

Sunday Evening News No. 88

Week 27 (2018-07-02 / 07-08)

Selected and edited by **BGF** Jany

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

and again, my selective selection of press releases, media reports, and publications. As always, you will find the daily up-to-date press reports and pictures here:

<https://www.biotech-gm-food.com/presse>

Press releases

EuGH- New breeding techniques – pressure on politicians:

BUND: Neue Gentechniken regulieren - Koalitionsvertrag umsetzen!

https://www.bund.net/fileadmin/user_upload_bund/publikationen/landwirtschaft/landwirtschaft_gentechnik_resolution_neue_gentechnik.pdf

Wahlfreiheit und Vorsorge sichern: 21 Verbände fordern mit Resolution die Regulierung und Kennzeichnung neuer Gentechniken

<https://www.bund.net/service/presse/pressemitteilungen/detail/news/wahlfreiheit-und-vorsorge-sichern-21-verbaende-fordern-mit-resolution-die-regulierung-und-kennzeichn/>

Arche Noah: **Neue Gentechnik-Verfahren – Neue Debatte?** Studien belegen die Risiken!

https://www.ots.at/presseaussendung/OTS_20180704_OTSO006/neue-gentechnik-verfahren-neue-debatte

Bioökonomie: **Genome Editing: Debatte vor EuGH-Entscheid**

<https://biooekonomie.de/nachrichten/genome-editing-debatte-vor-eugh-entscheid>

Kate Barlow: **Regulatory aspects of gene-edited crops: A Q&A with Jim Dunwell**

http://www.global-engage.com/agricultural-biotechnology/regulatory-aspects-of-gene-edited-crops-a-qa-with-jim-dunwell/?utm_content=73399338&utm_medium=social&utm_source=twitter

Again Seralini and the feeding study maybe also in respect to G.TWYST and GRACE

GMWATCH: Retraction by corruption

Corresponding to the Seralini-paper

<https://gmwatch.org/en/news/latest-news/18332>

please have a look on the paper of Novotny E (2018) below:

Cécile Thibert: **Lien entre OGM et cancer : l'étude était fausse**

<http://www.lefigaro.fr/sciences/2018/07/03/01008-20180703ARTFIG00322-une-grande-etude-europeenne-invalide-le-lien-entre-mais-ogm-et-cancer.php>

Gilles-Eric SERALINI

PRESS RELEASE: THE TOXICITIES OF ROUNDUP TOLERANT GMOs ARE DEMONSTRATED

<http://www.seralini.fr/wp-content/uploads/2018/06/Seralini-2018-press-release.pdf>

Nathan Rosenberg and Bryce Wilson Stucki

NEWS: CDC retracts finding that farmers have the highest suicide rate in the country

https://newfoodeconomy.org/update-cdc-retracts-finding-that-farmers-have-the-highest-suicide-rate-in-the-country/?utm_source=New+Food+Economy+Subscribers&utm_campaign=42e2b04fbe-EMAIL_CAMPAIGN_2018_06_28_08_15&utm_medium=email&utm_term=0_75a28a0eaf-42e2b04fbe-511579245

BfN: Naturbewusstseinsstudie **Deutsche sind für besseren Meeresschutz und gegen Gentechnik**

<https://www.berliner-zeitung.de/panorama/naturbewusstseinsstudie-deutsche-sind-fuer-besseren-meeresschutz-und-gegen-gentechnik-30918496#>

Die Naturbewusstseinsstudie 2017 sowie ein Informationspapier mit wesentlichen Aussagen der Studie steht zum Download unter: <https://www.bmu.de/PU496>

Kai Kupferschmidt: **Biologists raise alarm over changes to biopiracy rules.** *Science*. 361, Issue 6397, pp. 14 DOI: 10.1126/science.361.6397.14

<http://science.sciencemag.org/content/361/6397/14.full>

The Guardian: **Syrian seeds could save US wheat from climate menace**

<https://www.theguardian.com/world/2018/jul/06/syrian-seeds-could-save-us-wheat-from-climate-menace>

Scientific paper

Halford N.G. (2018): **Legislation governing genetically modified (GM) and genome edited crops in Europe: The need for change** J.Sci. Food and Agriculture.

<https://doi.org/10.1002/jsfa.9227>

The European Commission's assessment and approval process for genetically modified (GM) crops has resulted in only two GM crop varieties being licensed for cultivation in the European Union, one of which has been withdrawn. Unable to define GM crops satisfactorily, the European Commission has fallen back on a definition based on process. The shortcomings of this approach are all-too-clear as the Commission grapples with the advent of genome editing. This has led to a long and damaging delay in the Commission issuing an opinion on how genome edited crops should be regulated. At the same time, national bans imposed by Member States on GM crops without any evidence of safety concerns have been legalised. The Commission also faces the prospect of assessing an increasing number of GM and genome edited crops with deliberately altered composition. In this article, the operation of regulations covering GM crops in the European Union and the effect they have had on the development of plant biotechnology are reviewed, while the issues raised by new technologies are discussed. It is argued that there is an urgent need for the European Union to shift its position on plant biotechnology if agriculture is to meet the challenges of coming decades.

<https://onlinelibrary.wiley.com/doi/pdf/10.1002/jsfa.9227>

Frederiks C. and Wesseler J.H.H. (2018): **A comparison of the EU and US regulatory frameworks for the active substance registration of microbial biological control agents.**

Pest Management Science <https://doi.org/10.1002/ps.5133>

BACKGROUND: Microbial bio control agents (MBCA) are biopesticides based on living microbes. They provide a huge potential for the control of pests and diseases, but have trouble reaching the EU market. According to several authors, this is caused by the regulatory regime, which is less supportive compared to that of the US. The main objective of this paper is to present regulatory differences between the US and the EU and the resulting effects and developments of registration in both regions.

RESULTS: Results show that EU registration is more complex due to differences between EU and member state (MS) level processes, large actor heterogeneity and low flexibility. As a result, EU registration on average takes about 1.6 years more than US registration. Regulatory amendments improved EU level processes and led to a significant contraction of procedural timespans, but processes at MS level did not improve and have become a larger procedural obstacle.

CONCLUSION: Results correspond with the idea that EU registration is complex and lengthy compared to that of the US. In order to improve regulation, national level processes should be targeted for amendments. To that end, the authors suggest various ways of expanding registration capacity of MS.

<https://onlinelibrary.wiley.com/doi/pdf/10.1002/ps.5133>

Deplazes-Zemp A., Abiven S., Schaber P., Schaepman M., Schaepman-Strub G., Schmid B., Shimizu K.K. and Altermatt F. (2018): **The Nagoya Protocol could backfire on the Global South.** *Nature Ecology & Evolution* **2**, 917–919 (2018)

Regulations designed to prevent global inequalities in the use of genetic resources apply to both commercial and non-commercial research. Conflating the two may have unintended consequences for collaboration between the Global North and biodiverse countries in the Global South, which may promote global injustice rather than mitigate it.

<https://www.nature.com/articles/s41559-018-0561-z> pdf-file available

Suzuki T. et al. (2018): **Switchable genome editing via genetic code expansion.** *Scientific Reports* **8** (10051); DOI: [10.1038/s41598-018-28178-3](https://doi.org/10.1038/s41598-018-28178-3)

Multiple applications of genome editing by CRISPR-Cas9 necessitate stringent regulation and Cas9 variants have accordingly been generated whose activity responds to small ligands, temperature or light. However, these approaches are often impracticable, for example in clinical therapeutic genome editing *in situ* or gene drives in

which environmentally-compatible control is paramount. With this in mind, we have developed heritable Cas9-mediated mammalian genome editing that is acutely controlled by the cheap lysine derivative, Lys(Boc) (BOC). Genetic code expansion permitted non-physiological BOC incorporation such that Cas9 (Cas9^{BOC}) was expressed in a full-length, active form in cultured somatic cells only after BOC exposure. Stringently BOC-dependent, heritable editing of transgenic and native genomic loci occurred when Cas9^{BOC} was expressed at the onset of mouse embryonic development from cRNA or Cas9^{BOC} transgenic females. The tightly controlled Cas9 editing system reported here promises to have broad applications and is a first step towards purposed, spatiotemporal gene drive regulation over large geographical ranges.

<https://www.nature.com/articles/s41598-018-28178-3.pdf>

University of Bath

A novel switch to control genome editing

<https://phys.org/news/2018-07-genome.html#jCp>

Vogel P., Matin Moschref M., Qin Li Q., Tobias Merkle T., Karthika D. Selvasaravanan K.D., Li J.B. & Stafforst T. (2018): **Efficient and precise editing of endogenous transcripts with SNAP-tagged ADARs.** *Nature Methods* **15**, 535–538; DOI: [10.1038/s41592-018-0017-z](https://doi.org/10.1038/s41592-018-0017-z)

Molecular tools that target RNA at specific sites allow recoding of RNA information and processing. SNAP-tagged deaminases guided by a chemically stabilized guide RNA can edit targeted adenosine to inosine in several endogenous transcripts simultaneously, with high efficiency (up to 90%), high potency, sufficient editing duration, and high precision. We used adenosine deaminases acting on RNA (ADARs) fused to SNAP-tag for the efficient and concurrent editing of two disease-relevant signaling transcripts, *KRAS* and *STAT1*. We also demonstrate improved performance compared with that of the recently described Cas13b-ADAR.

<https://www.nature.com/articles/s41592-018-0017-z>

Universitaet Tübingen

Site-directed RNA editing as an alternative to genetic scissors

<https://phys.org/news/2018-07-site-directed-rna-alternative-genetic-scissors.html#jCp>

Čerevková A., Miklisová D., Szoboszlai M., Tebbe C.C., Cagáň L. (2018): **The responses of soil nematode communities to Bt maize cultivation at four field sites across Europe.** *Soil Biology and Biochemistry* **119**, 194–202; <https://doi.org/10.1016/j.soilbio.2018.01.023>

Transgenic maize expressing the *Bacillus thuringiensis* (Bt) insecticidal crystal (Cry1Ab) protein is poisonous to lepidopterans including the European Corn Borer (*Ostrinia nubilalis*). In many European countries, commercial cultivation of Bt maize is not allowed. One major reason is the potential variation of the environmental risk across different biogeographical regions. The aim of this study was to collect data about soil nematode communities as bioindicators of unintended effects across geographically diverse maize growing regions in Europe by sampling field sites in Denmark, Slovakia, and Sweden during 2013–2014, and in Spain during 2013. DKC3872YG (Bt maize line MON810) and its near-isogenic line DKC3871 were grown at the sites in Slovakia, Denmark, and Sweden and hybrids DKC6451YG (Bt maize line MON810) and its near-isogenic line DKC6450 were cultivated at the site in Spain. Dominating nematode genera in the maize fields regardless of the field site or maize variants were bacterial feeders *Rhabditis*, *Acroboloides*; root-fungal feeders *Filenchus*; fungal feeders *Aphelenchoides*, *Aphelenchus*; and omnivores *Eudorylaimus*. A significant effect of the field site location on the total nematode abundance, nematode abundance in trophic groups, diversity of nematode genera, and ecological and functional nematode indices was detected. Significant annual variation was found in the Plant parasite and Structure indices. There were significant differences in the abundances of omnivores and root-fungal feeders and in the Maturity, Channel, and Enrichment indices between Bt and non-Bt maize plots in Denmark in 2013, and in the abundance of fungal feeders in Sweden (2013). On the other hand, no difference was found between the Bt and non-Bt plots at the sites in Spain and Slovakia or at any of the sites in 2014. The effect of the field site location and season on the soil nematode community was more pronounced than that of the Bt genetic modification. We conclude that Bt maize had only a limited or no effect on soil nematode communities.

<https://www.sciencedirect.com/science/article/pii/S0038071718300233> pdf file available

Kumar M., Mohd Aslam Yusuf M.A., Nigam M., Manoj Kumar M. (2018): **An Update on Genetic Modification of Chickpea for Increased Yield and Stress Tolerance.** *Molecular Biotechnology*. <https://doi.org/10.1007/s12033-018-0096-1>

Chickpea is a highly nutritious grain legume crop, widely appreciated as a health food, especially in the Indian subcontinent. The major constraints on chickpea production are biotic (*Helicoverpa*, *bruchid*, *aphid*, *ascochyta*) and abiotic (drought, heat, salt, cold) stresses, which reduce the yield by up to 90%. Various strategies like conventional breeding, molecular breeding, and modern plant breeding have been used to overcome these problems. Conventionally, breeding programs aim at development of varieties that combine maximum number of traits through inter-specific hybridization, wide hybridization, and hybridization involving more than two

parents. Breeding is difficult in this crop because of its self-pollinating nature and limited genetic variation. Recent advances in in vitro culture and gene technologies offer unique opportunities to realize the full potential of chickpea production. However, as of date, no transgenic chickpea variety has been approved for cultivation in the world. In this review, we provide an update on the development of genetically modified chickpea plants, including those resistant to *Helicoverpa armigera*, *Callosobruchus maculatus*, *Aphis craccivora*, as well as to drought and salt stress. The genes utilized for development of resistance against pod borer, bruchid, aphid, drought, and salt tolerance, namely, Bt, alpha amylase inhibitor, ASAL, *P5CSF129A*, and *P5CS*, respectively, are discussed.

<https://link.springer.com/content/pdf/10.1007%2Fs12033-018-0096-1.pdf>

Xiang H. et al. (2018): **The evolutionary road from wild moth to domestic silkworm**, *Nature Ecology & Evolution*; DOI: [10.1038/s41559-018-0593-4](https://doi.org/10.1038/s41559-018-0593-4)

The Silk Road, which derives its name from the trade of silk produced by the domestic silkworm *Bombyx mori*, was an important episode in the development and interaction of human civilizations. However, the detailed history behind silkworm domestication remains ambiguous, and little is known about the underlying genetics with respect to important aspects of its domestication. Here, we reconstruct the domestication processes and identify selective sweeps by sequencing 137 representative silkworm strains. The results present an evolutionary scenario in which silkworms may have been initially domesticated in China as trimoulting lines, then subjected to independent spreads along the Silk Road that gave rise to the development of most local strains, and further improved for modern silk production in Japan and China, having descended from diverse ancestral sources. We find that genes with key roles in nitrogen and amino acid metabolism may have contributed to the promotion of silk production, and that circadian-related genes are generally selected for their adaptation. We additionally identify associations between several candidate genes and important breeding traits, thereby advancing the applicable value of our resources.

<https://www.nature.com/articles/s41559-018-0593-4>

and

Bob Yirka, Phys.org

Genetic study of silkworm helps unravel its long history of domestication

<https://phys.org/news/2018-07-genetic-silkworm-unravel-history-domestication.html#jCp>

Kooshapur H. et al. (2018): **Structural basis for terminal loop recognition and stimulation of pri-miRNA-18a processing by hnRNP A1**. *Nature Communications* 9 (2479); DOI: [10.1038/s41467-018-04871-9](https://doi.org/10.1038/s41467-018-04871-9)

Post-transcriptional mechanisms play a predominant role in the control of microRNA(miRNA) production. Recognition of the terminal loop of precursor miRNAs by RNA-binding proteins (RBPs) influences their processing; however, the mechanistic basis for how levels of individual or subsets of miRNAs are regulated is mostly unexplored. We previously showed that hnRNP A1, an RBP implicated in many aspects of RNA processing, acts as an auxiliary factor that promotes the Microprocessor-mediated processing of pri-mir-18a. Here, by using an integrative structural biology approach, we show that hnRNP A1 forms a 1:1 complex with pri-mir-18a where both RNA recognition motifs (RRMs) bind to cognate RNA sequence motifs in the terminal loop of pri-mir-18a. Terminal loop binding induces an allosteric destabilization of base-pairing in the pri-mir-18a stem that promotes its downstream processing. Our results highlight terminal loop RNA recognition by RBPs as a potential general principle of miRNA biogenesis and regulation.

<https://www.nature.com/articles/s41467-018-04871-9.pdf>

and

Helmholtz Association of German Research Centres

New insight into the maturation of miRNAs

<https://phys.org/news/2018-07-insight-maturation-mirnas.html#jCp>

Novotny E (2018): **Retraction by corruption: the 2012 Séralini paper**. *Journal of Biological Physics and Chemistry* 18 (2018) 32–56.

On 19 September 2012 a paper written by the group led by G.-E. Séralini was published online and then in print in the November 2012 issue of *Food and Chemical Toxicology*. The study reported in the paper examined the effects on the health of rats of a genetically engineered maize, Monsanto's NK603, and of the herbicide Roundup the maize is designed to tolerate. The paper elicited severe criticism from individual scientists and organizations, including some regulators and learned societies. Critical Letters to the Editor resulted in the retraction of the paper by the Editor-in-Chief of the journal, not on any scientific grounds but solely because the study was "inconclusive". Proponents of genetic engineering claim, wrongly, that there is now a consensus that genetically modified crops are safe to consume. To maintain that stance, it is necessary to destroy the credibility of any scientific evidence to the contrary and also the reputations of the researchers who obtained such evidence. In some cases even the institutions where the work was carried out and the journals publishing the results are attacked. Monsanto Company, in particular, has a huge financial stake in genetically modified crops and Roundup. Conflicts of interest of individuals, corporations and regulators have in the past triumphed over scientific evidence of harm. Private documents from the company, released by a law court in August 2017,

reveal covert manoeuvring by Monsanto to have the Séralini et al. paper retracted, in which the then Editor-in-Chief of the journal colluded. To this day the earlier, demonstrably flawed, research by Monsanto scientists finding NK603 to be “safe and nutritious” remains in print in the same journal. Meanwhile, the serious implications for public health have been disregarded by Monsanto, the critics and the regulators. Unfortunately, the “Séralini affair” is not unique

<http://www.seralini.fr/wp-content/uploads/2018/06/Novotny-JBPC-2018-On-Seralini-FCT-retraction.pdf>
(<http://www.seralini.fr/wp-content/uploads/2018/06/Novotny-JBPC-2018-On-Seralini-FCT-retraction.pdf>)

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. Most of the pdf files can be downloaded directly from the links.

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