

Sunday Evening News

Week 10 (2018-03-05 / 03-11)

Selected and edited by **BGF** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,
anbei meine selektive Auswahl an Presse- und Medienberichten sowie an wissenschaftlicher
Literatur. Wie immer alle Beiträge <https://www.biotech-gm-food.com/presse>

Dear all,

*Here a selection of press releases, media reports and scientific literature. As always, all
selected contributions are available: <https://www.biotech-gm-food.com/presse>*

London School of Economics and Political Science: **Ad hominem attacks on scientists are just as likely to undermine public faith in research as legitimate empirical critiques**
<http://blogs.lse.ac.uk/impactofsocialsciences/2018/03/06/ad-hominem-attacks-on-scientists-are-just-as-likely-to-undermine-public-faith-in-research-as-legitimate-empirical-critiques/>
and
<http://journals.plos.org/plosone/article/file?id=10.1371/journal.pone.0192025&type=printable>

O'Malley B.: **The question of trust in science requires many answers**
<http://www.universityworldnews.com/article.php?story=20180302092229937>

Ready for GMO 2.0?

<http://www.nutritionaloutlook.com/trends-business/ready-gmo-20>

Reinagel M.: **Meet GenED: The Next Generation of Biotechnology**
<https://foodandnutrition.org/from-the-magazine/meet-gened-next-generation-biotechnology/>
<https://geneticliteracyproject.org/2018/03/06/4-crispr-gene-edited-foods-coming-soon-grocery-store-near/>

Cerier S. - Genetic Literacy Project: **Viewpoint: Regulatory overreach looms as obstacle for New Breeding Techniques (NBTs) in agriculture**
<https://geneticliteracyproject.org/2018/03/05/viewpoint-regulatory-overreach-looms-obstacle-new-breeding-techniques-nbts-agriculture/>

Gabrielczyk T. (2018): **Bobek quells anti-GM peasant rebellion**. European Biotechnology Vol 17 Spring Edition 2018 pdf-file available

Oury J-P. (2018): **French scientists in revolt**
<https://www.europeanscientist.com/en/editors-corner/french-scientists-revolt/>

Kenny Walter K. - Digital Reporter: **Scientists Manipulate Crops to Need Less Water**
https://www.rdmag.com/article/2018/03/scientists-manipulate-crops-need-less-water?et_cid=6280690&et_rid=974038859&type=cta&et_cid=6280690&et_rid=974038859&linkid=content

Münkler H. – NZZ: **Wer nicht kämpfen will, hat schon verloren**
<https://www.nzz.ch/feuilleton/wer-nicht-kaempfen-will-hat-schon-verloren-ld.1363311>

Plant Breeding Innovation European Seed 5(1)
<http://www.european-seed.com/docs/books/volume-5/issue-1/?page=1>

Enorm-Magazin: **Genmais ist gut – oder?**
<https://enorm-magazin.de/genmais-ist-gut-oder>
bezieht sich auf die Studie vom BMBF 2015

Umweltinstitut München: **Gentechnik in der Zucht: Der Unwissenschaftliche Bericht**
<http://www.umweltinstitut.org/aktuelle-meldungen/meldungen/2018/gentechnik-in-der-zucht-der-unwissenschaftliche-bericht.html>

zu BVL-Bericht – Neue Züchtungsmethoden

Poland proposes a strategy to avoid GM soybean imports into Poland (valid also for non-GM soybeans produced outside EU). The TRIS database can be searched for the original document (see also attachment) with the term "2018/50"

<http://ec.europa.eu/growth/tools-databases/tris/en/index.cfm/search/?trisaction=search.detail&year=2018&num=50&mLang=EN>

Vosoughi S., Roy D., Sinan Aral S. (2018): **The spread of true and false news online**. *Science* 359, (6380), 1146-1151; DOI: 10.1126/science.aap9559

Lies spread faster than the truth

We investigated the differential diffusion of all of the verified true and false news stories distributed on Twitter from 2006 to 2017. The data comprise ~126,000 stories tweeted by ~3 million people more than 4.5 million times. We classified news as true or false using information from six independent fact-checking organizations that exhibited 95 to 98% agreement on the classifications. Falsehood diffused significantly farther, faster, deeper, and more broadly than the truth in all categories of information, and the effects were more pronounced for false political news than for false news about terrorism, natural disasters, science, urban legends, or financial information. We found that false news was more novel than true news, which suggests that people were more likely to share novel information. Whereas false stories inspired fear, disgust, and surprise in replies, true stories inspired anticipation, sadness, joy, and trust. Contrary to conventional wisdom, robots accelerated the spread of true and false news at the same rate, implying that false news spreads more than the truth because humans, not robots, are more likely to spread it.

<http://science.sciencemag.org/content/359/6380/1146.full>

Tagliabue G. (2018): **Comment on "Why are NGOs sceptical of genome editing?"** EMBO reports (2018) e45620

http://embor.embopress.org/content/early/2018/03/07/embr.201745620?utm_source=TrendMD&utm_medium=cpc&utm_campaign=EMBO_Rep_TrendMD_0 pdf-file available

Pearce W., Hartley S., Helliwell R. & O'Neill L. (2018): **Reply to Tagliabue**. EMBO reports (2018) e45954

<http://embor.embopress.org/content/early/2018/03/07/embr.201845954> pdf-file available

Shawn F. Dorius S.F., Carolyn J. Lawrence-Dill C.J. (2018): **Sowing the seeds of skepticism: Russian state news and the anti-GMO movement**.

Biotech news coverage in English-language Russian media fits the profile of the Russian information warfare strategy described in recent military reports. This raises the question of whether Russia views the dissemination of anti-GMO information as just one of many divisive issues it can exploit as part of its information war, or if GMOs serve more expansive disruptive purposes. Distinctive patterns in Russian news provide evidence that Russia is conducting a coordinated campaign to turn public opinion against genetically modified organisms. The recent branding of Russian agriculture as the ecologically clean alternative to genetically engineered foods is suggestive of an economic motive behind the information campaign against western biotechnologies.

<https://osf.io/preprints/socarxiv/26ubf/>

Lusk J.L., McFadden B.R. and Wilson N. (2018): **Do consumers care how a genetically engineered food was created or who created it?** *Food Policy* (2018),

<https://doi.org/10.1016/j.foodpol.2018.02.007>

This paper explores heterogeneity in consumer preferences for foods and policies that relate to different innovative plant breeding technologies. As a starting point in our analysis, we report results from almost four years of monthly surveys with U.S. consumers, which show slight food safety concern for genetically engineered food with no discernable trend of increased or decreased concern over time. We find small differences in consumer preferences for policies related to different plant breeding methods, with the strongest support for the notion that bioengineered crops should be regulated based on health and environmental outcomes rather than the process used to create new crops. Other survey results reveal support or opposition for genetically engineered food depends on consumers' perceptions of who created the technology. We also find that food safety concerns related to genetically engineered food are related to perceptions about the distribution of benefits from the technology across the food supply chain.

<https://www.sciencedirect.com/science/article/pii/S0306919218301106?via%3Dihub> pdf-file available

Wiedemann G., van Gessel N., Köchl F., Hunn L., Schulze K., Maloukh L., Nogué F., Decker E-L., Hartung F, Reski R. (2018): **RecQ helicases function in development, DNA-repair and gene targeting in *Physcomitrella patens***. *Plant Cell*. DOI: 10.1105/tpc.17.006372.

RecQ DNA helicases are genome surveillance proteins found in all kingdoms of life. They are characterized best in humans, as mutations in RecQ genes lead to developmental abnormalities and diseases. To better

understand RecQ-functions in plants we concentrated on *Arabidopsis thaliana* and *Physcomitrella patens*, the model species predominantly used for studies on DNA repair and gene targeting. Phylogenetic analysis of the six *P. patens* RecQ genes revealed their orthologs in humans and plants. Because *A. thaliana* and *P. patens* differ in their RecQ4 and RecQ6 genes, reporter and deletion moss mutants were generated and gene functions studied in reciprocal cross-species and cross-kingdom approaches. Both proteins can be found in meristematic moss tissues, although at low levels and with distinct expression patterns. PpRecQ4 is involved in embryogenesis and in subsequent development as demonstrated by sterility of PpRecQ4 mutants and by morphological aberrations. Additionally, PpRecQ4 displays an increased sensitivity to DNA damages and an increased rate of gene targeting. Therefore, we conclude that PpRecQ4 acts as a repressor of recombination. In contrast, PpRecQ6 is not obviously important for moss development or DNA repair but does function as a potent enhancer of gene targeting.

<http://www.plantcell.org/content/plantcell/early/2018/03/07/tpc.17.00632.full.pdf>

Devos Y., Ortiz-García S., Karen E. Hokanson K.E., Raybould A. (2018): **Teosinte and maize×teosinte hybrid plants in Europe—Environmental risk assessment and management implications for genetically modified maize.** *Agriculture, Ecosystems and Environment* 259 (2018) 19–27; <https://doi.org/10.1016/j.agee.2018.02.032>

The reporting of teosinte and maize×teosinte hybrid plants in maize fields in Spain and France has fuelled the continuing debate on the environmental risks and benefits of genetically modified (GM) crops in Europe. Concern has been expressed that GM maize may hybridise with teosinte or maize×teosinte hybrids, leading to the development of invasive weeds that pose unconsidered risks to the environment. In order to assess these risks, we hypothesised plausible pathways to harm from the cultivation and import of GM maize events MON810, Bt11, 1507 and GA21 for situations where GM maize plants and teosinte/maize×teosinte hybrids are sympatric. This enabled identification of events that must occur for harm to occur, and derivation of risk hypotheses about the likelihood and severity of these events. We tested these risk hypotheses using relevant available information. Overall, we conclude that the envisaged harmful effects to the environment arising from gene flow from GM maize to teosinte/maize×teosinte hybrids when cultivating or importing current commercial varieties of GM insect-resistant and herbicide-tolerant maize would be no greater than those from conventional maize: neither trait is likely to increase the abundance of teosinte or maize×teosinte progeny. Regardless of the likelihood of gene flow to teosinte or maize×teosinte hybrids, continuous cultivation of herbicide-tolerant maize, along with the repeated and exclusive application of the relevant herbicide, should be avoided in order to maintain the effectiveness of weed management. While scientific uncertainties about certain steps in the pathways remain, the risk assessment can be completed, using worst-case assumptions to handle these uncertainties.

<https://www.sciencedirect.com/science/article/pii/S0167880918301075> pdf-file available

van der Vlugt C.J.B., Brown D.D., Lehmann K., Leunda A., and Willemarck N. (2018): **A Framework for the Risk Assessment and Management of Gene Drive Technology in Contained Use.** *Applied Biosafety: Journal of ABSA International* 23(1) 25-31

The utilisation of the CRISPR/Cas9 technology has sparked a renewed interest in gene drive mechanisms. These mechanisms of biased inheritance may yield promising applications in the fields of vector control and nature conservation. However, the same properties that will enable these applications may also pose a risk if organisms that are equipped with gene drive cassettes are unintentionally released into the environment. Although several groups of scientists and regulators have started to address these safety concerns, there are currently no dedicated guidelines published on the required risk assessment and minimal control measures applicable to gene drive organisms in contained use. To fill this gap, this paper describes a fundamental approach to assessing the risks of these organisms while handled in a contained laboratory environment. Based on the likelihood that an adverse effect will arise from the handling of a gene drive organism and the severity of this effect, three risk classes for contained use activities are presented. Finally, specific minimum requirements regarding physical measures and working practices are proposed according to the presented risk classes and tailored to activities with rodents, insects, and fungi, which are most likely to be used for gene drive applications in the near future.

<http://journals.sagepub.com/doi/pdf/10.1177/1535676018755117>

Guan R-B., Li H.C., Fan Y-J, Hu S.R., Christiaens O., Smagghe G., Xue-Xia Miao X.X. (2018): **A nuclease specific to lepidopteran insects suppresses RNAi.** *JBC im Druck*

<http://www.jbc.org/cgi/doi/10.1074/jbc.RA117.001553>

More than 70% of all agricultural pests are insects in the order Lepidoptera, which, unlike other related insect orders, are not very sensitive to RNAi, limiting genetic studies of this insect group. However, the reason for this distinct lepidopteran characteristic is unknown. Previously, using transcriptome analysis of the Asian corn borer *Ostrinia furnacalis*, we identified a gene, termed *up56*, that is up-regulated in response to dsRNA. Here, we report that this Lepidoptera-specific gene encodes a nuclease that contributes to the RNAi insensitivity in this insect order. Its identity was experimentally validated, and sequence analysis indicated that *up56* encodes a previously uncharacterized protein with homologous sequences in seven other lepidopteran species. Its

computationally predicted three-dimensional structure revealed a high structural similarity to human exonuclease I. Exposure to dsRNA in *O. furnacalis* strongly up-regulated this gene's expression, and the protein could digest ss and ds RNA and DNA both *in vitro* and *in vivo*. Of note, we found that this up-regulation of *up56* expression is faster than that of the gene encoding the key RNAi-associated nuclease *Dicer*. *up56* knockdown in *O. furnacalis* significantly enhanced RNAi efficiency. Moreover, *up56* overexpression in *Drosophila melanogaster* suppressed RNAi efficiency. Finally, *up56* knockdown significantly increased the amount and diversity of small RNAs. Therefore, we renamed this protein RNAi efficiency-related nuclease (*REase*). In conclusion, we propose that *REase* may explain why lepidopterans are refractory to RNAi and represents a target for further research on RNAi efficiency in this insect order.

Hashemi A. (2018): **CRISPR–Cas System as a Genome Engineering Platform: Applications in Biomedicine and Biotechnology**. *Current Gene Therapy* 18, [10.2174/1566523218666180221110627](https://doi.org/10.2174/1566523218666180221110627)

Genome editing mediated by clustered regularly interspaced palindromic repeats (CRISPR) and its associated proteins (Cas) has recently been considered to be used as efficient, rapid and sitespecific tool in the modification of endogenous genes in biomedically important cell types and whole organisms. It has become a predictable and precise method of choice for genome engineering by specifying a 20-nt targeting sequence within its guide RNA. Firstly, this review aims to describe the biology of CRISPR system. Next, the applications of CRISPR–Cas9 in various ways, such as efficient generation of a wide variety of biomedically important cellular models as well as those of animals, modifying epigenomes, conducting genome-wide screens, gene therapy, labelling specific genomic loci in living cells, metabolic engineering of yeast and bacteria and endogenous gene expression regulation by an altered version of this system were reviewed.

<http://europepmc.org/abstract/med/29473500>

Kim J.-S. (2018): **Precision genome engineering through adenine and cytosine base editing**. *Nature Plants* 4,148–151; doi:10.1038/s41477-018-0115-z

Adenine base editors (ABEs), composed of an engineered deaminase and a catalytically impaired CRISPR–Cas9 variant, are powerful new tools for targeted base editing in cells and organisms. Together with cytosine base editors (CBEs), ABEs enable single-nucleotide conversions cleanly, efficiently and reversibly without double-stranded DNA cleavage, advancing genome editing in a new dimension.

<https://www.nature.com/articles/s41477-018-0115-z>

Kim S.-Il. et al, (2018):**Microhomology-assisted scarless genome editing in human iPSCs**. *Nature Communications* 9, Article number:939, DOI: [10.1038/s41467-018-03044-y](https://doi.org/10.1038/s41467-018-03044-y)

Gene-edited induced pluripotent stem cells (iPSCs) provide relevant isogenic human disease models in patient-specific or healthy genetic backgrounds. Towards this end, gene targeting using antibiotic selection along with engineered point mutations remains a reliable method to enrich edited cells. Nevertheless, integrated selection markers obstruct scarless transgene-free gene editing. Here, we present a method for scarless selection marker excision using engineered microhomology-mediated end joining (MMEJ). By overlapping the homology arms of standard donor vectors, short tandem microhomologies are generated flanking the selection marker. Unique CRISPR-Cas9 protospacer sequences nested between the selection marker and engineered microhomologies are cleaved after gene targeting, engaging MMEJ and scarless excision. Moreover, when point mutations are positioned unilaterally within engineered microhomologies, both mutant and normal isogenic clones are derived simultaneously. The utility and fidelity of our method is demonstrated in human iPSCs by editing the X-linked HPRT1 locus and biallelic modification of the autosomal APRT locus, eliciting disease-relevant metabolic phenotypes.

<https://www.nature.com/articles/s41467-018-03044-y.pdf>

and

Kyoto University

Gene editing method produces perfect pluripotent stem cell twins

<https://phys.org/news/2018-03-gene-method-pluripotent-stem-cell.html#iCp>

Cormac Sheridan C. (2018): **First off-the-shelf mesenchymal stem cell therapy nears European approval**. *Nature Biotechnology* 36 (3), 212-214

Boddu R.S., Divakar K. (2018) **Metagenomic Insights into Environmental Microbiome and Their Application in Food/Pharmaceutical Industry**. In: Patra J., Das G., Shin HS. (eds) *Microbial Biotechnology*. Springer, Singapore; DOI https://doi.org/10.1007/978-981-10-7140-9_2

To meet the increase in demand for food and health-related products, there was a promptly growing trend in the food and pharmaceutical manufacturing industries in recent years. Microbial process plays main role in the manufacturing of food products for enhancement of taste, aroma, shelf- life and other probiotic applications. Microbes and microbial enzymes were used for manufacturing of pharmaceutical ingredients/products through biocatalysis and biotransformation and also for degradation of toxic chemical compounds in pharmaceutical

industry waste. From a chosen environment, only small fraction of microbes can be cultured in the laboratory conditions, aforementioned industries critically depends on these cultivable microbial communities to make use of microbes and microbial metabolites/enzymes. The microbial metagenomics, a culture independent technique has become a revolutionary tool for biotechnological applications, especially in food and pharmaceutical industries, which takes an advantage of identification of all the possible genomic information from chosen microbiome and to apply them for needs of an industry. In the recent years, metagenomics has been adopted to screen antimicrobial resistant genes, enzymes used for biotransformation of pharmaceutical ingredients and degradation of toxic chemicals from pharmaceutical industry wastes. In this book chapter, we discuss application of metagenomics on probiotics, detection and resistance developed by pathogens present in natural/ packed foods. Also we discuss various metagenome derived enzymes (nitrilases, β -glucosidase, lipases and esterases) applied for chiral synthesis of pharmaceutical ingredients and degradation of recalcitrant chemical compounds (nitroaromatic, Cyanide) from pharmaceutical industry and an overview on predicting novel antimicrobial resistance genes from uncultivable microbiome.

https://link.springer.com/chapter/10.1007/978-981-10-7140-9_2

Burdock, G. A. and Wang, W. (2017): **Our unrequited love for natural ingredients**. Food and Chemical Toxicology 107, 37-46

<http://www.sciencedirect.com/science/article/pii/S0278691517303150>

and

<http://www.ask-force.org/web/Genomics/Burdock-Our-unrequited-love-for-natural-ingredients-2017.pdf>

Mikiashvili N and Yu J. (2018): **Changes in immunoreactivity of allergen-reduced peanuts due to post-enzyme treatment roasting**. Food Chemistry in press;

<https://doi.org/10.1016/j.foodchem.2018.02.119>

The objective of this study was to evaluate the effect of enzyme treatment and post-enzyme treatment roasting on allergenicity of raw peanut kernels. Raw peanuts were treated by single- and two-enzyme treatments, respectively. Enzyme-treated raw peanuts were dry roasted. Reductions of four major allergens (Ara h 1, 2, 3, and 6) and *in vitro* allergenicity of peanuts were evaluated. Quantitative measurements show that enzyme treatment of raw peanuts reduced Ara h 1, 2, 3 and 6 in raw peanuts by 99-100%, 95-99%, 35-46% and 85-88%, respectively. Roasting of enzyme-treated peanuts significantly reduced the total soluble protein ($P < 0.05$), Ara h 3 and 6 ($P < 0.0001$), slightly increased Ara h 1 in the extracts ($P < 0.05$), but did not significantly affect Ara h 2. Immunoblot shows that the IgE-bindings of both soluble and insoluble proteins of enzyme-treated peanuts were slightly enhanced by roasting but still tremendously lower than that of untreated peanuts.

<https://www.sciencedirect.com/science/article/pii/S0308814618303583>

Oostra V., Saastamoinen M., Zwaan B.J. & Wheat C.W. (2018): **Strong phenotypic plasticity limits potential for evolutionary responses to climate change**, Nature Communications [DOI: 10.1038/s41467-018-03384-9](https://doi.org/10.1038/s41467-018-03384-9)

[10.1038/s41467-018-03384-9](https://doi.org/10.1038/s41467-018-03384-9)

Phenotypic plasticity, the expression of multiple phenotypes from one genome, is a widespread adaptation to short-term environmental fluctuations, but whether it facilitates evolutionary adaptation to climate change remains contentious. Here, we investigate seasonal plasticity and adaptive potential in an Afrotropical butterfly expressing distinct phenotypes in dry and wet seasons. We assess the transcriptional architecture of plasticity in a full-factorial analysis of heritable and environmental effects across 72 individuals, and reveal pervasive gene expression differences between the seasonal phenotypes. Strikingly, intra-population genetic variation for plasticity is largely absent, consistent with specialisation to a particular environmental cue reliably predicting seasonal transitions. Under climate change, deteriorating accuracy of predictive cues will likely aggravate maladaptive phenotype-environment mismatches and increase selective pressures on reaction norms.

However, the observed paucity of genetic variation for plasticity limits evolutionary responses, potentially weakening prospects for population persistence. Thus, seasonally plastic species may be especially vulnerable to climate change.

<https://www.nature.com/articles/s41467-018-03384-9.pdf>

and

Wageningen University

Seasonally adaptable species may face greatest risk from climate change

<https://phys.org/news/2018-03-seasonally-species-greatest-climate.html#jCp>

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, especially to Klaus Ammann. Most of the pdf files can be downloaded directly from the links.

This file is saved at <https://www.biotech-gm-food.com/sunday-evening-news/> as well as at <https://www.wgg-ev.de/infos/wgg-nachrichten/>

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