

# Sunday Evening News No. 98

Week 41 (2018-10-08 / 10-14)

Selected and edited by **BGF** Jany

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Dear all,

This week there was nothing particularly exciting for the press. The CJEU-ruling is still present with comments.

## Press releases and media reports

### Ehrenhofer-Murray A.: **Chance verpasst; ein rückwärtsgewandtes Urteil des EuGH zu Genom-editierten Organismen.**

Das Urteil wird klare negative Auswirkungen auf Forschung und Entwicklung in Europa haben. Dabei wäre gerade hier eine zukunftsorientierte Perspektive wünschenswert.

BioSpektrum 24(6):573-573, DOI: 10.1007/s12268-018-0959-9

<http://link.springer-com-443.webvpn.jxutcm.edu.cn/content/pdf/10.1007%2Fs12268-018-0959-9.pdf>

### Hemberger J.: „Gravierende Nachteile im internationalen Vergleich“

<https://www.vdi-nachrichten.com/Gesellschaft/Gravierende-Nachteile-im-internationalen-Vergleich>

### Karberg S.: **Schere im Kopf**

Sind Eingriffe ins Erbgut mit neuen Gentechniken riskant? Mit der Beantwortung dieser Frage beauftragt der Staat ausgerechnet einen Anti-Gentechnik-Aktivistin.

<https://www.tagesspiegel.de/wissen/vom-interessenvertreter-zum-experten-schere-im-kopf/23161312.html>

### Alfons Deter A.: **Genome Editing: Bioökonomierat fordert neues EU-Gentechnikrecht**

<https://www.topagrar.com/news/Acker-Agrarwetter-Ackernews-Genome-Editing-Biooekonomierat-fordert-neues-EU-Gentechnikrecht-9945687.html>

### GM Watch: **ECJ ruling on "new GM" techniques: A victory, but vigilance needed**

<https://www.gmwatch.org/en/news/latest-news/18501>

### Fortuna G.: **Science and public opinion: Where do politicians stand?**

Policy makers, industry and civil society are trying to find a way to reconcile scientific evidence with public opinion's beliefs when it comes to food safety. However, this has proved time and again to be a difficult challenge.

<https://www.euractiv.com/section/agriculture-food/news/science-and-public-opinion-where-do-politicians-stand/>

### BMBF: **Mit vereinter Kraft für die Bioökonomie**

Bundesministerinnen Julia Klöckner und Anja Karliczek stärken die Bioökonomie-Politik der Bundesregierung

<https://www.bmbf.de/de/mit-vereinter-kraft-fuer-die-biooekonomie-5782.html>

### EU-Kommission: **Update of the 2012 Bioeconomy Strategy**

In 2017 the Commission carried out a review of its 2012 Bioeconomy Strategy. The review analysed the implementation of the strategy via its action plan, and examined the contribution of the bioeconomy to the EU circular economy objectives and to energy efficiency. In light of the findings of the review, the changed political context (SDGs, Paris Agreement) and the 2017 Communication on a renewed EU Industrial Policy Strategy, an update of the Bioeconomy Strategy and Action Plan is warranted.

[https://ec.europa.eu/info/law/better-regulation/initiatives/ares-2018-](https://ec.europa.eu/info/law/better-regulation/initiatives/ares-2018-975361?utm_source=POLITICO.EU&utm_campaign=658ea54183-EMAIL_CAMPAIGN_2018_10_10_06_28&utm_medium=email&utm_term=0_10959edeb5-658ea54183-189820221)

[975361?utm\\_source=POLITICO.EU&utm\\_campaign=658ea54183-](https://ec.europa.eu/info/law/better-regulation/initiatives/ares-2018-975361?utm_source=POLITICO.EU&utm_campaign=658ea54183-EMAIL_CAMPAIGN_2018_10_10_06_28&utm_medium=email&utm_term=0_10959edeb5-658ea54183-189820221)

[EMAIL\\_CAMPAIGN\\_2018\\_10\\_10\\_06\\_28&utm\\_medium=email&utm\\_term=0\\_10959edeb5-658ea54183-](https://ec.europa.eu/info/law/better-regulation/initiatives/ares-2018-975361?utm_source=POLITICO.EU&utm_campaign=658ea54183-EMAIL_CAMPAIGN_2018_10_10_06_28&utm_medium=email&utm_term=0_10959edeb5-658ea54183-189820221)

[189820221](https://ec.europa.eu/info/law/better-regulation/initiatives/ares-2018-975361?utm_source=POLITICO.EU&utm_campaign=658ea54183-EMAIL_CAMPAIGN_2018_10_10_06_28&utm_medium=email&utm_term=0_10959edeb5-658ea54183-189820221)

[http://ec.europa.eu/transparency/regdoc/rep/10102/2017/EN/SWD-2017-374-F1-EN-MAIN-PART-](http://ec.europa.eu/transparency/regdoc/rep/10102/2017/EN/SWD-2017-374-F1-EN-MAIN-PART-1.PDF?utm_source=POLITICO.EU&utm_campaign=658ea54183-EMAIL_CAMPAIGN_2018_10_10_06_28&utm_medium=email&utm_term=0_10959edeb5-658ea54183-189820221)

[1.PDF?utm\\_source=POLITICO.EU&utm\\_campaign=658ea54183-](http://ec.europa.eu/transparency/regdoc/rep/10102/2017/EN/SWD-2017-374-F1-EN-MAIN-PART-1.PDF?utm_source=POLITICO.EU&utm_campaign=658ea54183-EMAIL_CAMPAIGN_2018_10_10_06_28&utm_medium=email&utm_term=0_10959edeb5-658ea54183-189820221)

[EMAIL\\_CAMPAIGN\\_2018\\_10\\_10\\_06\\_28&utm\\_medium=email&utm\\_term=0\\_10959edeb5-658ea54183-](http://ec.europa.eu/transparency/regdoc/rep/10102/2017/EN/SWD-2017-374-F1-EN-MAIN-PART-1.PDF?utm_source=POLITICO.EU&utm_campaign=658ea54183-EMAIL_CAMPAIGN_2018_10_10_06_28&utm_medium=email&utm_term=0_10959edeb5-658ea54183-189820221)

[189820221](http://ec.europa.eu/transparency/regdoc/rep/10102/2017/EN/SWD-2017-374-F1-EN-MAIN-PART-1.PDF?utm_source=POLITICO.EU&utm_campaign=658ea54183-EMAIL_CAMPAIGN_2018_10_10_06_28&utm_medium=email&utm_term=0_10959edeb5-658ea54183-189820221)

<https://ec.europa.eu/research/bioeconomy/index.cfm?pg=policy&lib=strategy>

### Mancosu A.: **UK should diverge from EU rules on GMOs and NBTs after Brexit – study**

ECJ ruling on NBTs will drive research away from Europe

<https://iegpolicy.agribusinessintelligence.informa.com/PL217978/UK-should-diverge-from-EU-rules-on-GMOs-and-NBTs-after-Brexit--study>

**Graham Brookes: UK urged to 'bring back' sound science as the basis for regulating crop genetic innovations post-Brexit**

<https://pgeconomics.co.uk/press-releases/22/UK+urged+to+%E2%80%98bring+back%E2%80%99+sound+science+as+the+basis+for+regulating+crop+genetic+innovations+post-Brexit>

and the report:

<https://pgeconomics.co.uk/pdf/abc%20brexit%20report%20final.pdf>

**Retraction Watch: Spud dud, as agricultural industry potato paper gets pulled a decade after publication**

*Plant Physiology*, the official journal of the American Society of Plant Biologists, has retracted a 2004 article by a team of ag industry researchers, including a former husband-wife duo, for what could be misconduct by the husband.

<https://retractionwatch.com/2013/04/12/spud-dud-as-agricultural-industry-potato-paper-gets-pulled-a-decade-after-publication/>

**Rommens C.: Hidden Health Dangers: A Former Agbiotech Insider Wants His GMO Crops Pulled**

<https://www.independentsciencenews.org/health/hidden-health-dangers-former-agbiotech-insider-gmo-crops/>

**Sustainable Pulse: The Creator of GMO Potatoes Reveals The Dangerous Truth – Exclusive Interview**

[https://sustainablepulse.com/2018/10/09/the-creator-of-gmo-potatoes-reveals-the-dangerous-truth-exclusive-interview/#.W8HxX\\_ZCSUn](https://sustainablepulse.com/2018/10/09/the-creator-of-gmo-potatoes-reveals-the-dangerous-truth-exclusive-interview/#.W8HxX_ZCSUn)

**Proplanta: Wird das Glyphosat-Urteil gegen Monsanto gekippt?**

San Francisco- Wichtiger Teilerfolg für die Bayer AG: Im ersten US-Prozess um angebliche Krebsrisiken von Unkrautvernichtern der Tochter Monsanto mit dem umstrittenen Wirkstoff Glyphosat bahnt sich eine Kehrtwende an.

[https://www.proplanta.de/Agrar-Nachrichten/Unternehmen/Wird-das-Glyphosat-Urteil-gegen-Monsanto-gekippt\\_article1539250132.html](https://www.proplanta.de/Agrar-Nachrichten/Unternehmen/Wird-das-Glyphosat-Urteil-gegen-Monsanto-gekippt_article1539250132.html)

**The guardian: 'The world is against them': new era of cancer lawsuits threaten Monsanto**

<https://www.theguardian.com/science/2018/oct/07/monsanto-trial-cancer-appeal-glyphosate-chemical>

As always you will find the weekly overview of the press releases at: <https://www.biotech-gm-food.com/presse>

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**Publications:**

**Callaway E.: (2018): World's largest rice gene bank secures permanent funding**

The International Rice Research Institute is home to 136,000 varieties and aims to develop crops resistant to climate change. *Nature* | doi: 10.1038/d41586-018-07029-1

<https://www.nature.com/articles/d41586-018-07029-1>

**Reeves R.G., Voeneky S., Caetano-Anollés D., Beck F., Boëte C. (2018): Agricultural research, or a new bioweapon system? *Science* 362 (6410), 35-37, DOI: 10.1126/science.aat7664**

Insect-delivered horizontal genetic alteration is concerning

<http://science.sciencemag.org/content/362/6410/35.full>

**INRA: Stratégie de l'Inra en matière d'utilisation des technologies d'édition du génome végétal**

only a pdf-file available

Smyth S.J. and Lassoued R. (2018):

**Agriculture R&D Implications of the CJEU's Gene-Specific Mutagenesis Ruling**

Trends in Biotechnology, <https://doi.org/10.1016/j.tibtech.2018.09.004>

On 25 July 2018, the Court of Justice of the European Union (CJEU) ruled that gene-specific [mutagenesis](#) must be regulated as [genetically modified](#) organism (GMO) technologies. However, the costs to agricultural research and development (R&D) innovation will be staggering, not to mention the brain drain to other countries. As a result, Europe can now be known as the deathplace of agricultural breeding innovations.

<https://www.sciencedirect.com/science/article/pii/S0167779918302579>

Ishii T. (2018): Crop Gene-Editing: Should We Bypass or Apply Existing GMO Policy? Trends in Biotechnology: <https://doi.org/10.1016/j.tplants.2018.09.001>

Recent advances in crop gene-editing technologies allow for efficient site-specific [mutagenesis](#) without introducing exogenous DNA, potentially bypassing product-based [genetically modified organism \(GMO\)](#) regulations. Conversely, such plants can be subject to process-based GMO regulations. However, it is important to tailor existing GMO regulations with the aim to ensure social acceptance of gene-edited crops. <https://www.sciencedirect.com/science/article/pii/S1360138518301936>

Stanford University Medical Center (2018): **Researchers modify CRISPR to reorganize genome**

<https://phys.org/news/2018-10-crispr-genome.html#jCp>

Casacuberta J.M. & Puigdomènech P. (2018): **Proportionate and scientifically sound risk assessment of gene-edited plants.** EMBO Reports 19: e46907, DOI 10.15252/embr.201846907

<http://embor.embopress.org/content/early/2018/09/05/embr.201846907>

Salesse-Smith C.E., Sharwood, R.E., Busch F.A., Kromdijk J., Bardal V. & Stern D.B. (2018): **Overexpression of Rubisco subunits with RAF1 increases Rubisco content in maize.** Nature Plants 4,802–810 ; DOI: 10.1038/s41477-018-0252-4

Rubisco catalyses a rate-limiting step in photosynthesis and has long been a target for improvement due to its slow turnover rate. An alternative to modifying catalytic properties of Rubisco is to increase its abundance within  $C_4$  plant chloroplasts, which might increase activity and confer a higher carbon assimilation rate. Here, we overexpress the Rubisco large (LS) and small (SS) subunits with the Rubisco assembly chaperone RUBISCO ASSEMBLY FACTOR 1 (RAF1). While overexpression of LS and/or SS had no discernable impact on Rubisco content, addition of RAF1 overexpression resulted in a >30% increase in Rubisco content. Gas exchange showed a 15% increase in  $CO_2$  assimilation ( $A_{SAT}$ ) in UBI-LSSS-RAF1 transgenic plants, which correlated with increased fresh weight and in vitro  $V_{cmax}$  calculations. The divergence of Rubisco content and assimilation could be accounted for by the Rubisco activation state, which decreased up to 23%, suggesting that Rubisco activase may be limiting  $V_{cmax}$ , and impinging on the realization of photosynthetic potential from increased Rubisco content.

<https://www.nature.com/articles/s41477-018-0252-4>

Zhang J. et al. (2018). **Allele-defined genome of the autopolyploid sugarcane *Saccharum spontaneum* L.**, *Nature Genetics*. DOI: [10.1038/s41588-018-0237-2](https://doi.org/10.1038/s41588-018-0237-2)

Modern sugarcanes are polyploid interspecific hybrids, combining high sugar content from *Saccharum officinarum* with hardiness, disease resistance and ratooning of *Saccharum spontaneum*. Sequencing of a haploid *S. spontaneum*, AP85-441, facilitated the assembly of 32 pseudo-chromosomes comprising 8 homologous groups of 4 members each, bearing 35,525 genes with alleles defined. The reduction of basic chromosome number from 10 to 8 in *S. spontaneum* was caused by fissions of 2 ancestral chromosomes followed by translocations to 4 chromosomes. Surprisingly, 80% of nucleotide binding site-encoding genes associated with disease resistance are located in 4 rearranged chromosomes and 51% of those in rearranged regions. Resequencing of 64 *S. spontaneum* genomes identified balancing selection in rearranged regions, maintaining their diversity. Introgressed *S. spontaneum* chromosomes in modern sugarcanes are randomly distributed in AP85-441 genome, indicating random recombination among homologs in different *S. spontaneum* accessions. The allele-defined *Saccharum* genome offers new knowledge and resources to accelerate sugarcane improvement.

<https://www.nature.com/articles/s41588-018-0237-2.pdf>

University of Illinois at Urbana-Champaign

**Success is sweet: Researchers unlock the mysteries of the sugarcane genome**

<https://phys.org/news/2018-10-success-sweet-mysteries-sugarcane-genome.html#jCp>

Ankanahalli N., Urs N., Hu Y., Li P., Yuchi Z., Chen Y., Zhang Y. (2018): **Cloning and Expression of a Nonribosomal Peptide Synthetase to Generate Blue Rose.** *ACS Synth. Biol.*, Article ASAP, DOI: 10.1021/acssynbio.8b00187

Rose has been entwined with human culture and history. “Blue rose” in English signifies unattainable hope or an impossible mission as it does not exist naturally and is not breedable regardless of centuries of effort by gardeners. With the knowledge of genes and enzymes involved in flower pigmentation and modern genetic technologies, synthetic biologists have undertaken the challenge of producing blue rose by engineering the complicated vacuolar flavonoid pigmentation pathway and resulted in a mauve-colored rose. A completely different strategy presented in this study employs a dual expression plasmid containing bacterial *idgS* and *sfp* genes. The holo-IdgS, activated by Sfp from its apo-form, is a functional nonribosomal peptide synthetase that converts l-glutamine into the blue pigment indigoidine. Expression of these genes upon petal injection with agro-infiltration solution generates blue-hued rose flowers. We envision that implementing this proof-of-concept with obligatory modifications may have tremendous impact in floriculture to achieve a historic milestone in rose breeding.

<https://pubs.acs.org/doi/abs/10.1021/acssynbio.8b00187#cor1>

Wang P. et al. (2018): **High efficient multisites genome editing in allotetraploid cotton (*Gossypium hirsutum*) using CRISPR/Cas9 system.** *Plant Biotechnology Journal* (2018) 16, pp. 137–150; doi: 10.1111/pbi.12755

*Gossypium hirsutum* is an allotetraploid with a complex genome. Most genes have multiple copies that belong to At and Dt subgenomes. Sequence similarity is also very high between gene homologues. To efficiently achieve site/gene-specific mutation is quite needed. Due to its high efficiency and robustness, the CRISPR (clustered regularly interspaced short palindromic repeats)/ Cas9 system has exerted broad site-specific genome editing from prokaryotes to eukaryotes. In this study, we utilized a CRISPR/Cas9 system to generate two sgRNAs in a single vector to conduct multiple sites genome editing in allotetraploid cotton. An exogenously transformed gene *Discosoma red fluorescent protein2(DsRed2)* and an endogenous gene *GhCLA1* were chosen as targets. The DsRed2-edited plants in T0 generation reverted its traits to wild type, with vanished red fluorescence the whole plants. Besides, the mutated phenotype and genotype were inherited to their T1 progenies. For the endogenous gene *GhCLA1*, 75% of regenerated plants exhibited albino phenotype with obvious nucleotides and DNA fragments deletion. The efficiency of gene editing at each target site is 66.7–100%. The mutation genotype was checked for both genes with Sanger sequencing. Barcode-based high-throughput sequencing, which could be highly efficient for genotyping to a population of mutants, was conducted in *GhCLA1*-edited T0 plants and it matched well with Sanger sequencing results. No off-target editing was detected at the potential off-target sites. These results prove that the CRISPR/Cas9 system is highly efficient and reliable for allotetraploid cotton genome editing.

<https://www.ncbi.nlm.nih.gov/pubmed/28499063>

Tavares H. et al. (2018): **Selection and gene flow shape genomic islands that control floral guides.** *PNAS* <https://doi.org/10.1073/pnas.1801832115>

Genomes of closely-related species or populations often display localized regions of enhanced relative sequence divergence, termed genomic islands. It has been proposed that these islands arise through selective sweeps and/or barriers to gene flow. Here, we genetically dissect a genomic island that controls flower color pattern differences between two subspecies of *Antirrhinum majus*, *A.m.striatum* and *A.m.pseudomajus*, and relate it to clinal variation across a natural hybrid zone. We show that selective sweeps likely raised relative divergence at two tightly-linked *MYB*-like transcription factors, leading to distinct flower patterns in the two subspecies. The two patterns provide alternate floral guides and create a strong barrier to gene flow where populations come into contact. This barrier affects the selected flower color genes and tightly-linked loci, but does not extend outside of this domain, allowing gene flow to lower relative divergence for the rest of the chromosome. Thus, both selective sweeps and barriers to gene flow play a role in shaping genomic islands: sweeps cause elevation in relative divergence, while heterogeneous gene flow flattens the surrounding “sea,” making the island of divergence stand out. By showing how selective sweeps establish alternative adaptive phenotypes that lead to barriers to gene flow, our study sheds light on possible mechanisms leading to reproductive isolation and speciation.

<http://www.pnas.org/content/early/2018/10/04/1801832115.short?rss=1>

Abe T. et al. (2018): **AND-1 fork protection function prevents fork resection and is essential for proliferation,** *Nature Communications* 9, Article number: 3091 (2018). DOI: [10.1038/s41467-018-05586-7](https://doi.org/10.1038/s41467-018-05586-7)

AND-1/Ctf4 bridges the CMG helicase and DNA polymerase alpha, facilitating replication. Using an inducible degron system in avian cells, we find that AND-1 depletion is incompatible with proliferation, owing to cells accumulating in G2 with activated DNA damage checkpoint. Replication without AND-1 causes fork speed slow-down and accumulation of long single-stranded DNA (ssDNA) gaps at the replication fork junction, with these regions being converted to DNA double strand breaks (DSBs) in G2. Strikingly, resected forks and DNA damage accumulation in G2, but not fork slow-down, are reverted by treatment with mirin, an MRE11 nuclease inhibitor. Domain analysis of AND-1 further revealed that the HMG box is important for fast replication but not for proliferation, whereas conversely, the WD40 domain prevents fork resection and subsequent DSB-associated lethality. Thus, our findings uncover a fork protection function of AND-1/Ctf4 manifested via the WD40 domain that is essential for proliferation and averts genome instability.

Tokyo Metropolitan University

Unveiling the mechanism protecting replicated DNA from degradation

<https://phys.org/news/2018-10-unveiling-mechanism-replicated-dna-degradation.html#jCp>

Lenz T.L., Hafer N., Samonte I.E., Yeates S.E., Milinski M. (2018): **Cryptic haplotype-specific gamete selection yields offspring with optimal MHC immune genes.** *Evolution* <https://doi.org/10.1111/evo.13591>

Females choose specific mates in order to produce fitter offspring. However, several factors interfere with females' control over fertilization of their eggs, including sneaker males and phenotypically unpredictable allele segregation during meiosis. Mate choice at the individual level thus provides only a poor approximation for obtaining the best genetic match. Consequently, postcopulatory sperm selection by female oocytes has been proposed as a mechanism to achieve complementary combinations of parental haplotypes. Here, using controlled in vitro fertilization of three-spined stickleback eggs, we find haplotype-specific fertilization bias toward gametes with complementary major histocompatibility complex (MHC) immunogenes. The resulting zygote (and thus offspring) genotypes exhibit an intermediate level of individual MHC diversity that was previously shown to confer highest pathogen resistance. Our finding of haplotype-specific gamete selection

thus represents an intriguing mechanism for fine-tuned optimization of the offspring's immune gene composition and an evolutionary advantage in the Red Queen dynamics of host-parasite coevolution. <https://onlinelibrary.wiley.com/doi/epdf/10.1111/evo.13591>

Max Planck Society

**Female gametes prefer sperm with different immune genes**

<https://phys.org/news/2018-10-female-gametes-sperm-immune-genes.html#jCp>

Kruitwagen T, Chymkowitch P, Denoth-Lippuner A, Enserink J, Barral Y. (2018): **Centromeres License the Mitotic Condensation of Yeast Chromosome Arms.** *Cell* 175 (3) 1-16, <https://doi.org/10.1016/j.cell.2018.09.01>

During mitosis, chromatin condensation shapes chromosomes as separate, rigid, and compact sister chromatids to facilitate their segregation. Here, we show that, unlike wild-type yeast chromosomes, non-chromosomal DNA circles and chromosomes lacking a centromere fail to condense during mitosis. The centromere promotes chromosome condensation strictly in cis through recruiting the kinases Aurora B and Bub1, which trigger the autonomous condensation of the entire chromosome. Shugoshin and the deacetylase Hst2 facilitated spreading the condensation signal to the chromosome arms. Targeting Aurora B to DNA circles or centromere-ablated chromosomes or releasing Shugoshin from PP2A-dependent inhibition bypassed the centromere requirement for condensation and enhanced the mitotic stability of DNA circles. Our data indicate that yeast cells license the chromosome-autonomous condensation of their chromatin in a centromere-dependent manner, excluding from this process non-centromeric DNA and thereby inhibiting their propagation.

[https://www.cell.com/cell/pdf/S0092-8674\(18\)31184-X.pdf](https://www.cell.com/cell/pdf/S0092-8674(18)31184-X.pdf)

Pouyet F., Aeschbacher S., Thiéry A., Excoffier L. (2018): **Background selection and biased gene conversion affect more than 95% of the human genome and bias demographic inferences.** *eLife* 2018;7:e36317 doi: [10.7554/eLife.36317](https://doi.org/10.7554/eLife.36317)

Disentangling the effect on genomic diversity of natural selection from that of demography is notoriously difficult, but necessary to properly reconstruct the history of species. Here, we use high-quality human genomic data to show that purifying selection at linked sites (i.e. background selection, BGS) and GC-biased gene conversion (gBGC) together affect as much as 95% of the variants of our genome. We find that the magnitude and relative importance of BGS and gBGC are largely determined by variation in recombination rate and base composition. Importantly, synonymous sites and non-transcribed regions are also affected, albeit to different degrees. Their use for demographic inference can lead to strong biases. However, by conditioning on genomic regions with recombination rates above 1.5 cM/Mb and mutation types (C↔G, A↔T), we identify a set of SNPs that is mostly unaffected by BGS or gBGC, and that avoids these biases in the reconstruction of human history.

<https://elifesciences.org/articles/36317>

Swiss Institute of Bioinformatics

**The faulty yardstick in genomics studies and how to cope with it**

<https://phys.org/news/2018-10-faulty-yardstick-genomics-cope.html#jCp>

Binimelis R. & Wickson F. (2018): **The troubled relationship between GMOs and beekeeping: an exploration of socioeconomic impacts in Spain and Uruguay.** *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>

Vandamme E.J. and Mortelmans K. (2018): **A Century of Bacteriophage Research and Applications: Impact on Biotechnology, Health, Ecology and Economy.** *J. Chem Technology and Biotechnology*; <https://doi.org/10.1002/jctb.5810>

About one century ago bacteriophages, viruses that infect bacteria, were discovered and reported in the scientific literature. This review aims at a comprehensive survey of bacteriophage discovery, research and applications since the 1920s and its impact on molecular biology, biotechnology, health, ecology and economy. Phage therapy has been proven a valuable asset since the early 1920s to deal with pathogenic bacterial

infections. It has been practiced ever since, especially in the former Soviet Union and in Eastern Europe. The Western world remained skeptical and resorted to the widespread use of antibiotics since the 1940s. Now that antibiotic resistance among pathogenic bacteria has spread alarmingly and few really novel antibiotic compounds are in the pipeline, renewed attention is being directed to the use of phages as antibacterial agents in medicine. Because of this renewed interest in phage therapy in the Western world, novel applications with phages are being pursued in the human health, environmental and the agri-food sectors. This review will focus on 1) the history of early phage use and its successes and problems, 2) the study of phages as important tools in the development of molecular biology and biotechnology, 3) current developments in phage research including the use of phage endolysins for use in antibacterial treatment, 4) phage production systems including undesirable phage contamination of industrial fermentation processes based on bacteria, 5) recent applications in phage therapy and in phage based control, and 6) the roles of phages in nature and in the human gut.  
<https://onlinelibrary.wiley.com/doi/abs/10.1002/ictb.5810>

## Meetings

### Food Allergy Forum

Amsterdam, the Netherlands, on 1-3 April 2019.

<https://foodallergyforum.org/>

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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](http://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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