

Sunday Evening News

Week 02 (2018-01-15 / 01-21)

Selected and edited by **BGF** Jany

Bobek – EuGH: Schlussanträge von Generalanwalt Bobek zur Mutagenese und Gentechnik:

Pressemeldung: German: <http://bit.ly/2Dlgsav>

English: <https://curia.europa.eu/jcms/upload/docs/application/pdf/2018-01/cp180004en.pdf>

Vollständiger Text: deutsch:

<http://curia.europa.eu/juris/document/document.jsf?text=&docid=198532&pageIndex=0&oclang=DE&mode=req&dir=&occ=first&part=1&cid=779174#Footref12>

English:

<http://curia.europa.eu/juris/document/document.jsf?text=&docid=198532&pageIndex=0&oclang=EN&mode=req&dir=&occ=first&part=1&cid=779292>

Beiträge zu den Schlussanträgen / Press releases to the opinion

Juris (2018): **Schlussanträge zur Fortgeltung der "Mutagenese-Ausnahme" in GVO-Richtlinie**

<https://www.juris.de/jportal/portal/page/homerl.psm1?nid=jnachr-JUNA180100146&cmsuri=%2Fjuris%2Fde%2Fnachrichten%2Fzeigenachricht.jsp>

Abbott A. (2018): **Europe court suggests relaxed gene-editing rules**

Judicial opinion says restrictive regulations may not apply to plants and animals bred using CRISPR technique.

https://www.nature.com/articles/d41586-018-01013-5?WT.feed_name=subjects_climate-sciences

EuropaBio (2018): **One step closer to legal clarity in plant breeding / Our take on the CJEU Advocate General opinion**

http://www.europabio.org/agricultural-biotech/publications/one-step-closer-legal-clarity-plant-breeding?mc_cid=1000d8c51d&mc_eid=b89825d9e5

Press release:

<http://www.europabio.org/sites/default/files/One%20step%20closer%20to%20legal%20clarity%20in%20plant%20breeding.pdf>

epso First reaction (2018): **On the Advocate General's Opinion regarding mutagenesis and the Genetically Modified Organisms Directive**

http://www.epsoweb.org/webfm_send/2362

GAIN Report Number: E 18003 (2018): **Advisory Legal Opinion Expected for New Plant Breeding Techniques**

https://gain.fas.usda.gov/Recent%20GAIN%20Publications/Advisory%20Legal%20Opinion%20Expected%20for%20New%20Plant%20Breeding%20Techniques%20_Brussels%20USEU_EU-28_1-16-2018.pdf

GM-Watch (2018): **Modern mutagenesis techniques are genetic engineering and give rise to GMOs**

<http://gmwatch.org/en/news/archive/2018/18077>

Demeter-Statement (2018) **Demeter-Statement zur Position des Generalanwalts beim Europäischen Gerichtshof Gentechnik muss als solche erkenntlich sein und reguliert werden!**

<https://www.demeter.de/aktuell/gentechnik-kennzeichnen-und-regulieren>

BioAustria: (2018): **BIO AUSTRIA zu neuen Gentechnik-Verfahren: Gentechnikfreiheit Österreichs sichern**

Wahlfreiheit für Bäuerinnen und Bauern sowie Konsument/innen nur mit verpflichtender Kennzeichnung neuer Gentechnik gesichert

https://www.ots.at/presseaussendung/OTS_20180118_OTSO198/bio-austria-zu-neuen-gentechnik-verfahren-gentechnikfreiheit-oesterreichs-sichern

Informationsdienst Gentechnik: **Europäischer Generalanwalt: Wann ist Mutagenese Gentechnik?**

<https://www.keine-gentechnik.de/nachricht/32948/>

EuropaBio (2018) **Achieving the potential of genome editing - The perspective of the European Biotech Industry**

http://www.europabio.org/cross-sector/publications/achieving-potential-genome-editing?mc_cid=1000d8c51d&mc_eid=b89825d9e5

In den deutschen Medien fand die Pressemeldung des EuGH zu den Schlussanträgen von Generalanwalt Bobek kaum Beachtung.

Karberg S. – Der Tagesspiegel: **Crispr ist nicht immer Gentechnik**

Mit Genome Editing gezüchtete Organismen fallen nicht unbedingt unter die strenge Regulierung der EU.

<http://www.tagesspiegel.de/wissen/europaeischer-gerichtshof-vor-der-entscheidung-crispr-ist-nicht-immer-gentechnik/20864058.html>

and two english press releases

The Guardian **Gene edited crops should be exempted from GM food laws, says EU lawyer**

Technology can help foster specific positive traits in plants but can also have potentially dangerous 'off-target' effects, say critics

<https://www.theguardian.com/science/2018/jan/18/gene-edited-crops-should-be-exempted-from-gm-food-laws-says-eu-lawyer>

AG Bobek: **Organisms obtained by mutagenesis exempt from GMO Directive**

Organisms obtained by mutagenesis are, in principle, exempted from the obligations in the Genetically Modified Organisms Directive, according to **Advocate General Bobek**.

<http://www.scottishlegal.com/2018/01/18/ag-bobek-organisms-obtained-mutagenesis-exempt-gmo-directive/>

and the next top theme

Free-from food in focus

The free-from sector is growing ahead of the market thanks to consumer perceptions of health and wellness.

But which categories offer the most growth potential? And how can food manufacturers and marketers ensure that free-from food's 'health halo' does not slip?

Scientific References

Dossier: Public Participation, Legitimate Political Decisions, and Controversial Technologies
Christiansen A., Jonch-Clausen K., and Kappel K. (2018): **Does Controversial Science Call For Public Participation? The Case Of Gmo Skepticism**. *Les ateliers de l'éthique*, 12 (1), 26–50.
doi:10.7202/1042277ar

Many instances of new and emerging science and technology are controversial. Although a number of people, including scientific experts, welcome these developments, a considerable skepticism exists among members of the public. The use of genetically modified organisms (GMOs) is a case in point. In science policy and in science communication, it is widely assumed that such controversial science and technology require public participation in the policy-making process. We examine this view, which we call the Public Participation Paradigm, using the case of GMOs as an example. We suggest that a prominent reason behind the call for public participation is the belief that such participation is required for democratic legitimacy. We then show that the most prominent accounts of democratic legitimacy do not, in fact, entail that public participation is required in cases of controversial science in general, or in the case of GMOs in particular.

<https://www.erudit.org/fr/revues/ateliers/2017-v12-n1-ateliers03284/1042277ar/>

pdf-file: <https://www.erudit.org/fr/revues/ateliers/2017-v12-n1-ateliers03284/1042277ar.pdf>

Fernández Albújar, Gema and van der Meulen, Bernd, **The Legal GMO Concept Reassessment of the GMO Definition in the Light of New Breeding Techniques (NBTs)**

(December 29, 2017). European Institute for Food Law Working Paper Series 2017/03 . Available at SSRN: <https://ssrn.com/abstract=3094321>

What are GMOs in a legal sense? According to the EU definition a GMO is an organism 'in which the genetic material has been altered in a way that does not occur naturally by mating and/or natural recombination'. Does this definition refer to the organism, to the method by which it has been obtained or to both? This question has become acute with the emergence of New Breeding Techniques (NBTs) in particular when non-traditional methods have been used to achieve results that also could occur naturally. Are such products that could have been obtained by traditional breeding techniques GMOs? The French Conseil d'état has asked a preliminary ruling from the Court of Justice of the EU (CJEU). Unfortunately, the Conseil d'état failed to clearly phrase the question that needs to be answered. The authors express the hope that the CJEU nevertheless will be able to provide a meaningful answer. They provide an introduction to NBTs and argue in favour of a product based interpretation.

https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3094321 here also pdf-file available

reminder!

Braun M. & Dabrock P. (2017): **Mind the gaps!** Towards an ethical framework for genome editing. EMBO reports e45542, 2017

<http://embor.embopress.org/content/early/2017/12/27/embr.201745542>

pdf-file:

<http://embor.embopress.org/content/embor/early/2017/12/27/embr.201745542.full.pdf>

Breeding and New Technologies

Baldauf J.A., Marcon C., Lithio A., Vedder L., Altrogge L., Piepho H.-P., Schoof H., Nettleton D., and Hochholdinger F. (2018): **Single parent expression is a general mechanism that drives extensive complementation of non-syntenic genes in maize (*Zea mays* L.) hybrids**. Current Biology, Band 28, 2018; DOI: 10.1016/j.cub.2017.12.027

Maize (*Zea mays* L.) displays an exceptional degree of structural genomic diversity [1, 2]. In addition, variation in gene expression further contributes to the extraordinary phenotypic diversity and plasticity of maize. This study provides a systematic investigation on how distantly related homozygous maize inbred lines affect the transcriptomic plasticity of their highly heterozygous F₁ hybrids. The classical dominance model of heterosis explains the superiority of hybrid plants by the complementation of deleterious parental alleles by superior alleles of the second parent at many loci [3]. Genes active in one inbred line but inactive in another represent an extreme instance of allelic diversity defined as single-parent expression [4]. We observed on average ~1,000 such genes in all inbred line combinations during primary root development. These genes consistently displayed expression complementation (i.e., activity) in their hybrid progeny. Consequently, extreme expression complementation is a general mechanism that results on average in ~600 additionally active genes and their encoded biological functions in hybrids. The modern maize genome is complemented by a set of non-syntenic genes, which emerged after the separation of the maize and sorghum lineages and lack syntenic orthologs in any other grass species [5]. We demonstrated that non-syntenic genes are the driving force of gene expression complementation in hybrids. Among those, the highly diversified families of bZIP and bHLH transcription factors [6] are systematically overrepresented. In summary, extreme gene expression complementation extensively shapes the transcriptomic plasticity of maize hybrids and might therefore be one factor controlling the developmental plasticity of hybrids.

[http://www.cell.com/current-biology/abstract/S0960-9822\(17\)31660-3](http://www.cell.com/current-biology/abstract/S0960-9822(17)31660-3)

pdf-file: [http://www.cell.com/current-biology/pdf/S0960-9822\(17\)31660-3.pdf](http://www.cell.com/current-biology/pdf/S0960-9822(17)31660-3.pdf)

Tong Zhang T. et al. (2018): **Establishing RNA virus resistance in plants by harnessing CRISPR immune system**. doi: 10.1111/pbi.12881

Recently, CRISPR-Cas (clustered, regularly interspaced short palindromic repeats-CRISPR associated proteins) system has been used to produce plants resistant to DNA virus infections. However, there is no RNA virus control method in plants that uses CRISPR-Cas system to target the viral genome directly. Here we reprogrammed the CRISPR-Cas9 system from *Francisella novicida* confer molecular immunity against RNA viruses in *Nicotiana benthamiana* and Arabidopsis plants. Plants expressing Fn Cas9 and sgRNA specific for the cucumber mosaic virus (CMV) or tobacco mosaic virus (TMV) exhibited significantly attenuated virus infection symptoms and reduced viral RNA accumulation. Furthermore, in the transgenic virus-targeting plants, the resistance was inheritable and the progenies showed significantly less virus accumulation. These data reveals that the CRISPR/Cas9 system can be used to produce plant that stable resistant to RNA viruses, thereby broadening the use of such technology for virus control in agricultural field.

<http://onlinelibrary.wiley.com/doi/10.1111/pbi.12881/pdf>

Medina-Aparicio L, Dávila, S., Rebollar-Flores J.E., Calva E., and Hernández-Lucas I. (2018): **The CRISPR-Cas system in *Enterobacteriaceae*** . *Pathogens and Disease*, fty002, <https://doi.org/10.1093/femspd/fty002>

In nature, microorganisms are constantly exposed to multiple viral infections and thus have developed many strategies to survive phage attack and invasion by foreign DNA. One of such strategies is the CRISPR-Cas bacterial immunological system. This defense mechanism is widespread in prokaryotes including several families such as *Enterobacteriaceae*. Much knowledge about the CRISPR-Cas system has been generated, including its biological functions, transcriptional regulation, distribution, utility as a molecular marker, and as a tool for specific genome editing. This review focuses on these aspects and describes the state of the art of the CRISPR-Cas system in the *Enterobacteriaceae* bacterial family.

<https://academic.oup.com/femspd/advance-article-abstract/doi/10.1093/femspd/fty002/4794941>

Maselko M., Heinsch S.C., Chacón J.M., Harcombe W.R. & Smanski M.J. (2017): **Engineering species-like barriers to sexual reproduction** NATURE COMMUNICATIONS | 8: 883 | DOI: 10.1038/s41467-017-01007-3 | www.nature.com/naturecommunications

Controlling the exchange of genetic information between sexually reproducing populations has applications in agriculture, eradication of disease vectors, control of invasive species, and the safe study of emerging biotechnology applications. Here we introduce an approach to engineer a genetic barrier to sexual reproduction between otherwise compatible populations. Programmable transcription factors drive lethal gene expression in hybrid offspring following undesired mating events. As a proof of concept, we target the ACT1 promoter of the model organism *Saccharomyces cerevisiae* using a dCas9-based transcriptional activator. Lethal overexpression of actin results from mating this engineered strain with a strain containing the wild-type ACT1 promoter.

<https://www.nature.com/articles/s41467-017-01007-3>

pdf-file: <https://www.nature.com/articles/s41467-017-01007-3.pdf>

Jacob P. Avni A. and Bendahmane A. (2017): **Translational Research: Exploring and Creating Genetic Diversity**. *Trends in Plant Science*, 23 (1),

<https://doi.org/10.1016/j.tplants.2017.10.002>

The crop selection process has created a genetic bottleneck ultimately restricting breeding output. Wild relatives of major crops as well as the so-called 'neglected plant' species represent a reservoir of genetic diversity that remains underutilized. These species could be used as a tool to discover new alleles of agronomic interest or could be the target of breeding programs. Targeted induced local lesions in the genome (TILLING) can be used to translate in neglected crops what has been discovered in major crops and reciprocally. However, random mutagenesis, used in TILLING approaches, provides only a limited density of mutational events at a defined target locus. Alternatively, clustered regularly interspaced short palindromic repeats (CRISPR) associated 9 (Cas9) fused to a cytidine deaminase could serve as a localized mutagenic agent to produce high-density mutant populations. Artificial evolution is at hand.

[http://www.cell.com/trends/plant-science/pdf/S1360-1385\(17\)30232-7.pdf](http://www.cell.com/trends/plant-science/pdf/S1360-1385(17)30232-7.pdf)

Filipe Borges F. et al. (2018): **Transposon-derived small RNAs triggered by miR845 mediate genome dosage response in *Arabidopsis***. *Nature Genetics* (2018). DOI: [10.1038/s41588-017-0032-5](https://doi.org/10.1038/s41588-017-0032-5)

Chromosome dosage has substantial effects on reproductive isolation and speciation in both plants and animals, but the underlying mechanisms are largely obscure¹. Transposable elements in animals can regulate hybridity through maternal small RNA², whereas small RNAs in plants have been postulated to regulate dosage response via neighboring imprinted genes^{3,4}. Here we show that a highly conserved microRNA in plants, miR845, targets the tRNA^{Met} primer-binding site (PBS) of long terminal repeat (LTR) retrotransposons in *Arabidopsis* pollen, and triggers the accumulation of 21–22-nucleotide (nt) small RNAs in a dose-dependent fashion via RNA polymerase IV. We show that these epigenetically activated small interfering RNAs (easiRNAs) mediate hybridization barriers between diploid seed parents and tetraploid pollen parents (the 'triploid block'), and that natural variation for miR845 may account for 'endosperm balance' allowing the formation of triploid seeds. Targeting of the PBS with small RNA is a common mechanism for transposon control in mammals and plants, and provides a uniquely sensitive means to monitor chromosome dosage and imprinting in the developing seed.

<https://www.nature.com/articles/s41588-017-0032-5>

and <https://phys.org/news/2018-01-chromosomes-scientists-century-old-mystery-reproduction.html#jCp>

Jagadeesan, A. et al. (2018): **Reconstructing an African haploid genome from the 18th century**. *Nature Genetics* (2018); doi:10.1038/s41588-017-0031-6

A genome is a mosaic of chromosome fragments from ancestors who existed some arbitrary number of generations earlier. Here, we reconstruct the genome of Hans Jonatan (HJ), born in the Caribbean in 1784 to an enslaved African mother and European father. HJ migrated to Iceland in 1802, married and had two children. We genotyped 182 of his 788 descendants using single-nucleotide polymorphism (SNP) chips and whole-genome sequenced (WGS) 20 of them. Using these data, we reconstructed 38% of HJ's maternal genome and inferred that his mother was from the region spanned by Benin, Nigeria and Cameroon.

<https://www.nature.com/articles/s41588-017-0031-6>

Wagner R. de Souza et al. (2017): **Suppression of a single BAHD gene in *Setaria viridis* causes large, stable decreases in cell wall feruloylation and increases biomass digestibility.** *New Phytologist* (2017); doi: 10.1111/nph.14970

Feruloylation of arabinoxylan (AX) in grass cell walls is a key determinant of recalcitrance to enzyme attack, making it a target for improvement of grass crops, and of interest in grass evolution. Definitive evidence on the genes responsible is lacking so we studied a candidate gene that we identified within the BAHD acyl-CoA transferase family. We used RNA interference (RNAi) silencing of orthologs in the model grasses *Setaria viridis* (SvBAHD01) and *Brachypodium distachyon* (BdBAHD01) and determined effects on AX feruloylation. Silencing of SvBAHD01 in *Setaria* resulted in a c. 60% decrease in AX feruloylation in stems consistently across four generations. Silencing of BdBAHD01. In *Brachypodium* stems decreased feruloylation much less, possibly due to higher expression of functionally redundant genes. *Setaria* SvBAHD01 RNAi plants showed: no decrease in total lignin, approximately doubled arabinose acylated by p-coumarate, changes in two-dimensional NMR spectra of unfractionated cell walls consistent with biochemical estimates, no effect on total biomass production and an increase in biomass saccharification efficiency of 40 – 60%. We provide the first strong evidence for a key role of the BAHD01 gene in AX feruloylation and demonstrate that it is a promising target for improvement of grass crops for biofuel, biorefining and animal nutrition applications.

<http://onlinelibrary.wiley.com/doi/10.1111/nph.14970/epdf>

Muller A. et al. (2017): **Strategies for feeding the world more sustainably with organic agriculture** *Nature Communications* 8, Article number: 1290 (2017); doi:10.1038/s41467-017-01410-w

<https://www.nature.com/articles/s41467-017-01410-w.pdf> pdf-file available

Safety

do Amaral M.N. and Souza G.M. (2017): **The Challenge to Translate OMICS Data to Whole Plant Physiology: The Context Matters** *Front. Plant Sci.* 8:2146. doi: 10.3389/fpls.2017.02146 <https://www.frontiersin.org/articles/10.3389/fpls.2017.02146/full>

Ackah, V.B., Andoh-Odoom A.H, and Akonor P.T. (2017): **The status of food safety management systems in Ghana.** Council for Scientific and Industrial Research (CSIR), Food Research Institute, Ghana; <http://212.47.242.17:8080/jspui/handle/123456789/477>

In Ghana, there is not enough scientific information about the implementation of food safety management systems (FSMS). This study therefore aimed at getting insight into the current status of FSMS in Ghanaian food processing companies. This was a descriptive case study conducted in Tema. A questionnaire was administered to 70 companies which were randomly selected for the survey with a response rate of 65.7%. SPSS 17.1 was used to analyze the results obtained and STATA 12 used to determine the linkages between having a food safety management system in place and variables including market focus. The results indicated that more than 54% of the companies did not adhere to any quality assurance guideline. (56.5%) of the companies were not certified to any standards and 85% of the respondents cited cost as the main challenge in implementing a food safety management system. More than 40% of the companies had not been inspected by food regulation authorities since they were established. It has been recommended that Management of food processing companies must play an active role in adopting and implementing some form of food safety management system to guarantee a consistent production of safe products for consumers

<http://212.47.242.17:8080/jspui/handle/123456789/477>

Waiblinger, HU., Busch, U., Brünen-Nieweler, C. et al. (2018): **Official food control laboratories in Germany: results of GMO analyses from 2012 to 2016.** *J Consum Prot Food Saf* (2018). <https://doi.org/10.1007/s00003-017-1146-5>

<https://link.springer.com/article/10.1007/s00003-017-1146-5>

Kirschner A.K.T. et al. (2017): **Multiparametric monitoring of microbial faecal pollution reveals the dominance of human contamination along the whole Danube River, Water**

Research 124, 543-555; DOI: 10.1016/j.watres.2017.07.052
pdf-file: https://ac.els-cdn.com/S0043135417306255/1-s2.0-S0043135417306255-main.pdf?_tid=46251b1a-fe0e-11e7-8059-00000aacb361&acdnat=1516472472_e33eee138a749b5ebb193430c742e77e

Leclerc M., Emily Walker E., Antoine Messéan A., and Soubeyrand S. (2017): **Spatial exposure-hazard and landscape models for assessing the impact of GM crops on non-target organisms**. *Science of the Total Environment* 624, 470–479

The cultivation of Genetically Modified (GM) crops may have substantial impacts on populations of nontarget than the cultivated field, and, as landscape-scale experiments are difficult, if not impossible, modelling approaches are needed to address landscape risk management. We present an original stochastic and spatially explicit modelling framework for assessing the risk at the landscape level. We use techniques from spatial statistics for simulating simplified landscapes made up of (aggregated or non-aggregated) GM fields, neutral plants and NTO's habitat areas. The dispersal of toxic pollen grains is obtained by convolving the emission of GM plants and validated dispersal kernel functions while the locations of exposed individuals are drawn from a point process. By taking into account the adherence of the ambient pollen on plants, the loss of pollen due to climatic events, and, an experimentally validated mortality-dose function we predict risk maps and provide a distribution giving how the risk varies within exposed individuals in the landscape. Then, we consider the impact of the Bt maize on *Inachis io* in worst-case scenarios where exposed individuals are located in the vicinity of GM fields and pollen shedding overlaps with larval emergence. We perform a Global Sensitivity Analysis (GSA) to explore numerically how our input parameters influence the risk. Our results confirm the important effects of pollen emission and loss. Most interestingly they highlight that the optimal spatial distribution of GM fields that mitigates the risk depends on our knowledge of the habitats of NTOs, and finally, moderate the influence of the dispersal kernel function.

<https://www.sciencedirect.com/science/article/pii/S0048969717333879>

McArt SH, Urbanowicz C, McCoshum S, Irwin RE, Adler LS. (2017): **Landscape predictors of pathogen prevalence and range contractions in US bumblebees**. *Proc. R. Soc. B* 284: 20172181. <http://dx.doi.org/10.1098/rspb.2017.2181>

Several species of bumblebees have recently experienced range contractions and possible extinctions. While threats to bees are numerous, few analyses have attempted to understand the relative importance of multiple stressors. Such analyses are critical for prioritizing conservation strategies. Here, we describe a landscape analysis of factors predicted to cause bumblebee declines in the USA. We quantified 24 habitat, land-use and pesticide usage variables across 284 sampling locations, assessing which variables predicted pathogen prevalence and range contractions via machine learning model selection techniques. We found that greater usage of the fungicide chlorothalonil was the best predictor of pathogen (*Nosema bombi*) prevalence in four declining species of bumblebees. *Nosema bombi* has previously been found in greater prevalence in some declining US bumblebee species compared to stable species. Greater usage of total fungicides was the strongest predictor of range contractions in declining species, with bumblebees in the northern USA experiencing greater likelihood of loss from previously occupied areas. These results extend several recent laboratory and semi-field studies that have found surprising links between fungicide exposure and bee health. Specifically, our data suggest landscape-scale connections between fungicide usage, pathogen prevalence and declines of threatened and endangered bumblebees.

<http://rspb.royalsocietypublishing.org/content/royprsb/284/1867/20172181.full.pdf>

Spektrum: Insektensterben: Pestizide begünstigen Hummel-Parasiten

Weniger harmlos als bisher gedacht: Das Fungizid Chlorothalonil erweist sich als überraschend schädlich für Hummeln- durch eine Wirkung über Bande.

http://www.spektrum.de/news/pestizide-beguenstigen-hummel-parasiten/1532281?utm_medium=newsletter&utm_source=sdw-nl&utm_campaign=sdw-nl-daily&utm_content=heute

EFSA Guidance document: EFSA (European Food Safety Authority), 2018 Administrative guidance for the processing of applications for regulated products. EFSA supporting publication 2018: EN-1362. 13 pp. doi:10.2903/sp.efsa.2018. EN-1362

<http://onlinelibrary.wiley.com/doi/10.2903/sp.efsa.2018.EN-1362/epdf>