Sunday Evening News

Week 24 (2018-06-11 / 06-17)

Selected and edited by ***BGF*** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,
Dear all,

this week, probably the most important news for science and breeders. The Court of Justice of the European Union has informed that they will deliver the preliminary ruling on the C-528/16 case on **25 July at 09:30**.

and corresponding articles from “Nature”

Bioentrepreneur
Will the EU deregulate gene-edited plants?
http://blogs.nature.com/tradesecrets/2018/06/14/will-the-eu-deregulate-gene-edited-plants

Purnhagen K.P., Kok E., Kleter G., Schebesta H., Visser R.G.F. & Justus Wesseler J. (2018): **The European Union Court’s Advocate General’s Opinion and new plant breeding techniques**
NATURE BIOTECHNOLOGY VOLUME 36, (interesting paper!)

Presseberichte – Media reports

AgWeb Editors: **GM Wheat Found in Canada**
https://www.agprofessional.com/article/gm-wheat-found-canada

Lauren Krugel, The Canadian Press: **Genetically modified wheat found in Alberta, Japan halts shipments**
https://www.ctvnews.ca/business/genetically-modified-wheat-found-in-alberta-japan-halts-shipments-1.3975393

University of Copenhagen: **Genetic engineering researcher: Politicians are deaf to people's ethical concerns**
https://eurekalert.org/pub_releases/2018-06/uoc-ger061418.php

gmwatch: **EU-funded rat feeding studies do not refute the Séralini study**
https://www.gmwatch.org/en/news/latest-news/18310

Merck: **Merck nimmt Vordenkerrolle bei ethischen Fragestellungen der Genomeditierung ein**
https://www.finanznachrichten.de/nachrichten-2018-06/44031566-merck-nimmt-vordenkerrolle-bei-ethischen-fragestellungen-der-genomeditierung-ein-007.htm

Merck Drives Thought Leadership in Ethical Gene Editing
http://www.bioethics.net/2018/05/ethical-considerations-in-the-man ufacture-sale-and-distribution-of-genome-editing-technologies/

Frag den Staat: **Anfrage an Bundesamt für Naturschutz:** Fachstelle Gentechnik und Umwelt
https://fragdenstaat.de/anfrage/fachstelle-gentechnik-und-umwelt/

Alexander Bogner: **Schlaue Maschinen und der tumbe Homo sapiens**
Von KI bis zu Killerrobotern: Die Vergötzung der Technik in unserer Gegenwart ist nur die Kehrseite ihrer Dämonisierung.
https://diepresse.com/home/meinung/gastkommentar/5447795/Gastkommentar_Schlaue-Maschinen-und-der-tumbe-Homo-sapiens

more press releases or media reports: https://www.biotech-gm-food.com/presse

Scientific Papers

Wu T-Y, Gruissem W, Bhullar NK. (2018): **Targeting intra-cellular transport combined with efficient uptake and storage significantly increases grain iron and zinc levels in rice**. Plant Biotechnology Journal, doi: 10.1111/pbi.12943

Rice, a staple food for more than half of the world population, is an important target for iron and zinc biofortification. Current strategies mainly focus on the expression of genes for efficient uptake, long-distance transport and storage. Targeting intracellular iron mobilization to increase grain iron levels has not been reported. Vacuole is an important cell compartment for iron storage and the NATURAL RESISTANCE ASSOCIATED MACROPHAGE PROTEIN (NRAMP) family of transporters export iron from vacuoles to cytosol when needed. We developed transgenic Nipponbare rice lines expressing *AtNRAMP3* under the control of the *UBIQUITIN* or rice embryo/aleurone-specific *18-kDa Oleosin (Ole18)* promoter together with *NICOTIANAMINE SYNTHASE* (*AtNAS1)* and *FERRITIN* (*PvFER*), or expressing only *AtNRAMP3* and *PvFER* together. Iron and zinc were increased close to recommended levels in polished grains of the transformed lines, with maximum levels when *AtNRAMP3*, *AtNAS1* and *PvFER* were expressed together (12.67 μg/g DW iron and 45.60 μg/g DW zinc in polished grains of line NFON16). Similar high iron and zinc levels were obtained in transgenic Indica IR64 lines expressing the *AtNRAMP3*, *AtNAS1* and *PvFER* cassette (13.65 μg/g DW iron and 48.18 μg/g DW zinc in polished grains of line IR64_1), equalling more than 90% of the recommended iron increase in rice endosperm. Our results demonstrate that targeting intracellular iron stores in combination with iron and zinc transport and endosperm storage is an effective strategy for iron biofortification. The increases achieved in polished IR64 grains are of dietary relevance for human health and a valuable nutrition trait for breeding programmes.
https://onlinelibrary.wiley.com/doi/epdf/10.1111/pbi.12943
and
Peter Rüegg, ETH Zurich
Transporting micronutrients more efficiently
https://phys.org/news/2018-06-micronutrients-efficiently.html#jCp

Shiimori M., Garrett S.C., Graveley B.R., Michael P. Terns M.P. (2018): **Cas4 Nucleases Define the PAM, Length, and Orientation of DNA Fragments Integrated at CRISPR Loci.** *Molecular Cell* 70(5), 814-824; DOI: 10.1016/j.molcel.2018.05.002

To achieve adaptive and heritable immunity against viruses and other mobile genetic elements, CRISPR-Cas systems must capture and store short DNA fragments (spacers) from these foreign elements into host genomic CRISPR arrays. This process is catalyzed by conserved Cas1/Cas2 integration complexes, but the specific roles of another highly conserved protein linked to spacer acquisition, the Cas4 nuclease, are just now emerging. Here, we show that two Cas4 nucleases (Cas4-1 and Cas4-2) play critical roles in CRISPR spacer acquisition in *Pyrococcus furiosus*. The nuclease activities of both Cas4 proteins are required to process protospacers to the correct size. Cas4-1 specifies the upstream PAM (protospacer adjacent motif), while Cas4-2 specifies the conserved downstream motif. Both Cas4 proteins ensure CRISPR spacer integration in a defined orientation leading to CRISPR immunity. Collectively, these findings provide *in vivo* evidence for critical roles of Cas4 nucleases in protospacer generation and functional spacer integration at CRISPR arrays.
https://www.cell.com/molecular-cell/fulltext/S1097-2765(18)30352-6?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS1097276518303526%3Fshowall%3Dtrue
and
University of Georgia
Researchers discover roles and teamwork of CRISPR-Cas proteins
https://phys.org/news/2018-06-roles-teamwork-crispr-cas-proteins.html#jCp

Wang J., Gu L., Douglas C. Knipple D.C. (2018): Evaluation of some potential target genes and methods for RNAi-mediated pest control of the corn earworm Helicoverpa zea. Pesticide Biochemistry and Physiology; https://doi.org/10.1016/j.pestbp.2018.05.012

In this study, we explored the efficacy of knockdown four genes required for proper nervous system function by RNAi, in the corn earworm Helicoverpa zea (Boddie). Three of these genes encode components of validated insecticide target sites. We synthesized cDNA sequences orthologous to the Drosophila melanogaster genes Para (paralyticts), TipE (temperature-induced paralysis locus E), GluCl (glutamate-gated chloride channel), and Notch, and used these fragments to synthesize double-stranded RNAs (dsRNAs). We then performed experiments in an attempt to induce RNAi-mediated effects on gene expression and viability using three modes of delivery of the dsRNAs: microinjection of eggs, soaking of eggs and feeding of larvae. Microinjection of dsRNAs into eggs induced reduced hatch rates and knockdown of target gene expression for GluCl, para and TipE, but not for Notch. However, neither feeding nor soaking eggs in dsRNA solutions resulted in discernable RNAi effects. These results demonstrated the susceptibility to RNAi effects of the expression of H. zea genes encoding insecticide target sites, which suggests future avenues of research toward practical applications.
https://www.sciencedirect.com/science/article/abs/pii/S0048357518300749

Santos-Vigil K.I., Ilhuicatzi-Alvarado D., García-Hernández A.L. Juan S.Herrera-García J.S., Moreno-Fierros L. (2018): Study of the allergenic potential of *Bacillus thuringiensis* Cry1Ac toxin following intra-gastric administration in a murine model of food-allergy. **International Immunopharmacology 61, 185-196**; https://doi.org/10.1016/j.intimp.2018.05.029

Cry1Ac toxin, from *Bacillus thuringiensis*, is widely used as a biopesticide and expressed in genetically modified (GM) plants used for human and animal consumption. Since Cry1Ac is also immunogenic and able to activate macrophages, it is crucial to thoroughly evaluate the immunological effects elicited after intra-gastric administration. The allergenic potential of purified Cry1Ac was assessed and compared with that induced in a murine model of food-allergy to ovalbumin (OVA), in which animals are sensitized with the adjuvant Cholera toxin (CT). Mice were weekly intragastrically administered with: i) vehicle phosphate-buffered saline (PBS), ii) OVA, iii) OVA plus CT iv) Cry1Ac or v) OVA plus Cry1Ac. Seven weeks after, mice were intragastrically challenged and allergic reactions along with diverse allergy related immunological parameters were evaluated at systemic and intestinal level. The groups immunized with, Cry1Ac, OVA/Cry1Ac or OVA/CT developed moderate allergic reactions, induced significant IgE response and increased frequencies of intestinal granulocytes, IgE+ eosinophils and IgE+ lymphocytes. These same groups also showed colonic lymphoid hyperplasia, notably in humans, this has been associated with food allergy and intestinal inflammation. Although the adjuvant and allergenic potential of CT were higher than the effects of Cry1Ac, the results show that applied intra-gastrically at 50 µg doses, Cry1Ac is immunogenic, moderately allergenic and able to provoke intestinal lymphoid hyperplasia. Moreover, Cry1Ac is also able to induce anaphylaxis, since when mice were intragastrically sensitized with increasing doses of Cry1Ac, with every dose tested, a significant drop in rectal temperature was recorded after intravenous challenge.
https://www.sciencedirect.com/science/article/pii/S1567576918302467

Lai Y.-S. et al. (2018): **Salicylic acid-independent role of NPR1 is required for protection from proteotoxic stress in the plant endoplasmic reticulum**, *Proceedings of the National Academy of Sciences* 115 (22) E5203-E5212). DOI: 10.1073/pnas.1802254115

The unfolded protein response (UPR) is an ancient signaling pathway designed to protect cells from the accumulation of unfolded and misfolded proteins in the endoplasmic reticulum (ER). Because misregulation of the UPR is potentially lethal, a stringent surveillance signaling system must be in place to modulate the UPR. The major signaling arms of the plant UPR have been discovered and rely on the transcriptional activity of the transcription factors bZIP60 and bZIP28 and on the kinase and ribonuclease activity of IRE1, which splices mRNA to activate bZIP60. Both bZIP28 and bZIP60 modulate UPR gene expression to overcome ER stress. In this study, we demonstrate at a genetic level that the transcriptional role of bZIP28 and bZIP60 in ER-stress responses is antagonized by nonexpressor of PR1 genes 1 (NPR1), a critical redox-regulated master regulator of salicylic acid (SA)-dependent responses to pathogens, independently of its role in SA defense. We also establish that the function of NPR1 in the UPR is concomitant with ER stress-induced reduction of the cytosol and translocation of NPR1 to the nucleus where it interacts with bZIP28 and bZIP60. Our results support a cellular role for NPR1 as well as a model for plant UPR regulation whereby SA-independent ER stress-induced redox activation of NPR1 suppresses the transcriptional role of bZIP28 and bZIP60 in the UPR.
http://www.pnas.org/content/115/22/E5203
and
Michigan State University
Study shows how a gene helps plants manage their protein production in stressful times
https://phys.org/news/2018-06-gene-protein-production-stressful.html#jCp

Crits-Christoph A. et al. (2018): **Novel soil bacteria possess diverse genes for secondary metabolite biosynthesis**, *Nature;*. DOI: 10.1038/s41586-018-0207-y

In soil ecosystems, microorganisms produce diverse secondary metabolites such as antibiotics, antifungals and siderophores that mediate communication, competition and interactions with other organisms and the environment[1,2]. Most known antibiotics are derived from a few culturable microbial taxa[3], and the biosynthetic potential of the vast majority of bacteria in soil has rarely been investigated[4]. Here we reconstruct hundreds of near-complete genomes from grassland soil metagenomes and identify microorganisms from previously understudied phyla that encode diverse polyketide and nonribosomal peptide biosynthetic gene clusters that are divergent from well-studied clusters. These biosynthetic loci are encoded by newly identified members of the Acidobacteria, Verrucomicobia and Gemmatimonadetes, and the candidate phylum Rokubacteria. Bacteria from these groups are highly abundant in soils[5,6,7], but have not previously been genomically linked to secondary metabolite production with confidence. In particular, large numbers of biosynthetic genes were characterized in newly identified members of the Acidobacteria, which is the most abundant bacterial phylum across soil biomes[5]. We identify two acidobacterial genomes from divergent lineages, each of which encodes an unusually large repertoire of biosynthetic genes with up to fifteen large polyketide and nonribosomal peptide biosynthetic loci per genome. To track gene expression of genes encoding polyketide synthases and nonribosomal peptide synthetases in the soil ecosystem that we studied, we sampled 120 time points in a microcosm manipulation experiment and, using metatranscriptomics, found that gene clusters were differentially co-expressed in response to environmental perturbations. Transcriptional co-expression networks

for specific organisms associated biosynthetic genes with two-component systems, transcriptional activation, putative antimicrobial resistance and iron regulation, linking metabolite biosynthesis to processes of environmental sensing and ecological competition. We conclude that the biosynthetic potential of abundant and phylogenetically diverse soil microorganisms has previously been underestimated. These organisms may represent a source of natural products that can address needs for new antibiotics and other pharmaceutical compounds.
https://www.nature.com/articles/s41586-018-0207-y
and
University of California - Berkeley
Genetic soil prospecting yields wealth of potential antibiotics
https://phys.org/news/2018-06-genetic-soil-prospecting-yields-wealth.html#jCp

Karasawa M. et al. (2018): **Whole-Cell Biotransformation of Benzene to Phenol Catalysed by Intracellular Cytochrome P450BM3 Activated by External Additives**, *Angewandte Chemie International Edition* (2018). https://doi.org/10.1002/anie.201804924
An Escherichia coli whole-cell biocatalyst for the direct hydroxylation of benzene to phenol has been developed. By adding amino acid derivatives as decoy molecules to culture medium, wild-type cytochrome P450BM3 (P450BM3) expressed in E.coli can be activated and non-native substrates hydroxylated, without supplementing NADPH. The yield of phenol reached 44% when N-heptyl-L-prolyl-L-phenylalanine (C7-Pro-Phe) was employed as the decoy molecule. It was shown that decoy molecules, especially those lacking fluorination, reached the cytosol of E. coli, thus imparting in vivo catalytic activities for oxyfunctionalisation of non-native substrates onto intracellular P450BM3.
https://onlinelibrary.wiley.com/doi/pdf/10.1002/anie.201804924
and
Nagoya University
Tricking bacteria into hydroxylating benzene
https://phys.org/news/2018-06-bacteria-hydroxylating-benzene.html#jCp

Rasmussen L.V. et al. (2018): **Social-ecological outcomes of agricultural intensification**. *Nature Sustainability* **1**, 275–282 (2018)
Land-use intensification in agrarian landscapes is seen as a key strategy to simultaneously feed humanity and use ecosystems sustainably, but the conditions that support positive social-ecological outcomes remain poorly documented. We address this knowledge gap by synthesizing research that analyses how agricultural intensification affects both ecosystem services and human well-being in low- and middle-income countries. Overall, we find that agricultural intensification is rarely found to lead to simultaneous positive ecosystem service and well-being outcomes. This is particularly the case when ecosystem services other than food provisioning are taken into consideration.
https://www.nature.com/articles/s41893-018-0070-8 pdf-file available

Brookes G. & Barfoot P. (2018): **New published research paper - Farm income and production impacts of using GM crop technology 1996–2016.** GM Crops & Food - Biotechnology in Agriculture and the Food Chain;
https://doi.org/10.1080/21645698.2018.1464866
This paper estimates the value of using genetically modified (GM) crop technology in agriculture at the farm level. It follows and updates earlier annual studies which examined impacts on yields, key variable costs of production, direct farm (gross) income and impacts on the production base of the four main crops of soybeans, corn, cotton and canola. The commercialisation of GM crops has occurred at a rapid rate since the mid 1990s, with important changes in both the overall level of adoption and impact occurring in 2016. This annual updated analysis shows that there continues to be very significant net economic benefits at the farm level amounting to $18.2 billion in 2016 and $186.1 billion for the period 1996–2016 (in nominal terms). These gains have been divided 48% to farmers in developed countries and 52% to farmers in developing countries. About 65% of the gains have derived from yield and production gains with the remaining 35% coming from cost savings. The technology has also made important contributions to increasing global production levels of the four main crops, having, for example, added 213 million tonnes and 405 million tonnes respectively, to the global production of soybeans and maize since the introduction of the technology in the mid 1990s.
https://www.tandfonline.com/doi/pdf/10.1080/21645698.2018.1464866?needAccess=true

Miller H.I. & Silva B. (2018): **The flower industry gets the genetic engineering blues**. GM Crops & Food Biotechnology in Agriculture and the Food Chain
https://doi.org/10.1080/21645698.2018.1471962
The genetic engineering of plants over the past two decades has led to significant scientific, commercial and humanitarian successes, with more than 2.1 billion hectares cultivated worldwide. The vast majority of cultivation has been huge-scale commodity crops – corn, cotton, canola, soybean, sugar beet and alfalfa - while specialty crops such as fruits, nuts, vegetables and ornamental plants have been underrepresented. The

commercialization of genetically engineered (GE) flowers has been especially neglected. Various laboratories worldwide are conducting research on various traits and flowers, the most intense interest focusing on carnation, rose, chrysanthemum and petunia, but the expense and uncertainty of government regulation is a hindrance. There are untapped economic opportunities in this sector, but for it to blossom, a regulatory climate that can spur development is critical. We need regulation that is scientifically defensible and risk-based.
https://www.tandfonline.com/doi/abs/10.1080/21645698.2018.1471962?journalCode=kgmc20
https://www.tandfonline.com/eprint/waDfSezRKKJRRXu9tBAK/full pdf-file available

Scheurer S. and Schülke S.(2018): **Interaction of non-specific Lipid-Transfer Proteins from foods with plant-derived lipids and its impact on allergic sensitization**. Front. Immunol. | doi: 10.3389/fimmu.2018.01389

On-specific lipid transfer proteins (nsLTPs) represent a family of ubiquitous plant proteins belonging to the prolamin superfamily. nsLTPs are characterized by a globular α-helical structure stabilized by four disulfide bonds and a hydrophobic cavity which acts as ligand-binding site for a broad spectrum of lipids and hydrophobic molecules. nsLTPs are involved in membrane biogenesis and in the adaption of plants to abiotic and biotic stress. They display anti-microbial activity by the ability to permeabilize the cell membrane of phytopathogens. Moreover, in the presence of lipids, nsLTPs are suggested to activate the plant immune system by a receptor-dependent mechanism.

Moreover, nsLTPs from pollen and plant-derived food, in particular type 1 nsLTPs (9 kDa), are described as potent allergens. Within the nsLTP family Pru p 3 from peach is the clinically most relevant allergen which can cause genuine food allergy and frequently elicits severe clinical reactions. So far, the allergenic properties of nsLTPs are attributed to both their low molecular mass and their high thermal and proteolytic stability which allow them to reach the immune system in a biological intact form. Recently, the interaction of nsLTPs with lipids has been suggested to increase their allergenic properties and to promote the allergic sensitization to these proteins.

This review will summarize the current knowledge on diversity of lipid ligands of plant LTPs, and illustrate recent studies performed with allergenic nsLTPs to investigate the effect of lipid binding on the structural modification and IgE-binding properties of proteins, and finally the potential effect on the innate immune responses
https://www.frontiersin.org/articles/10.3389/fimmu.2018.01389/abstract

Wie immer wird für Hinweise und der Zusendung von Publikationen und sonstigen Informationen gedankt. pdf-Dateien können meist direkt aus den links heruntergeladen werden.

Bitte besuchen sie auch die Webseite des Wissenschaftlerkreis Grüne Gentechnik e.V. (WGG): www.wgg-ev.de . Hier finden Sie weitere interessante Informationen.

*As always, I thank you all for hints and for publications. M*ost of the pdf files can be downloaded directly from the links.

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