

Sunday Evening News No. 95

Week 38 (2018-09-17 / 09-23)

Selected and edited by **BGF** Jany

Press releases:

Sarantis Michalopoulos: EFSA boss: **Our advice should not be misused for short-term political interests**

<https://www.euractiv.com/section/agriculture-food/interview/efsa-boss-our-advice-should-not-be-misused-for-short-term-political-interests/>

A difficult balance: Science, politics and policy-making on food

https://www.euractiv.com/section/agriculture-food/special_report/a-difficult-balance-science-politics-and-policy-making-on-food/

Éanna Kelly: **Scientists urge new EU rules on gene editing crops**

Restrictive regulations could be 'fatal' for Crispr-edited crop research in Europe, researchers warn. Meanwhile, there are hints the UK government could consider relaxing restrictions on gene edited crops post-Brexit

<https://sciencebusiness.net/news/scientists-urge-new-eu-rules-gene-editing-crops>

William F. Engdahl: **GMO-Lobby will EU-Gerichtsurteil zur Genmanipulation korrumpieren**

<https://www.contra-magazin.com/2018/09/gmo-lobby-will-eu-gerichtsurteil-zur-genmanipulation-korrumpieren/>

Anna Lederle: **Neues Gentechnikrecht für die Genschere?**

<https://www.europeanscientist.com/de/landwirtschaft/neues-gentechnikrecht-fuer-die-genschere/>

Ludger Wess: **Sondersteuer für die Biotech-Branche?**

Private Vereine wollen über die Zulassung von Gentechnikprodukten entscheiden. Die „vorsorgeorientierte Risikoprüfung“ aber sollen die Biotech-Unternehmen bezahlen.

<https://www.laborjournal.de/editorials/1593.lasso>

The Logical Indian Crew: **16 Yrs Since Bt Cotton Was Introduced For Commercial Cultivation – Was The Decision Correct?**

Bt Cotton was officially approved for commercial production in India in 2002. Since then, after 16 years, the share of Bt Cotton in the country's cotton growing area has risen to more than 90%. This has made India one of the largest countries using Bt cotton.

<https://thelogicalindian.com/awareness/bt-cotton-correct/>

Angela Logomasini: **U.S. Should Stop Funding the International Agency for Research on Cancer**

Misleading Classifications Promote Counterproductive Bans and Adverse Market Impacts

<https://cei.org/content/us-should-stop-funding-international-agency-research-cancer>

More press releases or media reports on: <https://www.biotech-gm-food.com/presse>

Publications:

Fritsche S., Poovaiah C., MacRae E. and Thorlby G. (2018): **A New Zealand Perspective on the Application and Regulation of Gene Editing.** Front. Plant Sci.,

<https://doi.org/10.3389/fpls.2018.01323>

New Zealand (NZ) is a small country with an export-led economy with above 90% of primary production exported. Plant-based primary commodities derived from the pastoral, horticultural and forestry sectors account for around half of the export earnings. Productivity is characterized by a history of innovation and the early adoption of advanced technologies. Gene editing has the potential to revolutionize breeding programmes, particularly in NZ. Here, perennials such as tree crops and forestry species are key components of the primary production value chain but are challenging for conventional breeding and only recently domesticated. Uncertainty over the global regulatory status of gene editing products is a barrier to invest in and apply editing techniques in plant breeding. NZ's major trading partners including Europe, Asia and Australia are currently evaluating the regulatory status of these technologies and have not made definitive decisions. NZ is one of the few countries where the regulatory status of gene editing has been clarified. In 2014, the NZ Environmental Protection Authority ruled that plants produced via gene editing methods, where no foreign DNA remained in the edited plant, would not be regulated as GMOs. However, following a challenge in the

High Court, this decision was overturned such that NZ currently controls all products of gene editing as GMOs. Here, we illustrate the potential benefits of integrating gene editing into plant breeding programmes using targets and traits with application in NZ. The regulatory process which led to gene editing's current GMO classification in NZ is described and the importance of globally harmonized regulations, particularly to small export-driven nations is discussed.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.01323/full>

Shao Q, Punt M and Wessler J (2018): **New Plant Breeding Techniques Under Food Security Pressure and Lobbying.** *Front. Plant Sci.* 9:1324; doi: 10.3389/fpls.2018.01324

Different countries have different regulations for the approval and cultivation of crops developed by using new plant breeding technologies (NPBTs) such as gene editing. In this paper, we investigate the relationship between global food security and the level of NPBT regulation assuming a World Nation Official (WNO) proposes advice on global NPBT food policies. We show that a stricter NPBT food regulation reduces food security as measured by food availability, access, and utilization. We also find that political rivalry among interest groups worsens the food security status, given the NPBT food technology is more productive and the regulatory policy is influenced by lobbying. When the WNO aims to improve food security and weighs the NPBT food lobby contribution more than the non-NPBT food lobby's in the lobbying game, the total lobbying contributions will be the same for the WNO, and the NPBT food lobby will be more successful in the political process. The NPBT food lobby, however, under food security loses its advantage in the political competition, and this may result in a strict NPBT food policy. Under food security problems implementing stricter NPBT food regulations results in welfare losses.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.01324/full>

Moldovan A. (2018): **On Appeals to Nature and their Use in the Public Controversy over Genetically Modified Organisms.** *Informal Logic*, 38 (3), 409–437;

<https://doi.org/10.22329/il.v38i3.5050>

In this paper I discuss appeals to nature, a particular kind of argument that has received little attention in argumentation theory. After a quick review of the existing literature, I focus on the use of such arguments in the public controversy over the acceptability of genetically-modified organisms in the food industry. Those who reject this biotechnology invoke its unnatural character. Such arguments have received attention in bioethics, where they have been analyzed by distinguishing different meanings that “nature” and “natural” might have. I argue that in many such appeals to nature the main deficiency of these arguments is semantic, in particular, that these words cannot be assigned a determinate meaning at all. In doing so, I rely on semantic externalism, a widely accepted theory of linguistic meaning.

https://informallogic.ca/index.php/informal_logic/article/view/5050

Vargas-Albores F., Martínez-Córdova L.R., Marcel Martínez-Porchas M., Kadiya Calderón K. & Asunción Lago-Lestón A. (2018): **Functional metagenomics: a tool to gain knowledge for agronomic and veterinary sciences.** *Biotechnology and Genetic Engineering Reviews*;

<https://doi.org/10.1080/02648725.2018.1513230>

The increased global demand for food production has motivated agroindustries to increase their own levels of production. Scientific efforts have contributed to improving these production systems, aiding to solve problems and establishing novel conceptual views and sustainable alternatives to cope with the increasing demand. Although microorganisms are key players in biological systems and may drive certain desired responses toward food production, little is known about the microbial communities that constitute the microbiomes associated with agricultural and veterinary activities. Understanding the diversity, structure and *in situ* interactions of microbes, together with how these interactions occur within microbial communities and with respect to their environments (including hosts), constitutes a major challenge with an enormous relevance for agriculture and biotechnology. The emergence of high-throughput sequencing technologies, together with novel and more accessible bioinformatics tools, has allowed researchers to learn more about the functional potential and functional activity of these microbial communities. These tools constitute a relevant approach for understanding the metabolic processes that can occur or are currently occurring in a given system and for implementing novel strategies focused on solving production problems or improving sustainability. Several ‘omics’ sciences and their applications in agriculture are discussed in this review, and the usage of functional metagenomics is proposed to achieve substantial advances for food agroindustries and veterinary sciences.

<https://www.tandfonline.com/doi/full/10.1080/02648725.2018.1513230>

Rezaeigolestani M, Hashemi M. (2018): **A Review of Pesticide Residues in Agricultural and Food Products of Iran.** *J Fasting Health* 6 (1): 1-6; Doi:10.22038/jfnh.2018.33593.1125

Pest control strategies are essential to reducing food waste and providing fresh, safe food products. However, the excessive and uncontrolled use of pesticides have caused severe environmental and health problems. The present study aimed to evaluate the level of pesticide residues in food products in Iran through reviewing the current literature.

A comprehensive literature review was conducted via searching in databases such as PubMed, Google Scholar, ScienceDirect, and SID to identify the abstracts and titles of the relevant papers using English and Persian keywords, including ‘pesticide residues’, ‘Iran’, and ‘food’ or their Persian equivalents.

Several studies have investigated the level of pesticide contamination in various food materials in Iran, the majority of which have been focused on the foods of vegetal origin (e.g., cucumbers, tomatoes, and melons).

Various pesticides, including organophosphorus, pyrethroids and organochlorines, were assessed in these studies, and organochlorines were the main tested pesticides in foods of animal origin. According to the review, illegal levels of pesticides are still detected in foods of vegetal and animal origin in some areas of the country.

Although pesticide residues in food materials are an important health issue, it seems that the national efforts to determine the level of these substances in foodstuffs are inadequate. Therefore, national food safety authorities and researchers must pay special attention to improving the current status of pesticide use in food products.

http://jnfh.mums.ac.ir/article_11331_c10efe91d8ff999dc55dda29c5890cf3.pdf

Cheng Zhang et al. (2018): **Structural Basis for the RNA-Guided Ribonuclease Activity of CRISPR-Cas13d.** *Cell* (2018). DOI: [10.1016/j.cell.2018.09.001](https://doi.org/10.1016/j.cell.2018.09.001)

CRISPR-Cas endonucleases directed against foreign nucleic acids mediate prokaryotic adaptive immunity and have been tailored for broad genetic engineering applications. Type VI-D CRISPR systems contain the smallest known family of single effector Cas enzymes, and their signature Cas13d ribonuclease employs guide RNAs to cleave matching target RNAs. To understand the molecular basis for Cas13d function and explain its compact molecular architecture, we resolved cryoelectron microscopy structures of Cas13d-guide RNA binary complex and Cas13d-guide-target RNA ternary complex to 3.4 and 3.3 Å resolution, respectively. Furthermore, a 6.5 Å reconstruction of apo Cas13d combined with hydrogen-deuterium exchange revealed conformational dynamics that have implications for RNA scanning. These structures, together with biochemical and cellular characterization, provide insights into its RNA-guided, RNA-targeting mechanism and delineate a blueprint for the rational design of improved transcriptome engineering technologies.

[https://www.cell.com/cell/fulltext/S0092-8674\(18\)31173-5?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867418311735%3FshowaIl%3Dtrue](https://www.cell.com/cell/fulltext/S0092-8674(18)31173-5?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867418311735%3FshowaIl%3Dtrue)

Salk Institute

Decoding the structure of an RNA-based CRISPR system

<https://phys.org/news/2018-09-decoding-rna-based-crispr.html#jCp>

Søren Lykke-Andersen, Britt Kidmose Ardal, Anne Kruse Hollensen, Christian Kroun Damgaard, Torben Heick Jensen. **Box C/D snoRNP Autoregulation by a cis-Acting snoRNA in the NOP56 Pre-mRNA.** *Molecular Cell*, 2018; DOI: [10.1016/j.molcel.2018.08.017](https://doi.org/10.1016/j.molcel.2018.08.017)

Box C/D snoRNAs constitute a class of abundant **noncoding RNAs** that associate with common core proteins to form catalytic snoRNPs. Most of these operate in *trans* to assist the maturation of rRNAs by guiding and catalyzing the 2'-O-methylation of specific **nucleotides**. Here, we report that the human intron-hosted box C/D snoRNA *snoRD86* acts in *cis* as a sensor and master switch controlling levels of the limiting snoRNP core protein NOP56, which is important for proper **ribosome biogenesis**. Our results support a model in which *snoRD86* adopts different RNP conformations that dictate the usage of nearby alternative splice donors in the *NOP56 pre-mRNA*. Excess snoRNP core proteins prevent further production of NOP56 and instead trigger the generation of a cytoplasmic *snoRD86*-containing *NOP56*-derived lncRNA via the **nonsense-mediated decay** pathway. Our findings reveal a feedback mechanism based on **RNA structure** that controls the precise coordination between box C/D snoRNP core proteins and global snoRNA levels.

<https://www.sciencedirect.com/science/article/pii/S1097276518306774?via%3Dihub>

Kaletsky R. et al. (2018): **Transcriptome analysis of adult *Caenorhabditis elegans* cells reveals tissue-specific gene and isoform expression.** *PLOS Genetics* (2018). DOI: [10.1371/journal.pgen.1007559](https://doi.org/10.1371/journal.pgen.1007559)

The biology and behavior of adults differ substantially from those of developing animals, and cell-specific information is critical for deciphering the biology of multicellular animals. Thus, adult tissue-specific transcriptomic data are critical for understanding molecular mechanisms that control their phenotypes. We used adult cell-specific isolation to identify the transcriptomes of *C. elegans*' four major tissues (or "tissue-ome"), identifying ubiquitously expressed and tissue-specific "enriched" genes. These data newly reveal the hypodermis' metabolic character, suggest potential worm-human tissue orthologies, and identify tissue-specific changes in the Insulin/IGF-1 signaling pathway. Tissue-specific alternative splicing analysis identified a large set of collagen isoforms. Finally, we developed a machine learning-based prediction tool for 76 sub-tissue cell types, which we used to predict cellular expression differences in IIS/FOXO signaling, stage-specific TGF-β activity, and basal vs. memory-induced CREB transcription. Together, these data provide a rich resource for understanding the biology governing multicellular adult animals.

<https://journals.plos.org/plosgenetics/article/file?id=10.1371/journal.pgen.1007559&type=printable>

Princeton University

In a tiny worm, a close-up view of where genes are working

<https://phys.org/news/2018-09-tiny-worm-close-up-view-genes.html#jCp>

Waage J. et al. (2018): **Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis.** *Nature Genetics* 50,1072–1080

Allergic rhinitis is the most common clinical presentation of allergy, affecting 400 million people worldwide, with increasing incidence in westernized countries^{1,2}. To elucidate the genetic architecture and understand the underlying disease mechanisms, we carried out a meta-analysis of allergic rhinitis in 59,762 cases and 152,358 controls of European ancestry and identified a total of 41 risk loci for allergic rhinitis, including 20 loci not previously associated with allergic rhinitis, which were confirmed in a replication phase of 60,720 cases and 618,527 controls. Functional annotation implicated genes involved in various immune pathways, and fine mapping of the HLA region suggested amino acid variants important for antigen binding. We further performed genome-wide association study (GWAS) analyses of allergic sensitization against inhalant allergens and nonallergic rhinitis, which suggested shared genetic mechanisms across rhinitis-related traits. Future studies of the identified loci and genes might identify novel targets for treatment and prevention of allergic rhinitis. <https://www.nature.com/articles/s41588-018-0157-1>

Binimelis R. and Wickson F. (2018): **The troubled relationship between GMOs and beekeeping: an exploration of socioeconomic impacts in Spain and Uruguay**. Journal Agroecology and Sustainable Food Systems <https://doi.org/10.1080/21683565.2018.1514678>

There has been a persistent conflict over agricultural biotechnology, and existing governance institutions relying on traditional processes of scientific risk assessment have failed to address the sociopolitical dimensions of this disagreement. Although there are demands to incorporate socioeconomic impact (SEI) assessment into regulatory deliberations, these often neglect to look beyond the technology in isolation to also include the networks of relations agricultural biotechnologies require and create. This paper argues that understanding the impacts of genetically modified organisms (GMOs) cultivation requires attentiveness to the operational context of the technology as well as a wide range of actors and potential pathways of harm. In order to do this and contribute new empirical research, this paper adopts a system-based perspective and focuses on socioeconomic impacts for a particular actor that is both critically important and highly vulnerable for sustainable agri-food systems: beekeepers. The paper explores the European Court of Justice ruling on the contamination of beehive products with GMOs. It then describes consequent legislative developments and the socioeconomic impacts observed in the wake of this in both Spain and Uruguay. The paper documents the distributive injustice being experienced by beekeepers and highlights the significance of assessing socioeconomic considerations from a systems-based understanding of agriculture and biotechnologies. <https://www.tandfonline.com/doi/abs/10.1080/21683565.2018.1514678?journalCode=wjsa21> pdf-file available

Odemer R. and Odemer F. (2018): **Honey bee workers reared in a neonicotinoid contaminated in-hive environment**. Biorxiv; doi: <https://doi.org/10.1101/420919>

With the currently updated risk assessment of three neonicotinoid pesticides, the European Food Safety Authority has confirmed that different applications of these substances represent a risk to wild and managed bees and their use was therefore severely restricted. However, to close further gaps in knowledge, this experiment covers exposure of honey bee worker brood reared in a neonicotinoid contaminated in-hive environment with focus on the individual. In a worst case scenario, mini-hives were fed chronically with a sublethal concentration of clothianidin (15 ug/kg), which is highly toxic to bees already in small amounts. Freshly hatched workers from these colonies were subsequently marked and introduced into non-contaminated colonies, where their lifespan and behavior was monitored. Nineteen days after exposure, clothianidin treated bees had no reduced lifespan or showed any signs of behavioral impairment when compared to the control, demonstrating that social buffering is not a simple substitution of dead bees by rearing more brood. Our results suggest that the social environment plays a crucial role for the individual in terms of superorganism resilience. These findings are discussed in context with the current use of lower tier test systems in risk assessment and contrary results obtained from laboratory experiments. <https://www.biorxiv.org/content/early/2018/09/18/420919>

Fitz E., Wanka F. and Seiboth B. (2018): **The promoter toolbox for recombinant gene expression in *Trichoderma reesei***. Front. Bioeng. Biotechnol. | doi: 10.3389/fbioe.2018.00135

The ascomycete *Trichoderma reesei* is one of the main fungal producers of cellulases and xylanases based on its high production capacity. Its enzymes are applied in food, feed, and textile industry or in lignocellulose hydrolysis in biofuel and biorefinery industry. Over the last years, the demand to expand the molecular toolbox for *T. reesei* to facilitate genetic engineering and improve the production of heterologous proteins grew. An important instrument to modify the expression of key genes are promoters to initiate and control their transcription. To date, the most commonly used promoter for *T. reesei* is the strong inducible promoter of the main cellobiohydrolase cel7a. Beside this one, there is a number of alternative inducible promoters derived from other cellulase- and xylanase encoding genes and a few constitutive promoters. With the advances in genomics and transcriptomics the identification of new constitutive and tunable promoters with different expression strength was simplified. In this review, we will discuss new developments in the field of promoters and compare their advantages and disadvantages. Synthetic expression systems constitute a new option to control gene expression and build up complex gene circuits. Therefore, we will address common structural features of promoters and describe options for promoter engineering and synthetic design of promoters. The availability of well-characterized gene expression control tools is essential for the analysis of gene function, detection of bottlenecks in gene networks and yield increase for biotechnology applications. <https://www.frontiersin.org/articles/10.3389/fbioe.2018.00135/abstract>

Kuchheuser P., Dünnebier K., Hoffbauer J., Butschke A., Birringer M. (2018): **Alert notifications concerning food contact material published in the Rapid Alert System for Food and Feed between 2012 and 2017.** J Consum Prot Food Saf. <https://doi.org/10.1007/s00003-018-1182-9>

Das Europäische Schnellwarnsystem für Lebensmittel und Futtermittel (RASFF) dient europäischen Mitgliedstaaten als Instrument für einen schnellen Informationsaustausch über Gesundheitsrisiken durch Lebensmittel, Futtermittel und Lebensmittelkontaktmaterialien. Eine differenzierte Auswertung der übermittelten Meldungen zu Lebensmittelkontaktmaterialien über einen längeren Zeitraum lag bislang nicht vor. Daher wurde eine Analyse der zwischen 2012 und 2017 veröffentlichten Warnmeldungen, mit Fokus auf Art und Material betroffener Lebensmittelkontaktmaterialien sowie zugrundeliegende Gesundheitsrisiken, durchgeführt. Die Auswertung konzentriert sich explizit auf Warnmeldungen, welche im Schnellwarnsystem ein rasches Tätigwerden zuständiger Kontaktstellen erforderten und vorrangig behandelt wurden. Als häufige Gesundheitsrisiken erwiesen sich der Übergang von Metallionen, die Migration von primären aromatischen Aminen sowie die Migration von Ausgangsstoffen der Kunststoffherstellung aus Kontaktmaterialien in Lebensmittelsimulanzien. Die entsprechenden Warnmeldungen wurden hinsichtlich Art und Material der betroffenen Lebensmittelkontaktmaterialien sowie auf ursächliche Substanzen untersucht. Ein Übergang von Blei und Cadmium ließ sich häufig bei Gläsern, Bechern, Tassen und Geschirr aus dekoriertem Glas oder glasierter Keramik feststellen. Eine Migration von primären aromatischen Aminen wurde insbesondere bei Erzeugnissen aus Kunststoff oder Nylon nachgewiesen. Betroffen waren meist Pfannenwender oder Servierlöffel. Auch das Humankanzerogen 4,4'-Methyldianilin befand sich unter den migrierenden Substanzen. Eine Migration von Ausgangsstoffen der Kunststoffherstellung wie Melamin und Formaldehyd ließ sich vermehrt bei Lebensmittelkontaktmaterialien aus Melaminharz identifizieren, insbesondere bei Geschirr. <https://link.springer.com/content/pdf/10.1007%2Fs00003-018-1182-9.pdf>

Wu H., Zheng J., Zhang G., Caihuan Huang C., Shiyi Ou S. (2018): **The Formation of Acrylamide from and Its Reduction by 3-Aminopropanamide Occur Simultaneously During Thermal Treatment.** Food Science: <https://doi.org/10.1111/1750-3841.14355>

3-Aminopropanamide (3-APA) is the direct precursor of acrylamide produced in the Maillard reaction between asparagine and reducing sugars. In this research, we found that 3-APA could reduce acrylamide by the formation of adducts between acrylamide and 3-APA *via* Michael addition. The effects of temperature, heating duration and 3-APA/acrylamide ratio on the reduction of acrylamide were investigated. Addition of 3-APA to acrylamide at a molar ratio of 5:3 at 160 °C for 20 min reduced acrylamide by up to 47.29%. The major adduct was identified as 3,3',3'-nitrilotris, and its cytotoxicity on Caco-2 cells was evaluated to be much lower than acrylamide. The viability of Caco-2 cells retained at 88.31% and 86.43% after incubation with 16 mM 3,3',3'-nitrilotris for 24 and 48 hr, respectively, while those incubated with the same concentration of acrylamide were 23.33% and 19.12%, respectively. <https://onlinelibrary.wiley.com/doi/pdf/10.1111/1750-3841.14355>

Konferenzen – Meetings:

Internationale Konferenz: **Genome Editing / CRISPR als Herausforderung für das Life Sciences-Recht**

11. und 12. Oktober 2018 Pro lure Auditorium, Universität Basel Juristische Fakultät Peter Merian-Weg 8 CH-4002 Basel

Registration: Per E-Mail: ZLSR-ius@unibas.ch

<https://ius.unibas.ch/de/aktuelles/events-details/news/genome-editing-crispr-als-herausforderung-fuer-das-life-sciences-recht/>

Konferenz "**Genome Editing under Gene Technology Law**" in Berlin am 6. November 2018 <https://www.jura.uni-bonn.de/aktuelles/veranstaltungen-und-termine/ansicht/news/konferenz-genome-editing-under-gene-technology-law-in-berlin-am-6-november-2018/>

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.

Nelkenstrasse 36
D-76351 Linkenheim-Hochstetten
jany@biotech-gm-food.com

Postfach 120721
D-60114 Frankfurt/Main
kd.jany@wgg-ev.de