

Sunday Evening News No. 110

Week 03 (2019-01-014 – 2019-20-01)

Selected and edited by **BGF** Jany

Dear all,
this week the media focused on three topics.

1. The article by Fernbach et al. in Nature Human Behaviour on the knowledge of opponents of genetic engineering. There were 27 articles in Germany and Austria countries. Only two are listed here. Especially interesting is the one from Austria.
Fernbach et al. see below and also the reaction by GM Watch: **Are GM food opponents stupid?**

taz: **Große Klappe, nichts dahinter**

Eine psychologische Studie zeigt: Erbitterte Gentechnik-Feinde sind nicht nur häufig ignorant, sondern überschätzen auch ihr Wissen
<http://www.taz.de/!5563219/>

Der Standard: **Warum viele radikale Gentechnikgegner ahnungslos sind**

Befragungen von rund 2.500 Personen zeigten eindeutige Zusammenhänge
<https://www.derstandard.de/story/2000096211137/erbittertegentechnik-gegner-wissen-viel-weniger-ueber-gentechnik-also-sie-glauben>

2. The ban on the use of glyphosate / Roundup-Pro-360 in France.

<http://lyon.tribunal-administratif.fr/A-savoir/Communiqués/Annulation-de-l-autorisation-de-mise-sur-le-marche-du-Roundup-Pro-360>

https://www.lepoint.fr/economie/glyphosate-le-roundup-pro-360-interdit-en-france-par-la-justice-15-01-2019-2286066_28.php#xtmc=roundup&xtnp=1&xtr=1

3. The risk assessment of glyphosate by the Federal Institute for Risk Assessment (BfR), Berlin

The Guardian: **EU glyphosate approval was based on plagiarised Monsanto text, report finds**

Study for European parliament 'explains why EU assessors brushed off warnings of pesticide's dangers', says MEP

<https://www.theguardian.com/environment/2019/jan/15/eu-glyphosate-approval-was-based-on-plagiarised-monsanto-text-report-finds>

RT-deutsch: **Plagiat-Experte: Glyphosat-Gutachten der EU wurde wortwörtlich bei Monsanto abgeschrieben**

<https://deutsch.rt.com/europa/82592-plagiat-experte-glyphosat-gutachten-wurde-wortwoertlich-von-monsanto-abgeschrieben/>

BfR-reply

https://www.bfr.bund.de/en/press_information/2019/02/european_assessment_of_glyphosate_is_quality_assured_and_independent_industry_reports_are_routinely_part_of_assessment_reports-239502.html

National Academies of Sciences, Engineering, and Medicine. 2019. **Forest Health and Biotechnology: Possibilities and Considerations**. Washington, DC: The National Academies Press. <https://doi.org/10.17226/25221>.

<https://www.nap.edu/catalog/25221/forest-health-and-biotechnology-possibilities-and-considerations>
<http://www8.nationalacademies.org/onpinews/newsitem.aspx?RecordID=25221>

John Innes Centre: **Application for Field Trial of Genetically Modified Organisms: High Iron Wheat and CRISPR Brassica**

<https://www.jic.ac.uk/news/application-field-trial-2019/>

GM-Watch: **A YEAR IN REVIEW: GMO industry suffers major setbacks**

Part 1: Landmark victories leave agrochemical giants reeling

<https://www.gmwatch.org/en/news/latest-news/18697-a-year-in-review-part-1-gmo-industry-suffers-major-setbacks>

International Green Week 2019, Berlin, IGW (Grüne Woche 2019)

IGW is a one-of-a-kind international exhibition of the food, agriculture and gardening industries.

Bio-Oekonomierat: **Genome Editing: Europa benötigt ein neues Gentechnikrecht**

http://biooekonomierat.de/fileadmin/Publikationen/berichte/BOERMEMO_07_final.pdf

Grain Club: **Grain Club auf Internationaler Grüner Woche Politik muss Gentechnikrecht modernisieren**

<https://www.presseportal.de/pm/105718/4168842>

Schirmacher H.: **„Wir fordern ein neues Regelwerk“**

<https://www.agrarzeitung.de/nachrichten/politik/gentechnik-wir-fordern-ein-neues-regelwerk-85848?crefresh=1>

Struck J.: **Gentechnikrecht muss überarbeitet werden**

<https://www.agrarzeitung.de/nachrichten/politik/pflanzenzucht-gentechnikrecht-muss-ueberarbeitet-werden-85873>

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

Fernbach P.M., Light N., Scott S.E., Inbar Y. & Paul Rozin P. (2019): **Extreme opponents of genetically modified foods know the least but think they know the most.** *Nature Human Behaviour*; DOI: [10.1038/s41562-018-0520-3](https://doi.org/10.1038/s41562-018-0520-3), <https://www.nature.com/articles/s41562-018-0520-3>

There is widespread agreement among scientists that genetically modified foods are safe to consume^{1,2} and have the potential to provide substantial benefits to humankind³. However, many people still harbour concerns about them or oppose their use^{4,5}. In a nationally representative sample of US adults, we find that as extremity of opposition to and concern about genetically modified foods increases, objective knowledge about science and genetics decreases, but perceived understanding of genetically modified foods increases. Extreme opponents know the least, but think they know the most. Moreover, the relationship between self-assessed and objective knowledge shifts from positive to negative at high levels of opposition. Similar results were obtained in a parallel study with representative samples from the United States, France and Germany, and in a study testing attitudes about a medical application of genetic engineering technology (gene therapy). This pattern did not emerge, however, for attitudes and beliefs about climate change.

<https://www.nature.com/articles/s41562-018-0520-3> pdf-file available

https://www.nature.com/articles/s41562-018-0520-3.epdf?referrer_access_token=RFjditi7HYesvrvwSfy7WBNRgN0jAJWeI9jnR3Z0Tv0NCPz-KWDa8SCyuAJLdVClz2ISGO2G0jLidVKBpsJP90X2Ze37IY_xhfvHFGWhgca7-UUoLH8Er9QHZ1CAPto2KNm_6yHitVA7JoMwkFX67jagDT6LOxDcf5R94xfGsFn9rb74grZguv1-C6w0G_wphryx0Y-zz37VqkBrTBO8QRtlRX45e25C4ziQfKkY3I-QRQ7dGOesfzPI8hqNhCAXvgYjoy0xP1rza8bv3oTisk1EXTue9-N7zObnbXDJ6CPop_7JLgQOZiC172bxfCBr&tracking_referrer=www.theguardian.com

<https://www.nature.com/articles/s41562-018-0520-3> pdf-file available

<https://www.nature.com/articles/s41562-018-0520-3> pdf-file available

University of Colorado at Boulder

Genetically modified food opponents know less than they think, research finds

Read more at: <https://phys.org/news/2019-01-genetically-food-opponents.html#jCp>

Reaction of GM Watch: **Are GM food opponents stupid?**

<https://www.gmwatch.org/en/news/latest-news/18711>

Critchley C., Nicol D., Bruce G., Walshe J., Treleaven T. and Tuch B. (2019) **Predicting Public Attitudes Toward Gene Editing of Germlines: The Impact of Moral and Hereditary Concern in Human and Animal Applications.** *Front. Genet.* 9:704. doi: [10.3389/fgene.2018.00704](https://doi.org/10.3389/fgene.2018.00704)

Background and Objective: New and more efficient methods of gene editing have intensified the ethical and legal issues associated with editing germlines. Yet no research has separated the impact of hereditary concern on public attitudes from moral concern. This research compares the impact these two concerns have on public attitudes across five applications including, the prevention of human disease, human and animal research, animals for the use of human food and the enhancement of human appearance. Methods: A sample of 1004 Australians responded to either a telephone ($n = 501$; randomly selected) or online survey ($n = 503$; sourced by Qualtrics). Both samples were representative in terms of States and Territories as well as gender (51% female), though the online sample was younger ($M = 40.64$, $SD = 16.98$; Range = 18–87) than the telephone sample ($M = 54.79$, $SD = 18.13$; Range = 18–96). A 5 (application) by 3 (type of cell) within groups design was utilized, where all respondents reported their level of approval with scientists editing genes across the 15 different contexts. Multilevel modeling was used to examine the impact of moral (embryo vs. germ) and hereditary (germ vs. somatic) concern on attitudes across all applications. Results: Australians were comfortable with editing human and animal embryos, but only for research purposes and to enhance human health. The effect of moral concern was stronger than hereditary concern, existing in all applications except for the use of animals for human purposes. Hereditary concern was only found to influence attitudes in two applications: improving

human health and human research. Moral concern was found to be accentuated amongst, women, more religious individuals and those identifying as Australian, while hereditary concern was strongest amongst non-Australians, those with stronger trust in scientists, and more religious respondents. Conclusion: Moral and hereditary concerns are distinct, and require different approaches to public education, engagement and possibly regulation. Further research needs to explore hereditary concern in relation to non-human applications, and the reasons underlying cultural and gender differences

Benbrook, C.M. (2019): How did the US EPA and IARC reach diametrically opposed conclusions on the genotoxicity of glyphosate-based herbicides? *Environ Sci Eur* (2019) 31: 2. <https://doi.org/10.1186/s12302-018-0184-7>

Background

The US EPA considers glyphosate as “not likely to be carcinogenic to humans.” The International Agency for Research on Cancer (IARC) has classified glyphosate as “probably carcinogenic to humans (Group 2A).” EPA asserts that there is no convincing evidence that “glyphosate induces mutations in vivo via the oral route.” IARC concludes there is “strong evidence” that exposure to glyphosate is genotoxic through at least two mechanisms known to be associated with human carcinogens (DNA damage, oxidative stress). Why and how did EPA and IARC reach such different conclusions?

Results

A total of 52 genotoxicity assays done by registrants were cited by the EPA in its 2016 evaluation of technical glyphosate, and another 52 assays appeared in the public literature. Of these, one regulatory assay (2%) and 35 published assays (67%) reported positive evidence of a genotoxic response. In the case of formulated, glyphosate-based herbicides (GBHs), 43 regulatory assays were cited by EPA, plus 65 assays published in peer-reviewed journals. Of these, none of the regulatory, and 49 published assays (75%) reported evidence of a genotoxic response following exposure to a GBH. IARC considered a total of 118 genotoxicity assays in six core tables on glyphosate technical, GBHs, and aminomethylphosphonic acid (AMPA), glyphosate’s primary metabolite. EPA’s analysis encompassed 51 of these 118 assays (43%). In addition, IARC analyzed another 81 assays exploring other possible genotoxic mechanisms (mostly related to sex hormones and oxidative stress), of which 62 (77%) reported positive results. IARC placed considerable weight on three positive GBH studies in exposed human populations, whereas EPA placed little or no weight on them.

Conclusions

EPA and IARC reached diametrically opposed conclusions on glyphosate genotoxicity for three primary reasons: (1) in the core tables compiled by EPA and IARC, the EPA relied mostly on registrant-commissioned, unpublished regulatory studies, 99% of which were negative, while IARC relied mostly on peer-reviewed studies of which 70% were positive (83 of 118); (2) EPA’s evaluation was largely based on data from studies on technical glyphosate, whereas IARC’s review placed heavy weight on the results of formulated GBH and AMPA assays; (3) EPA’s evaluation was focused on typical, general population dietary exposures assuming legal, food-crop uses, and did not take into account, nor address generally higher occupational exposures and risks. IARC’s assessment encompassed data from typical dietary, occupational, and elevated exposure scenarios. More research is needed on real-world exposures to the chemicals within formulated GBHs and the biological fate and consequences of such exposures.

<https://link.springer.com/article/10.1186%2Fs12302-018-0184-7>

<https://link.springer.com/content/pdf/10.1186%2Fs12302-018-0184-7.pdf>

Custers R, Casacuberta JM, Eriksson D, Sági L and Schiemann J (2019) Genetic Alterations That Do or o Not Occur Naturally; Consequences for Genome Edited Organisms in the Context of Regulatory Oversight. *Front. Bioeng. Biotechnol.* 6: 213.

<https://doi.org/10.3389/fbioe.2018.00213>

The ability to successfully exploit genome edited organisms for the benefit of food security and the environment will essentially be determined by the extent to which these organisms fall under specific regulatory provisions. In many jurisdictions the answer to this question is considered to depend on the genetic characteristics of the edited organism, and whether the changes introduced in its genome do (or do not) occur naturally. We provide here a number of key considerations to assist with this evaluation as well as a guide of concrete examples of genetic alterations with an assessment of their natural occurrence. These examples support the conclusion that for many of the common types of alterations introduced by means of genome editing, the resulting organisms would not be subject to specific biosafety regulatory provisions whenever novelty of the genetic combination is a crucial determinant.

<https://www.frontiersin.org/articles/10.3389/fbioe.2018.00213/full>

Metje-Sprink J, Menz J, Modrzejewski D and Sprink T (2019): DNA-Free Genome Editing: Past, Present and Future. *Front. Plant Sci.* 9:1957. <https://doi.org/10.3389/fpls.2018.01957>

Genome Editing using engineered endonuclease (GEEN) systems rapidly took over the field of plant science and plant breeding. So far, Genome Editing techniques have been applied in more than fifty different plants; including model species like *Arabidopsis*; main crops like rice, maize or wheat as well as economically less important crops like strawberry, peanut and cucumber. These techniques have been used for basic research as proof-of-concept or to investigate gene functions in most of its applications. However, several market-oriented traits have been addressed including enhanced agronomic characteristics, improved food and feed quality, increased tolerance to abiotic and biotic stress and herbicide tolerance. These technologies are evolving at a tearing pace and especially the field of CRISPR based Genome Editing is advancing incredibly fast. CRISPR-

Systems derived from a multitude of bacterial species are being used for targeted Gene Editing and many modifications have already been applied to the existing CRISPR-Systems such as (i) alter their protospacer adjacent motif (ii) increase their specificity (iii) alter their ability to cut DNA and (iv) fuse them with additional proteins. Besides, the classical transformation system using *Agrobacteria tumefaciens* or *Rhizobium rhizogenes*, other transformation technologies have become available and additional methods are on its way to the plant sector. Some of them are utilizing solely proteins or protein-RNA complexes for transformation, making it possible to alter the genome without the use of recombinant DNA. Due to this, it is impossible that foreign DNA is being incorporated into the host genome. In this review we will present the recent developments and techniques in the field of DNA-free Genome Editing, its advantages and pitfalls and give a perspective on technologies which might be available in the future for targeted Genome Editing in plants. Furthermore, we will discuss these techniques in the light of existing– and potential future regulations.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.01957/full>

Eriksson D., Kershen D., Nepomuceno A., Pogson B.J., Prieto H., Purnhagen K., Smyth S, Wesseler J., Whelan A. (2019): **A comparison of the EU regulatory approach to directed mutagenesis with that of other jurisdictions, consequences for international trade and potential steps forward.** *New Phytol.* ;doi: 10.1111/nph.15627

A special regulatory regime applies to products of recombinant nucleic acid modifications. A ruling from the European Court of Justice has interpreted this regulatory regime in a way that it also applies to emerging mutagenesis techniques. Elsewhere regulatory progress is also ongoing. In 2015, Argentina launched a regulatory framework, followed by Chile in 2017 and recently Brazil and Colombia. In March 2018, the USDA announced that it will not regulate genome-edited plants differently if they could have also been developed through traditional breeding. Canada has an altogether different approach with their Plants with Novel Traits regulations. Australia is currently reviewing its Gene Technology Act. This article illustrates the deviation of the European Union's (EU's) approach from the one of most of the other countries studied here. Whereas the EU does not implement a case-by-case approach, this approach is taken by several other jurisdictions. Also, the EU court ruling adheres to a process-based approach while most other countries have a stronger emphasis on the regulation of the resulting product. It is concluded that, unless a functioning identity preservation system for products of directed mutagenesis can be established, the deviation results in a risk of asynchronous approvals and disruptions in international trade

<https://nph.onlinelibrary.wiley.com/doi/epdf/10.1111/nph.15627>

Shen B-R. et al. (2018): **Engineering a New Chloroplastic Photorespiratory Bypass to Increase Photosynthetic Efficiency and Productivity in Rice.** *Molecular Plant* (2018); <https://doi.org/10.1016/j.molp.2018.11.013>

Over the past few years, three photorespiratory bypasses have been introduced into plants, two of which led to observable increases in photosynthesis and biomass yield. However, most of the experiments were carried out using *Arabidopsis* under controlled environmental conditions, and the increases were only observed under low-light and short-day conditions. In this study, we designed a new photorespiratory bypass (called GOC bypass), characterized by no reducing equivalents being produced during a complete oxidation of glycolate into CO₂ catalyzed by three rice-self-originating enzymes, i.e., glycolate oxidase, oxalate oxidase, and catalase. We successfully established this bypass in rice chloroplasts using a multi-gene assembly and transformation system. Transgenic rice plants carrying GOC bypass (GOC plants) showed significant increases in photosynthesis efficiency, biomass yield, and nitrogen content, as well as several other CO₂-enriched phenotypes under both greenhouse and field conditions. Grain yield of GOC plants varied depending on seeding season and was increased significantly in the spring. We further demonstrated that GOC plants had significant advantages under high-light conditions and that the improvements in GOC plants resulted primarily from a photosynthetic CO₂-concentrating effect rather than from improved energy balance. Taken together, our results reveal that engineering a newly designed chloroplastic photorespiratory bypass could increase photosynthetic efficiency and yield of rice plants grown in field conditions, particularly under high light.

<https://www.cell.com/action/showPdf?pii=S1674-2052%2818%2930370-8>

Li. Z. et al. (2019): **Responses of soil enzymatic activities to transgenic *Bacillus thuringiensis* (Bt) crops - A global meta-analysis.** *Science of The Total Environment* 651 (2), 1830-1838 <https://doi.org/10.1016/j.scitotenv.2018.10.073>

Transgenic *Bacillus thuringiensis* (Bt) crops have been widely planted, and the resulting [environmental risks](#) have attracted extensive attention. To foresee the impacts of Bt crops on soil quality, it is essential to understand how Bt crops alter the soil enzymatic activities and what the important influencing factors are. We compiled data from 41 published papers that studied soil enzymatic activities with Bt crops and their non-Bt counterparts. The results showed that [dehydrogenase](#) and urease significantly increased, but neutral [phosphatase](#) significantly decreased under Bt crop cultivations without Bt residues incorporation. The activities of dehydrogenase, β -glucosidase, urease, nitrate reductase, alkaline phosphatase, and aryl sulfatase significantly increased under Bt crop cultivation with Bt residues incorporation. The response ratios of other enzymes were not significantly changed. Generally, the response ratios of soil enzymes were greater with Bt residues incorporation than those of Bt crop cultivations without Bt residues incorporation. Further, the response ratios of soil enzymes varied with Bt crop types and growth periods. It was the strongest under Bt cotton among Bt crops, and the significant responses usually appeared in the middle growth stages. The responses of soil enzymes ascribed more to the properties of Bt crops than to [soil properties](#) across sites. Given - significant responses of some soil enzymes to Bt crops, we recommended that [soil environmental risks](#) should be carefully evaluated over the transgenic crops.

<https://www.sciencedirect.com/science/article/pii/S0048969718339469>

Bao Z. et al. (2018): **Genome-scale engineering of *Saccharomyces cerevisiae* with single-nucleotide precision**. *Nature Biotechnology* **36**, 505–508 (). DOI: [10.1038/nbt.4132](https://doi.org/10.1038/nbt.4132)

We developed a CRISPR–Cas9- and homology-directed-repair-assisted genome-scale engineering method named CHAnGE that can rapidly output tens of thousands of specific genetic variants in yeast. More than 98% of target sequences were efficiently edited with an average frequency of 82%. We validate the single-nucleotide resolution genome-editing capability of this technology by creating a genome-wide gene disruption collection and apply our method to improve tolerance to growth inhibitors.

<https://www.nature.com/articles/nbt.4132>

Peters J. M. et al. (2019): **Enabling genetic analysis of diverse bacteria with Mobile-CRISPRi**. *Nature Microbiology*, 2019; DOI: [10.1038/s41564-018-0327-z](https://doi.org/10.1038/s41564-018-0327-z)

The vast majority of bacteria, including human pathogens and microbiome species, lack genetic tools needed to systematically associate genes with phenotypes. This is the major impediment to understanding the fundamental contributions of genes and gene networks to bacterial physiology and human health. Clustered regularly interspaced short palindromic repeats interference (CRISPRi), a versatile method of blocking gene expression using a catalytically inactive Cas9 protein (dCas9) and programmable single guide RNAs, has emerged as a powerful genetic tool to dissect the functions of essential and non-essential genes in species ranging from bacteria to humans^{1,2,3,4,5,6}. However, the difficulty of establishing effective CRISPRi systems across bacteria is a major barrier to its widespread use to dissect bacterial gene function. Here, we establish ‘Mobile-CRISPRi’, a suite of CRISPRi systems that combines modularity, stable genomic integration and ease of transfer to diverse bacteria by conjugation. Focusing predominantly on human pathogens associated with antibiotic resistance, we demonstrate the efficacy of Mobile-CRISPRi in gammaproteobacteria and Bacillales Firmicutes at the individual gene scale, by examining drug–gene synergies, and at the library scale, by systematically phenotyping conditionally essential genes involved in amino acid biosynthesis. Mobile-CRISPRi enables genetic dissection of non-model bacteria, facilitating analyses of microbiome function, antibiotic resistances and sensitivities, and comprehensive screens for host–microorganism interactions.

<https://www.nature.com/articles/s41564-018-0327-z>

David J. Krause et al. (2018): Functional and evolutionary characterization of a secondary metabolite gene cluster in budding yeasts, *Proceedings of the National Academy of Sciences* (115 (43) 11030-11035. <https://doi.org/10.1073/pnas.1806268115>

Secondary metabolites are key in how organisms from all domains of life interact with their environment and each other. The iron-binding molecule pulcherrimin was described a century ago, but the genes responsible for its production in budding yeasts have remained uncharacterized. Here, we used phylogenomic footprinting on 90 genomes across the budding yeast subphylum Saccharomycotina to identify the gene cluster associated with pulcherrimin production. Using targeted gene replacements in *Kluyveromyces lactis*, we characterized the four genes that make up the cluster, which likely encode two pulcherriminic acid biosynthesis enzymes, a pulcherrimin transporter, and a transcription factor involved in both biosynthesis and transport. The requirement of a functional putative transporter to utilize extracellular pulcherrimin-complexed iron demonstrates that pulcherriminic acid is a siderophore, a chelator that binds iron outside the cell for subsequent uptake. Surprisingly, we identified homologs of the putative transporter and transcription factor genes in multiple yeast genera that lacked the biosynthesis genes and could not make pulcherrimin, including the model yeast *Saccharomyces cerevisiae*. We deleted these previously uncharacterized genes and showed they are also required for pulcherrimin utilization in *S. cerevisiae*, raising the possibility that other genes of unknown function are linked to secondary metabolism. Phylogenetic analyses of this gene cluster suggest that pulcherrimin biosynthesis and utilization were ancestral to budding yeasts, but the biosynthesis genes and, subsequently, the utilization genes, were lost in many lineages, mirroring other microbial public goods systems that lead to the rise of cheater organisms.

US Department of Energy

Scientists identify gene cluster in budding yeasts with major implications for renewable energy

<https://phys.org/news/2019-01-scientists-gene-cluster-budding-yeasts.html#jCp>

EFSA (European Food Safety Authority), Hart A, Maxim L, Siegrist M, Von Goetz N, da Cruz C, Merten C, Mosbach-Schulz O, Lahaniatis M, Smith A and Hardy A, 2019. **Guidance on Communication of Uncertainty in Scientific Assessments**. EFSA Journal 2019;17(1):5520, 73 pp. <https://doi.org/10.2903/j.efsa.2019.5520>

This document provides guidance for communicators on how to communicate the various expressions of uncertainty described in EFSA's document: ‘Guidance on uncertainty analysis in scientific assessments’. It also contains specific guidance for assessors on how best to report the various expressions of uncertainty. The document provides a template for identifying expressions of uncertainty in scientific assessments and locating the specific guidance for each expression. The guidance is structured according to EFSA's three broadly defined categories of target audience: ‘entry’, ‘informed’ and ‘technical’ levels. Communicators should use the guidance for entry and informed audiences, while assessors should use the guidance for the technical level. The guidance was formulated using evidence from the scientific literature, grey literature and two EFSA research

studies, or based on judgement and reasoning where evidence was incomplete or missing. The limitations of the evidence sources inform the recommendations for further research on uncertainty communication <https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2019.5520>

Nawaz M.A. et al. (2019): Addressing concerns over the fate of DNA derived from genetically modified food in the human body: A review. Food and Chemical Toxicology 124,423-430, doi: 10.1016/j.fct.2018.12.030.

Global commercialization of GM food and feed has stimulated much debate over the fate of GM food-derived DNA in the body of the consumer and as to whether it poses any health risks. We reviewed the fate of DNA derived from GM food in the human body. During mechanical/chemical processing, integrity of DNA is compromised. Food-DNA can survive harsh processing and digestive conditions with fragments up to a few hundred bp detectable in the gastrointestinal tract. Compelling evidence supported the presence of food (also GM food) derived DNA in the blood and tissues of human/animal. There is limited evidence of food-born DNA integrating into the genome of the consumer and of horizontal transfer of GM crop DNA into gut-bacteria. We find no evidence that transgenes in GM crop-derived foods have a greater propensity for uptake and integration than the host DNA of the plant-food. We found no evidence of plant-food DNA function/expression following transfer to either the gut-bacteria or somatic cells. Strong evidence suggested that plant-food-miRNAs can survive digestion, enter the body and affect gene expression patterns. We envisage that this multi-dimensional review will address questions regarding the fate of GM food-derived DNA and gene-regulatory-RNA in the human body.

<https://www.sciencedirect.com/science/article/pii/S0278691518309037?via%3Dihub>

Gupta R.S., Warren C.M., Bridget M., Smith B.M., et al. (2019): Prevalence and Severity of Food Allergies Among US Adults. JAMA Netw Open. 2019;2(1): e185630; doi:10.1001/jamanetworkopen.2018.5630

Question: What are the prevalence and severity of food allergy in US adults?

Findings: In a population-based survey study of 40 443 US adults, an estimated 10.8% were food allergic at the time of the survey, whereas nearly 19% of adults believed that they were food allergic. Nearly half of food-allergic adults had at least 1 adult-onset food allergy, and 38% reported at least 1 food allergy-related emergency department visit in their lifetime.

Meaning: The findings suggest that food allergies are common and severe among US adults, often starting in adulthood.

<https://jamanetwork.com/journals/jamanetworkopen/fullarticle/2720064>

Meeting

Professor Niggli am 15.3. in Berlin: "**Gentechnik & Ökolandwirtschaft – Warum nicht?**" // HU-Veranstaltungsreihe „Wissenschaft im Sauriersaal“

<https://www.hu-berlin.de/de/foerdern/was/projekte/presentation/wissenschaft-im-sauriersaal>

Deutsche Biotechnologietage 2019

9. und 10. April in Würzburg

<https://www.biotechnologietage.de/de/>

13 / 14 May 2019: 8th INTERNATIONAL BIOECONOMY CONFERENCE at Halle (Germany)

<https://www.bioeconomy-conference.de/startseite/>

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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