as a Research Assistant and most recently in the BRACT crop transformation group. Since moving to BRACT he has become interested in Genome Editing which BRACT are currently utilising and developing.
Molnár, Attila
Attila Molnar is a Chancellor’s Fellow at the University of Edinburgh. His group studies the synthesis and action of RNA silencing-associated small RNAs with particular emphasis on epigenetic modifications driven by endogenous and virus-derived small RNA molecules. The Molnar group also develops new genome editing tools and strategies for functional genomics.

Puchta, Holger
Prof. Dr. Holger Puchta is head of the Botanical Institute and holds the chair of plant molecular biology and biochemistry at the Karlsruhe Institute of Technology (KIT) in Germany. He studied biochemistry at the universities of Tübingen and Munich, and after his PhD at the Max-Planck-Institute for Biochemistry in Munich he joined as a postdoc the laboratory of Barbara Hohn at the Friedrich Miescher Institute in Basel, Switzerland to work on DNA recombination in plants. As a group leader he was from 1995 to 2002 at the Institute for Plant Genetics in Gatersleben (IPK) and habilitated in genetics at the university of Halle, Germany. He was worldwide the first scientist to show that by induction of double strand breaks by site specific nucleases different kinds of controlled changes in the plant genome can be achieved. His current research interest centres round the development of sophisticated tools for plant genome engineering and the characterization of the DNA repair and recombination machinery of plants.

Ricroch, Agnes
- Woman in Biotechnology Law and Regulation - 2015
- Laureate 2012 Special Prize of Academy of Agriculture of France
- Group leader ‘Durability-Innovation-Resources-Ethics’, University Paris-Sud, Paris-Saclay
- Associate Professor in Evolutionary Genetics and Plant Breeding, AgroParisTech
- Adjunct Professor at Pennsylvania State University, College of Agricultural Sciences, USA
- Fellow of the Academy of Agriculture of France and Deputy Secretary of Life Sciences Section of the Academy of Agriculture of France

Education
- MA in Plant Biology and Physiology – University of Pierre et Marie Curie, Paris, 1985
- PhD in Genetics and Plant Breeding – University of Paris Sud, Orsay, 1990
- HDR ‘Habilitation à diriger des recherches’ (Accreditation to Supervise Research) – University of Paris Sud, Orsay, 2003

Editor of 4 books on plant biotech


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**Schiemann, Joachim**

Prof. Dr. Joachim Schiemann has been director of the Institute for Biosafety in Plant Biotechnology at Julius Kuehn Institute (JKI), Federal Research Centre for Cultivated Plants, until his retirement in September 2016. Since 2006 he is Honorary Professor at University of Lüneburg. He has been coordinating several national and EU-funded cluster projects on biosafety research, recently the project GRACE (GMO Risk Assessment and Communication of Evidence; http://www.grace-fp7.eu). From 2000 to 2003 he was member of the Scientific Committee on Plants of the European Commission, Health & Consumer Protection Directorate-General, and from 2003 to 2009 member of the Panel on Genetically Modified Organisms of the European Food Safety Authority (EFSA). From 2002 to 2012 he was member of the Executive Committee of the International Society for Biosafety Research (ISBR), from 2004 to 2008 President of ISBR. Since 2004 he has been member of the Steering Council of the European Technology Platform “Plants for the Future”.

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**Stoger, Eva**

Eva Stoger is Professor of Molecular Plant Physiology and head of the Department of Applied Genetics and Cell Biology at the University of Natural Resources and Life Sciences in Vienna, Austria. She worked previously at the University of Florida (US), the John Innes Centre (UK), and at the Aachen Technical University (Germany). She received several awards including the Sofia-Kovalevskaja Prize awarded by the Alexander-von-Humboldt Foundation. Her main research interests are in the area of cereal biotechnology, endomembrane dynamics and the production of high-value recombinant proteins in seed crops.

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**Telugu, Bhanu**

Dr. Telugu holds a primary appointment with University of Maryland- College Park, where he is an Assistant Professor in the Department of Animal and Avian Sciences. He also holds a “Visiting Scientist” appointment with USDA, ARS, Beltsville. The laboratory has two research interests, Genetic engineering/Biotechnology and Reproductive Biology.

The laboratory employs genome editing tools such as CRISPRs and TALENS, and induced pluripotent stem cells (iPSC) for site specifically altering the genome in large animal model pig for biomedical and agricultural applications. Specifically, genome editing tools are employed to alter alleles to facilitate “rational selection” of agricultural traits. For biomedical applications, the laboratory is engaged in developing porcine models of human disease such as diabetes,
cardiovascular disease and obesity, where pig is a preferred animal model. For more detailed information, please contact the PI: btelugu@umd.edu

Whitworth M., Kristin
Kristin Whitworth is a research scientist at the University of Missouri. Kristin focused her PhD work on the transcriptional profiling in pig preimplantation embryos and extraembryonic membranes and using histone deacetylase inhibitors such as Scriptaid and SAHA to improve cloning efficiencies. Kristin is now heavily focusing her research efforts on using gene editing tools such as CRISPR/Cas9 to create disease resistant swine models.

Panel members
Bohanec, Borut
Dr. Borut Bohanec, (born 1954, Ljubljana Slovenia) is a professor of plant breeding and plant biotechnology, the Head of Agronomy Department (2006-2014) and Head of the Chair of genetics, biotechnology, statistics and plant breeding (since 1998) at the Biotechnical Faculty, University of Ljubljana. He is a lecturer of under and postgraduate courses in the fields of Genetics, Plant biotechnology and Plant breeding. He served as coordinator of postgraduate studies of biotechnology (2002-2008). He was a supervisor (or co-supervisor) of 12 PhD thesis, 6 Master thesis and 33 Bachelor thesis.

His predominant research interests are the development of biotechnological methods used in plant breeding and genetics. Topics included research on haploid induction (buckwheat, cabbage, onion, pumpkins, Mimulus), mutations and somaclonal variation (hop, olives), somatic embryogenesis (onion), interspecific hybridization (cucurbits, Sambucus species), genetic transformation (tobacco, onion, Mimulus, Hypericum, Lotus) and molecular phylogeny (alliums, clovers and others). Part of his studies is related to the use of flow cytometry as a method for ploidy determination, measurements of genome size and quantification of GFP expression. Currently he leads projects related to genome editing of horticultural plants. Dr. Bohanec is a co-author of 82 peer-reviewed publications, one patent, 10 book chapters, two professional books and one university textbook. He is a member of editorial board of four international journals Acta Biologica Cracoviensia Series Botanica (Krakow), Folia Horticulturae (Krakow), Archives of Biological Sciences (Belgrade), temporary editor of the Turkish Journal of Biology (Bolu) and referee of several scientific journals.

According to his expertise he is also actively involved in spreading knowledge to a broader public of experts and layman in the field. In this regard, he is the author of more than 60 newspaper articles, interviews and public debates on television and radio. He is also involved in activities related to public awareness of the consequences and benefits of genetically modified varieties and as such he was invited to give a speech at a TEDx Talk (GMO controversies - science vs. public fear: 24. 10. 2010). He also co-authored general public book titled “Yes to GMOs! For us and the environment” (2016).
Frebort, Ivo
Ivo Frébort is the founder and Executive Director of the Centre of the Region Haná for Biotechnological and Agricultural Research, Olomouc, Czech Republic. He graduated at the Palacký University Olomouc in Analytical Chemistry, received Ph.D. in Bioresources Science at Tottori University in Japan and did his postdoc at the University of Tübingen, Germany. Since 2005 he has been appointed full professor and since 2014 serves as a Dean of the Faculty of Science, Palacký University Olomouc. He published more than 100 scientific papers mainly in biochemistry research, enzymology and molecular biology and has been a principal investigator or co-investigator of more than 30 research projects. Some of his latest publications deal with biotechnological approaches, including cloning and preparation of GM barley with increased draught tolerance. He is also a member of the Executive Board of the European Federation of Biochemistry.

Rakosy-Tican, Elena
Prof. Elena Rakosy-Tican is specialized in the field of plant biotechnology starting from 1985, she developed research on plant somatic hybridization and genetic transformation. In the last years the main subject of her research was potato improvement by biotechnological tools. She introduced in this context the concept of combinatorial biotechnology. She published many papers and participated in many international conferences. Elena used to be an active member of Pannonian Plant Biotechnology Association. As a teacher she developed the first MSc course in Plant genetic engineering (1998) in Romania and introduced different new lectures and practicals in the field including a new one semester lecture and seminar on Bioethics.

Sweet, Jeremy
Jeremy Sweet has spent the last 27 years conducting research on the risk assessment of GMOs. Much of this work was conducted at NIAB Cambridge studying environmental and agronomic impacts, and gene flow to crops and wild relatives. He was coordinator of the UK BRIGHT project which studied herbicide tolerance, and he was also coordinator of the European Science Foundation programme “Assessing the Impact of GMOs” that brought together all the major research groups in this area in Europe. He was a coordinator of the EU SIGMEA project analysing data on gene flow and gene impacts and was a participant in the EU CO-EXTRA programme and the BBSRC Gene flow project led by Mike Wilkinson. He was work package leader in the GRACE EU project on Systematic Reviewing of the impacts of GM plants. He was an advisory Board member of the EU Pegasus project on GM animals, the EU Price Project on coexistence, the DEMETRA Life project, the EU COST Action on GM trees, the ESEGMO project in Finland and he served on the Steering Committee of the Swiss NFP59 programme on GMOs. He is a member of the EFSA GMO Panel, providing scientific opinions on the risks associated with GMO applications in the EU. He has served as chairman of the Environmental, Post Market Environmental Monitoring and GM Fish Working Groups of the EFSA GMO Panel. He was a member of the GM Insects
working group developing the EFSA Guidance Document. He was a member of the BBSRC/Phyconet Management Board and is currently participating in the ALGEBRA project on GM algae and in an EFSA study of RNAi GM plants. He is an author in over 50 scientific papers on GMOs and of 2 books.

He is director of JT Environmental Consultants Ltd which provides research and advice on GMOs to the European Commission, European governments, FAO/UNIDO/UNEP and scientific organisations and academies of several countries. He lectures on risk assessment of GMOs on postgraduate courses at the Universities of Marche (Ancona) and Ghent, and other training courses for FAO, UNEP, EC and other organisations.

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**Twardowski, Tomasz**

Prof. Tomasz Twardowski is chairman of Polish Biotechnology Committee of Polish Academy of Sciences and former head of the Polish Biotechnology Federation and former Editor-in-Chief of only Polish quarterly “Biotechnologia”. He is a researcher who has spent the last few years promoting the achievements of genetic engineering in Poland. In his opinion biotechnology is one of five modern technologies, next to telecommunications, nanotechnology, power engineering and new materials, that will determine the world's economic development in the next several decades. Professor Twardowski has been conducting research at the PAS Institute of Bioorganic Chemistry in Poznań since 1974.

His scientific and research interests are divided between molecular research of plant system and legal and social aspects of modern biotechnology. Predominately, Twardowski is concerned with the regulatory mechanisms of protein biosynthesis in eukaryotic systems, especially plants. The results of his latest research, carried out with a team of scientists from the Institute of Bioorganic Chemistry, concerned correlation of structure and function of small non-coding RNA. In the past he with the team discovered a relationship between the structure of certain fragments of ribosomal ribonucleic acids and their function in ribonucleic acid within protein biosynthesis. Twardowski also conducts research on the use of proteins that can bind large amounts of iron in the body. One such protein is ferritin. He was trying to find out how to use ferritin in treating anemia, and this procedure was patented.

Over the years, Twardowski has taken part in many science festivals, lectures and debates. He has been active in the Polish Biotechnology Federation, of which he is president in 2003-2009. He has been editor-in-chief of the scientific quarterly Biotechnologia since 1988 to 2010. In January 2008, he received the "Promoter of Science 2007" title in a competition held by the Polish Press Agency (PAP) and the Ministry of Science and Higher Education. This award was very important for him, especially since promoting science is largely unappreciated in Poland. Promoting science is still only a hobby of Professor Twardowski. In 2011 his activities have been honored by Polish Academy of Sciences Medal for scientific achievements.
Professor Tomasz Twardowski has represented Poland in the work of biotechnology teams set up by the United Nations Environment Program (UNEP) and the Organization for Economic Cooperation and Development (OECD). He is a member of ExBo of European Federation of Biotechnology [2010 – present] Poland’s Central Commission for Academic Titles and Degrees (1997 – present), vice-chairman of the Biotechnology Committee (1991-2009) and chairman of this Committee [2012 –present]. He has been a scientific consultant for institutions such as the State Committee for Scientific Research (KBN), the Ministry of the Environment, and the Ministry of Agriculture and Rural Development. He has won many awards and distinctions. For his contribution to Polish science, he received the Knight's Cross of the Polonia Restituta Order in 2001 and 2012.

Organiser

Balázs, Ervin

Ervin Balázs, general director at the Centre for Agricultural Research Martonvásár Hungary, a former founding general director of the Agricultural Biotechnology Center Gödöllő, lead a unit on molecular virology and genetic engineering of crops, which also includes a service facility for plant breeders to use all current molecular tools. He spent several years abroad, working at Cornell University, Plant Pathology Department, Ithaca N.Y.USA, thanBMC Strasbourg, France, and at the Friedrich Miescher Institute, Basel, Switzerland. He has been involved in exploring Cauliflower Mosaic Virus genome, including its promoters, and later he has developed a plant transformation vector based on 19S promoter of the virus. During the last two decades he has produced several transgenic virus resistant plants, such as tobacco, potato and pepper. He is an advocate of the introduction of the new technology into the daily agricultural practice and supports internationally harmonized regulation of the biotechnology. He published more than hundred scientific papers. Elected to be member of the Hungarian Academy of Sciences, and has been awarded with the Blaise Pascal International Research Chair (2001) and with the International Institute of Biotechnology (Royal Society of Arts, London) lecture award in 2005. He served as Panel chair of the Hungarian Higher Education Accreditation Committee between 2012-2016. He is the president of the Hungarian Unesco Committee for Natural Sciences.
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