

Sunday Evening News No. 111

Week 04 (2019-21-01 – 2019-27-01)

Selected and edited by **BGF** Jany

Dear all,

In the press and the media there was hardly anything worth reporting. Germany remains rigid in the cold and the states are in part paralyzed by the shutdown.

For the German speaking colleagues / Nur die deutschsprachigen Kollegen.

In Deutschland wurde die Arbeit von Willett W. et al. (2019): „Food in the Anthropocene: the EAT–Lancet Commission on healthy diets from sustainable food systems“ bislang kaum diskutiert oder fand noch kein Eingang in die Medien Die Grünen und Greenpeace sind vielleicht noch nicht aufmerksam auf sie geworden. Anders in den USA.

Rohm B.: Für Erde und Gesundheit: Forscher entwickeln die perfekte Ernährung

Der eigene Speiseplan ist mit den Problemen unseres Planeten eng verknüpft. Experten haben nun eine Ernährung entworfen, die die globalen Probleme lösen soll – von Schadstoffemissionen bis hin zu Krankheiten.

https://utopia.de/fuer-erde-und-gesundheit-forscher-entwickeln-die-perfekte-ernaehrung-123236/?utm_source=Interessenten&utm_campaign=18cc43ff34-Newsletter+Do+19KW4&utm_medium=email&utm_term=0_af58dac727-18cc43ff34-264788737

Spiegel online.de: Iss nur 43 Gramm Fleisch pro Tag, rette die Welt

Zehn Milliarden Menschen gesund ernähren und gleichzeitig die Umwelt schützen? Das geht, glauben Forscher. In fünf radikalen Schritten.

<http://www.spiegel.de/gesundheit/ernaehrung/gesunde-ernaehrung-43-gramm-fleisch-pro-tag-und-die-welt-ist-gerettet-a-1248387.html>

OÖNachrichten: Warum wir weniger rotes Fleisch essen sollten

<https://www.nachrichten.at/nachrichten/gesundheits/warum-wir-weniger-rotes-fleisch-essen-sollten;art114,3095518>

Conrow J.: Study suggests science education improves attitudes about GMO food

<https://allianceforscience.cornell.edu/blog/2019/01/study-suggests-science-education-improves-attitudes-gmo-food/>

Sosland J.: Researchers seek go-ahead for GM wheat field trials

<https://www.world-grain.com/articles/11532-researchers-seek-go-ahead-for-gm-wheat-field-trials>

Eenennaam A.V.: Proposed U.S. regulation of gene-edited food animals is not fit for purpose

<https://geneticliteracyproject.org/2019/01/24/proposed-u-s-regulation-of-gene-edited-food-animals-is-not-fit-for-purpose/>

tg-transkript: CJEU ruling triggers exodus of EU plant research

<https://european-biotechnology.com/up-to-date/backgrounds-stories/story/cjeu-ruling-triggers-exodus-of-eu-plant-research.html>

Robin Wyers R.: Will CRISPR gene editing fuel trade tensions between post-Brexit UK and the EU?

<https://geneticliteracyproject.org/2019/01/23/will-crispr-gene-editing-fuel-trade-tensions-between-post-brexit-uk-and-the-eu/>

GM-Watch: Deceptive reporting of GMO90+ EU-funded feeding study on GM maize

GMO90+ study is falsely claimed to show the GM diets had no adverse effects and to refute the Séralini long-term study on GM maize and Roundup

<https://www.gmwatch.org/en/news/latest-news/18720>

The daily up-date of the press releases: <https://www.biotech-gm-food.com/presse>

Publikations:

Willett W. et al. (2019): **Food in the Anthropocene: the EAT–Lancet Commission on healthy diets from sustainable food systems.** Lancet. [https://doi.org/10.1016/S0140-6736\(18\)31788-4](https://doi.org/10.1016/S0140-6736(18)31788-4)

[https://www.thelancet.com/pdfs/journals/lancet/PIIS0140-6736\(18\)31788-4.pdf?utm_campaign=tleat19&utm_source=HubPage&code=lancet-site](https://www.thelancet.com/pdfs/journals/lancet/PIIS0140-6736(18)31788-4.pdf?utm_campaign=tleat19&utm_source=HubPage&code=lancet-site)

pdf-file available

Elder L. Greene S., Lizotte M.K. (2018): **The gender gap on public opinion towards genetically modified foods,** *The Social Science Journal* 55 (4); 500-509.

Ever since genetically modified (GM) foods were introduced into the food supply in the 1990s they have provoked debate and concern. The number of GM foods approved by the U.S. Food and Drug Administration and offered on supermarket shelves has steadily grown at the same time that public wariness about the safety of GM foods has increased. Studies within the [scientific literature](#) show a strikingly large gender gap in attitudes towards GM foods with women consistently more skeptical than men. However, there have been few efforts to understand the [determinants](#) of the gender gap on GM foods within the [political science](#) literature. This study employs a 2014 Pew [Research Center](#) survey on science issues to test several possible explanations for the gender gap in attitudes towards GM foods rooted in the different life experiences of women and men. The results show that while being a parent predicts more skeptical views about [genetically modified foods](#) overall it does not explain the gender gap in attitudes. In contrast, knowledge about science and having confidence in science do play a significant role in mediating the gender gap. By exploring the robust and pervasive gender gap on the issue of GM foods, this study sheds light on the fundamentally different ways men and women approach political issues.

<https://www.sciencedirect.com/science/article/abs/pii/S0362331918300260?via%3Dihub>

Rippe K.P. and Willemsen A (2018) **The Idea of Precaution: Ethical Requirements for the Regulation of New Biotechnologies in the Environmental Field.** *Front. Plant Sci.* 9:1868. | doi: 10.3389/fpls.2018.01868

The rapid emergence of new biotechnologies for selectively altering genetic material—so-called genome editing—has sparked public controversy about how their development and application in the environmental fields are to be regulated. Since the use of these new technologies harbors not only considerable potential but also risks of serious damage whose occurrence is uncertain due to their application in complex environmental systems, many national and international legal authorities are currently adhering to policies of precaution. According to critics, however, precautionary measures and the legal principle of precaution on which they are based are unduly restrictive in the case of the new biotechnologies, hindering advancements in both research and various fields of application. At the same time, legal notions of precaution are highly ambiguous within and across different national and international formulations, thereby further complicating the controversy about their implications. This paper goes beyond the concept of precaution as found in environmental law by examining the ethical significance and the ethical justification of precautionary measures in the environmental field. In particular, it clarifies the criterion of potential damage, disambiguates different types of epistemic bases in precaution decisions, and considers the relevance and implications of different ethical risk theories as to their response to epistemic uncertainty and vagueness. The two main conclusions are that, first, irrespective of the ethical risk theory embraced, there is an ethical obligation to take precautionary measures whenever serious damage is possible and the probability of damage occurring epistemically uncertain or vague. Regarding the risk assessment, it is argued that the burden of proof lies not with those who fear the occurrence of serious environmental damage. Rather, it is up to those whose actions give rise to such fears to demonstrate that serious damage is extremely improbable or scientifically absurd. Second, the moral responsibility to determine precaution situations and to specify appropriate precautionary measures is attributed not only to state authorities but also to industrial players as well as research communities. Based on these two conclusions, recommendations are given as to how the precautionary principle should be incorporated in political and legal decision-making.

<http://www.readcube.com/articles/10.3389/fpls.2018.01868>

Bogner A and Torgersen H (2018): **Precaution, Responsible Innovation and Beyond – In Search of a Sustainable Agricultural Biotechnology Policy.** *Front. Plant Sci.* 9:1884. | doi: 10.3389/fpls.2018.01884

The recent ruling by the European Court of Justice on gene edited plants highlighted regulatory inadequacy as well as a decades-old political problem, namely how to reconcile diverging expectations regarding agricultural biotechnology in Europe. Over time, regulators had tried out various tools to address concerns and overcome implementation obstacles. While initially focussing on risk (with the Precautionary Principle), they later tried to better embed technology in society (e.g., through Responsible Research and Innovation). The PP got criticized early-on; meanwhile, it seems to have lost much of its salience. Responsible Research and Innovation (RRI) is associated with problems of participation and political impact, often rendering it a public awareness tool only. We discuss problems with both approaches and conclude that also RRI falls short of facilitating technology implementation in the way regulators might have had in mind. Rather than leaving political decisions to technical risk assessment or ethics and public awareness, we argue for re-establishing a broad yet sober process of opinion formation and informed decision-making in agricultural policy.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.01884/full>

Agapito-Tenfen S.Z., Okoli A.S., Bernstein M.J., Wikmark O.-G. and Myhr AI (2018): **Revisiting Risk Governance of GM Plants: The Need to Consider New and Emerging Gene-Editing Techniques.** *Front. Plant Sci.* 9:1874. | doi: 10.3389/fpls.2018.01874

New and emerging gene-editing techniques make it possible to target specific genes in species with greater speed and specificity than previously possible. Of major relevance for plant breeding, regulators and scientists are discussing how to regulate products developed using these gene-editing techniques. Such discussions include whether to adopt or adapt the current framework for GMO risk governance in evaluating the impacts of gene-edited plants, and derived products, on the environment, human and animal health and society. Product classification or definition is one of several aspects of the current framework being criticized. Further, knowledge gaps related to risk assessments of gene-edited organisms—for example of target and off-target effects of intervention in plant genomes—are also of concern. Resolving these and related aspects of the current framework will involve addressing many subjective, value-laden positions, for example how to specify protection goals through ecosystem service approaches. A process informed by responsible research and innovation practices, involving a broader community of people, organizations, experts, and interest groups, could help scientists, regulators, and other stakeholders address these complex, value-laden concerns related to gene-editing of plants with and for society.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.01874/full>

Glandorf D.C.M. (2019): **Re-evaluation of biosafety questions on genetically modified biocontrol bacteria.** *Eur J Plant Pathol* (2019) 153:243–251 |

<https://doi.org/10.1007/s10658-018-1598-1>

Microorganisms have the potential to promote plant health and can be used to increase agricultural production that depends less on chemical control. The implementation of EU Directive 2009/128/EC, also called the Sustainable Use Directive, has led to a renewed interest in microbial biocontrol of plant diseases. Technological developments in biotechnology such as high throughput sequencing and genome editing using CRISPR/Cas open new possibilities for biocontrol applications of microorganisms. Some of these developments may involve the use of genetic modification to increase efficacy. This reopens biosafety questions posed for genetically modified microorganisms with respect to their environmental release. However, over the last decades quite some experience has been gained with genetically modified microorganisms, which could also be considered for the risk assessment of microorganisms obtained by recent techniques in biotechnology. This paper describes experience gained from risk assessment studies with genetically modified microbial biocontrol agents under field conditions. The use of this experience in addressing current biosafety questions in biotechnology is discussed.

<https://link.springer.com/article/10.1007%2Fs10658-018-1598-1> pdf-file available

Kausch A.P. et al. (2019): **Edit at Will: Genotype Independent Plant Transformation in the Era of Advanced Genomics and Genome Editing,** *Plant Science* |

<https://doi.org/10.1016/j.plantsci.2019.01.006>

The combination of advanced genomics, genome editing and plant transformation biology presents a powerful platform for basic plant research and crop improvement. Together these advances provide the tools to identify genes as targets for direct editing as single base pair changes, deletions, insertions and site specific homologous recombination. Recent breakthrough technologies using morphogenic regulators in plant transformation creates the ability to introduce reagents specific toward their identified targets and recover stably transformed and/or edited plants which are genotype independent. These technologies enable the possibility to alter a trait in any variety, without genetic disruption which would require subsequent extensive breeding, but rather to deliver the same variety with one trait changed. Regulatory issues regarding this technology will predicate how broadly these technologies will be implemented. In addition, education will play a crucial role for positive public acceptance. Taken together these technologies comprise a platform for advanced breeding which is an imperative for future world food security.

<https://www.sciencedirect.com/science/article/pii/S0168945218312056?via%3Dihub>

Jupe F., Rivkin A.C., Michael T.P., Zander M., Motley S.T., Sandoval J.P. et al. (2019): **The complex Architecture and epigenomic impact of plant T-DNA insertions.** *PLoS Genet* 15(1): e1007819. | <https://doi.org/10.1371/journal.pgen.1007819>

The bacterium *Agrobacterium tumefaciens* has been the workhorse in plant genome engineering. Customized replacement of native tumor-inducing (Ti) plasmid elements enabled insertion of a sequence of interest called Transfer-DNA (T-DNA) into any plant genome. Although these transfer mechanisms are well understood, detailed understanding of structure and epigenomic status of insertion events was limited by current technologies. Here we applied two single-molecule technologies and analyzed *Arabidopsis thaliana* lines from three widely used T-DNA insertion collections (SALK, SAIL and WISC). Optical maps for four randomly selected T-DNA lines revealed between one and seven insertions/rearrangements, and the length of individual insertions from 27 to 236 kilobases. *De novo* nanopore sequencing-based assemblies for two segregating lines partially resolved T-DNA structures and revealed multiple translocations and exchange of chromosome arm ends. For the current TAIR10 reference genome, nanopore contigs corrected 83% of non-centromeric misassemblies. The unprecedented contiguous nucleotide-level resolution enabled an in-depth study of the epigenome at T-DNA insertion sites. SALK_059379 line T-DNA insertions were enriched for 24nt small interfering RNAs (siRNA) and dense cytosine DNA methylation, resulting in transgene silencing via the RNA-directed DNA methylation pathway. In contrast, SAIL_232 line T-DNA insertions are predominantly targeted by

21/22nt siRNAs, with DNA methylation and silencing limited to a reporter, but not the resistance gene. Additionally, we profiled the H3K4me3, H3K27me3 and H2A.Z chromatin environments around T-DNA insertions using ChIP-seq in SALK_059379, SAIL_232 and five additional T-DNA lines. We discovered various effects ranging from complete loss of chromatin marks to the *de novo* incorporation of H2A.Z and trimethylation of H3K4 and H3K27 around the T-DNA integration sites. This study provides new insights into the structural impact of inserting foreign fragments into plant genomes and demonstrates the utility of state-of-the-art long-range sequencing technologies to rapidly identify unanticipated genomic changes.

<https://journals.plos.org/plosgenetics/article/file?id=10.1371/journal.pgen.1007819&type=printable>

Salk Institute

New technologies enable better-than-ever

<https://phys.org/news/2019-01-technologies-enable-better-than-ever-genetically.html#jCp>

Helen L. Hicks H.L. et al. (2018): **The factors driving evolved herbicide resistance at a national scale.** *Nature Ecology & Evolution* **2**, 529–536 | <https://doi.org/10.1038/s41559-018-0470-1>

Repeated use of xenobiotic chemicals has selected for the rapid evolution of resistance, threatening health and food security at a global scale. Strategies for preventing the evolution of resistance include cycling and mixtures of chemicals and diversification of management. We currently lack large-scale studies that evaluate the efficacy of these different strategies for minimizing the evolution of resistance. Here we use a national-scale data set of occurrence of the weed *Alopecurus myosuroides* (black-grass) in the United Kingdom to address this. Weed densities are correlated with assays of evolved resistance, supporting the hypothesis that resistance is driving weed abundance at a national scale. Resistance was correlated with the frequency of historical herbicide applications, suggesting that evolution of resistance is primarily driven by intensity of exposure to herbicides, but was unrelated directly to other cultural techniques. We find that populations resistant to one herbicide are likely to show resistance to multiple herbicide classes. Finally, we show that the economic costs of evolved resistance are considerable: loss of control through resistance can double the economic costs of weeds. This research highlights the importance of managing threats to food production and healthcare systems using an evolutionarily informed approach in a proactive not reactive manner.

<https://www.nature.com/articles/s41559-018-0470-1>

Champer J, Joan Chung J., Lee J.Y., Liu C., Yang E., Wen Z., Clark A.G., Messer P.W. (2019):

Molecular safeguarding of CRISPR gene drive experiments. *eLife* | DOI: [10.7554/eLife.41439](https://doi.org/10.7554/eLife.41439)

CRISPR-based gene drives have sparked both enthusiasm and deep concerns due to their potential for genetically altering entire species. This raises the question about our ability to prevent the unintended spread of such drives from the laboratory into a natural population. Here, we experimentally demonstrate the suitability of synthetic target sites and split drives as flexible safeguarding strategies for gene drive experiments

<https://www.biorxiv.org/content/biorxiv/early/2018/09/08/411876.full.pdf>

Packer E., eLife

Scientists demonstrate effective strategies for safeguarding CRISPR gene-drive experiments

<https://phys.org/news/2019-01-scientists-effective-strategies-safeguarding-crispr.html#jCp>

Tait-Burkard C., et- al. (2018): **Livestock 2.0 – genome editing for fitter, healthier, and more productive farmed Animals.** *Genome Biology* **19**:204 | <https://doi.org/10.1186/s13059-018-1583-1>

The human population is growing, and as a result we need to produce more food whilst reducing the impact of farming on the environment. Selective breeding and genomic selection have had a transformational impact on livestock productivity, and now transgenic and genome-editing technologies offer exciting opportunities for the production of fitter, healthier and more-productive livestock. Here, we review recent progress in the application of genome editing to farmed animal species and discuss the potential impact on our ability to produce food.

<https://genomebiology.biomedcentral.com/track/pdf/10.1186/s13059-018-1583-1>

Duke, S.O., Powles, S B., Sammons, R.D. (2018): **Glyphosate – How it Became a Once in a Hundred Year Herbicide and Its Future** . *Outlooks on Pest Management*, **29** (6), 247-251 | DOI: https://doi.org/10.1564/v29_dec_03

<https://www.ingentaconnect.com/content/resinf/opm/2018/00000029/00000006/art00003>

El-Azaz J. Cánovas F.M., Ávila C., Fernando de la Torre F. (2018): **The arogenate dehydratase ADT2 is essential for seed development in Arabidopsis.** *Plant and Cell Physiology*, **59** (12), Pages 2409–2420 | <https://doi.org/10.1093/pcp/pcy200>

Phenylalanine (Phe) biosynthesis in plants is a key process, as Phe serves as a precursor of proteins and phenylpropanoids. The prephenate pathway connects chorismate, the final product of the shikimate pathway, with the biosynthesis of Phe and tyrosine. Two alternative routes of Phe biosynthesis have been reported: one depending on arogenate, and the other on phenylpyruvate. Whereas the arogenate pathway is considered the main route, the role of the phenylpyruvate pathway remains unclear. Here, we report that a deficiency in ADT2, a bifunctional arogenate dehydratase (ADT)/prephenate dehydratase (PDT) enzyme, causes embryo

arrest and seed abortion. This result makes a clear distinction between the essential role of *ADT2* and the five remaining *ADT* genes from Arabidopsis, which display mostly overlapping functions. We have found that PHA2, a monofunctional PDT from yeast, restores the *adt2* phenotype when it is targeted within the plastids, but not when it is expressed in the cytosol. Similar results can be obtained by expressing *ADT3*, a monofunctional ADT. These results suggest that Phe can be synthesized from phenylpyruvate or arogenate when the bifunctional *ADT2* is replaced by other ADT or PDT enzymes during seed formation, highlighting the importance of Phe biosynthesis for embryo development, and providing further insights into the plasticity of Phe biosynthesis. <https://academic.oup.com/pcp/article/59/12/2409/5115989>

University of Malaga: **Researchers identify gene essential for plants to survive**
<https://phys.org/news/2019-01-gene-essential-survive.html#jCp>

Kameron Wittmeyer K. et al. (2018): **The dominant and poor penetrant phenotypes of the maize mutation Unstable factor for orange1 are caused by DNA methylation changes at a linked transposon.** *The Plant Cell*, tpc.00546. | DOI: <https://doi.org/10.1105/tpc.18.00546>

The maize mutant Unstable factor for orange1 (*Ufo1*) has been implicated in the epigenetic modifications of pericarp color1 (*p1*), which regulates the production of flavonoid pigments phlobaphenes. Here we show that the *ufo1* gene maps to a genetically recalcitrant region near the centromere on chromosome 10. Transcriptome analysis of the *Ufo1-1* mutant allele and wild type plants identified a candidate gene in the mapping region using a comparative sequence-based approach. The candidate gene, GRMZM2G053177 is overexpressed by >45-fold in multiple tissues of *Ufo1-1*. Ectopic overexpression of this gene explains the dominance of *Ufo1-1* and its phenotypes. In the mutant stock, GRMZM2G053177 has a unique transcript which originates within a CACTA transposon inserted in the first intron of the gene, and it is missing the first four codons of the wild type transcript. Expression of GRMZM2G053177 is regulated by the DNA methylation status of the CACTA transposon, explaining the incomplete penetrance and poor expressivity of *Ufo1-1*. Transgenic overexpression lines of GRMZM2G053177~ [*Ufo1-1*] phenocopy the *p1* induced pigmentation in coleoptile, tassel, leaf sheath, husk, pericarp, and cob glumes. Transcriptome analysis from *Ufo1* vs. wild type tissues show several stress induced pathways related to abiotic and biotic stress. Thus, this study addresses the enigma of *Ufo1* in maize, unsolved >50 years. <http://www.plantcell.org/content/plantcell/early/2018/12/18/tpc.18.00546.full.pdf>

Mingzhu Fan et al. **A Trihelix Family Transcription Factor Is Associated with Key Genes in Mixed-Linkage Glucan Accumulation,** *Plant Physiology* (2018). DOI: [10.1104/pp.18.00978](https://doi.org/10.1104/pp.18.00978)
<http://www.plantphysiol.org/content/178/3/1207>

Mixed-linkage glucan (MLG) is a polysaccharide that is highly abundant in grass endosperm cell walls and present at lower amounts in other tissues. Cellulose synthase-like F (CSLF) and cellulose synthase-like H genes synthesize MLG, but it is unknown if other genes participate in the production and restructuring of MLG. Using *Brachypodium distachyon* transcriptional profiling data, we identified a *B. distachyon* trihelix family transcription factor (*BdTHX1*) that is highly coexpressed with the *B. distachyon* CSLF6 gene (*BdCSLF6*), which suggests that *BdTHX1* is involved in the regulation of MLG biosynthesis. To determine the genes regulated by this transcription factor, we conducted chromatin immunoprecipitation sequencing (ChIP-seq) experiments using immature *B. distachyon* seeds and an anti-*BdTHX1* polyclonal antibody. The ChIP-seq experiment identified the second intron of *BdCSLF6* as one of the most enriched sequences. The binding of *BdTHX1* to the *BdCSLF6* intron sequence was confirmed using electrophoretic mobility shift assays (EMSA). ChIP-seq also showed that a gene encoding a grass-specific glycoside hydrolase family 16 endotransglucosylase/hydrolase (*BdXTH8*) is bound by *BdTHX1*, and the binding was confirmed by EMSA. Radio-chemical transglucanase assays showed that *BdXTH8* exhibits predominantly MLG:xyloglucan endotransglucosylase activity, a hetero-transglycosylation reaction, and can thus produce MLG-xyloglucan covalent bonds; it also has a lower xyloglucan:xylo-glucan endotransglucosylase activity. *B. distachyon* shoots regenerated from transformed calli overexpressing *BdTHX1* showed an abnormal arrangement of vascular tissue and seedling-lethal phenotypes. These results indicate that the transcription factor *BdTHX1* likely plays an important role in MLG biosynthesis and restructuring by regulating the expression of *BdCSLF6* and *BdXTH8*

<http://www.plantphysiol.org/content/plantphysiol/178/3/1207.full.pdf>

US Department of Energy: **How plants regulate sugar deposition in cell walls**
<https://phys.org/news/2019-01-sugar-deposition-cell-walls.html#jCp>

Lyons B.A. et al (2019): **Conversion messages and attitude change: Strong arguments, not costly signals.** *Public Understanding of Science*. | DOI: [10.1177/0963662518821017](https://doi.org/10.1177/0963662518821017)

A conversion narrative recounts the process that led the speaker to reject one belief for a different, usually incompatible, alternative. However, researchers know little about whether, when, and, if so, how such messages affect audience attitudes about controversial science. Using a general US population-sample experiment, we assessed the attitudinal impact of three versions of a statement by Mark Lynas, an environmental activist who converted from opposing to championing genetically modified crops. Participants were exposed to (1) a one-sided pro-genetically modified message by Lynas, (2) a two-sided pro-genetically modified message in which Lynas indicates but does not detail his conversion, or (3) a two-sided pro-genetically modified message in which Lynas explains the process that prompted his conversion. We find that his conversion messages influenced attitudes by way of perceived argument strength, but not speaker credibility. This finding implies such messages induce greater elaboration, which may lead to durable attitudes that predict behavior.

<https://journals.sagepub.com/doi/10.1177/0963662518821017>

Annenberg Public Policy Center of the University of Pennsylvania: **Can a critic-turned-believer sway others? The case of genetically modified foods**

<https://phys.org/news/2019-01-critic-turned-believer-sway-case-genetically-foods.html#jCp>

Nagashima A. et al. (2018): **Transcriptional regulators involved in responses to volatile organic compounds in plants**. *Journal of Biological Chemistry*, 2018; jbc.RA118.005843 DOI: [10.1074/jbc.RA118.005843](https://doi.org/10.1074/jbc.RA118.005843)

Field studies have shown that plants growing next to herbivore-infested plants acquire higher resistance to herbivore damage. This increased resistance is partly due to regulation of plant gene expression by volatile organic compounds (VOCs) released by plants that sense environmental challenges such as herbivores. The molecular basis for VOC sensing in plants, however, is poorly understood. Here, we report the identification of TOPLESS-like proteins (TPLs) that have VOC-binding activity and are involved in VOC sensing in tobacco. While screening for volatiles that induce stress-responsive gene expression in tobacco BY-2 cell and tobacco plants, we found that some sesquiterpenes induce the expression of stress-responsive genes. These results provided evidence that plants sense these VOCs and motivated us to analyze the mechanisms underlying volatile sensing using tobacco as a model system. Using a pull-down assay with caryophyllene derivative-linked beads, we identified TPLs as transcriptional co-repressors that bind volatile caryophyllene analogs. Overexpression of TPLs in cultured BY-2 cells or tobacco leaves reduced caryophyllene-induced gene expression, indicating that TPLs are involved in the responses to caryophyllene analogs in tobacco. We propose that unlike animals, which use membrane receptors for sensing odorants, a transcriptional co-repressor plays a role in sensing and mediating VOC signals in plant cells.

<http://www.jbc.org/content/early/2018/12/28/jbc.RA118.005843>

Ramsey S.D. et al. (2018): **"Varroa destructor feeds primarily on honey bee fat body tissue and not hemolymph."** *PNAS* | www.pnas.org/cgi/doi/10.1073/pnas.1818371116

The parasitic mite *Varroa destructor* is the greatest single driver of the global honey bee health decline. Better understanding of the association of this parasite and its host is critical to developing sustainable management practices. Our work shows that this parasite is not consuming hemolymph, as has been the accepted view, but damages host bees by consuming fat body, a tissue roughly analogous to the mammalian liver. Both hemolymph and fat body in honey bees were marked with fluorescent biostains. The fluorescence profile in the guts of mites allowed to feed on these bees was very different from that of the hemolymph of the host bee but consistently matched the fluorescence profile unique to the fat body. Via transmission electron microscopy, we observed externally digested fat body tissue in the wounds of parasitized bees. Mites in their reproductive phase were then fed a diet composed of one or both tissues. Mites fed hemolymph showed fitness metrics no different from the starved control. Mites fed fat body survived longer and produced more eggs than those fed hemolymph, suggesting that fat body is integral to their diet when feeding on brood as well. Collectively, these findings strongly suggest that *Varroa* are exploiting the fat body as their primary source of sustenance: a tissue integral to proper immune function, pesticide detoxification, overwinter survival, and several other essential processes in healthy bees. These findings underscore a need to revisit our understanding of this parasite and its impacts, both direct and indirect, on honey bee health.

<https://www.pnas.org/content/pnas/early/2019/01/08/1818371116.full.pdf>

University of Maryland: **Honey bee parasites feed on fatty organs, not blood**

<https://phys.org/news/2019-01-honey-bee-parasites-fatty-blood.html#jCp>

Wie immer wird für Hinweise und der Zusendung von Publikationen und sonstigen Informationen gedankt. pdf-Dateien können meist direkt aus den links heruntergeladen werden.

Bitte besuchen sie auch die Webseite des Wissenschaftlerkreis Grüne Gentechnik e.V. (WGG): www.wgg-ev.de.

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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