

Sunday Evening News

Week 08 (2018-02-19 / 02-25)

Selected and edited by **BGF** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,
hier eine Auswahl von Pressemeldungen und Medienberichten. Aber wie immer alle Beiträge
<https://www.biotech-gm-food.com/presse>

Dear all,

Here a selection of press releases and media reports. But as always, all selected contributions are available: <https://www.biotech-gm-food.com/presse>

Golden Rice gazetted in Au and NZ - now approved for sale

Goldener Reis in Au und NZ - jetzt zum Verkauf zugelassen

<http://www.foodstandards.gov.au/code/changes/gazette/Pages/AmendmentNo177.aspx>

Kuntz M. – European Scientist:

Are Sciences and Economics Outdated? Or rather plagued by ideology?

<https://www.europeanscientist.com/en/features/european-sciences-economics-outdated-rather-plagued-ideology/>

Consumer and Society

Campaigners try to politicize European decision-making

<http://consumerandsociety.com/2018/02/22/campaigners-try-politicize-european-decision-making/>

Regalado A., Wünnenberg I. – Technology Review

Gesunde Gentechnik?

Per Gen-Editing entwickeln Biotech-Firmen neue Pflanzen-Sorten, die gesünder und nahrhafter sein sollen.

Dieses Jahr könnten die ersten Lebensmittel daraus auf dem Teller landen.

<https://www.heise.de/tr/artikel/Gesunde-Gentechnik-3966578.html>

Fisser D.

Interview mit BfR-Präsident Hensel Risikoforscher: Darum haben Deutsche so viel Angst vor Glyphosat

<https://www.noz.de/deutschland-welt/politik/artikel/1023042/risikoforscher-darum-haben-deutsche-so-viel-angst-vor-glyphosat>

Pestizide jetzt wirksam reduzieren – Bündnis90/Die Grünen (only in German)

<http://dip21.bundestag.de/dip21/btd/19/008/1900835.pdf>

EFSA

Climate change and food safety – complete the EFSA survey

The [survey is online](#) until the 7 March and takes less than 10 minutes to complete.

<https://www.efsa.europa.eu/en/press/news/180221>

16.01.2016 SCoPAFF: Maize 59122 and MON87427xMON89034xNK603, maize 59122,
Vote taken “no opinion”

https://ec.europa.eu/food/sites/food/files/plant/docs/sc_modif-genet_20180116_sum.pdf

26.02. 2018 Appeal Committee: Genetically Modified Food and Feed and Environmental Risk; On the Agenda: Maize 59122 and MON87427xMON89034xNK603

https://ec.europa.eu/food/committees/appeal/gmffer_en

Result? Probably as usually “no opinion”

Scientific literature

Tagliabue G., Kuntz M., Miller H.I., and Ammann K. (2018): **A Plea for the Renewal of the ISBR.** *Trends in Biotechnology*, 36(3), 229-231
www.sciencedirect.com/science/article/pii/S0167779917302834 pdf-file available

Urnov F.D. (2018): **Genome Editing B.C. (Before CRISPR): Lasting Lessons from the “Old Testament”** *The CRISPR Journal* 1, (1); DOI: 10.1089/crispr.2018.29007.fyu
Genome editing with engineered nucleases, a powerful tool for understanding biological function and revealing causality, was built in a joint effort by academia and industry in 1994–2010. Use of CRISPR-Cas9 is the most recent (2013–), and facile, implementation of the resulting editing toolbox. Principles and methods of genome editing from the pre-CRISPR era remain relevant and continue to be useful.
<http://online.liebertpub.com/doi/pdf/10.1089/crispr.2018.29007.fyu>

Jon Cohen J. (2018): **Genome editor CRISPR’s latest trick? Offering a sharper snapshot of activity inside the cell.** *Science*
<http://www.sciencemag.org/news/2018/02/genome-editor-crispr-s-latest-trick-offering-sharper-snapshot-activity-inside-cell>

Ledford H. (2018): **CRISPR hack transforms cells into data recorders**
Gene-editing tool can be harnessed to give a close-up view of life's most basic processes.
Nature 554, 414;
<https://www.nature.com/magazine-assets/d41586-018-02068-0/d41586-018-02068-0.pdf>

Tang W., Liu D.R. (2018): **Rewritable multi-event analog recording in bacterial and mammalian cells.** *Science* 10.1126/science.aap8992
We present two CRISPR-mediated analog multi-event recording apparatus (CAMERA) systems that use base editors and Cas9 nucleases to record cellular events in bacteria and mammalian cells. The devices record signal amplitude or duration as changes in the ratio of mutually exclusive DNA sequences (CAMERA 1), or as single-base modifications (CAMERA 2). We achieved recording of multiple stimuli in bacteria or mammalian cells, including exposure to antibiotics, nutrients, viruses, light, and changes in Wnt signaling. When recording to multi-copy plasmids, reliable readout requires as few as 10-100 cells. The order of stimuli can be recorded through an overlapping guide RNA design and memories can be erased and re-recorded over multiple cycles. CAMERA systems serve as “cell data recorders” that write a history of endogenous or exogenous signaling events into permanent DNA sequence modifications in living cells.
<http://science.sciencemag.org/content/early/2018/02/14/science.aap8992.long> pdf-file available

Madrid J.L.C. et al. (2018): **Transportability of non-target arthropod field data for the use in environmental risk assessment of genetically modified maize in Northern Mexico.** *J Appl Entomol.* 2018;1–14; DOI: 10.1111/jen.12499
In country, non-target arthropod (NTA) field evaluations are required to comply with the regulatory process for cultivation of genetically modified (GM) maize in Mexico. Two sets of field trials, Experimental Phase and Pilot Phase, were conducted to identify any potential harm of insect-protected and glyphosate-tolerant maize (MON-89Ø34-3× MON-88Ø17-3 and MON-89Ø34-3 × MON-Ø6Ø3-6) and glyphosate tolerant maize (MON-ØØ6Ø3-6) to local NTAs compared to conventional maize. NTA abundance data were collected at 32 sites, providing high geographic and environmental diversity within maize production areas from four ecological regions (ecoregions) in northern Mexico. The most abundant herbivorous taxa collected included field crickets, corn flea beetles, rootworm beetles, cornsilk flies, aphids, leafhoppers, plant bugs and thrips while the most abundant beneficial taxa captured were soil mites, spiders, predatory ground beetles, rove beetles, springtails (Collembola), predatory earwigs, ladybird beetles, syrphid flies, tachinid flies, minute pirate bugs, parasitic wasps and lacewings. Across the taxa analysed, no statistically significant differences in abundance were detected between GM maize and the conventional maize control for 69 of the 74 comparisons (93.2%) indicating that the single or stacked insect-protected and herbicide-tolerant GM traits generally exert no marked adverse effects on the arthropod populations compared with conventional maize. The distribution of taxa observed in this study provides evidence that irrespective of variations in overall biodiversity of a given ecoregion, important herbivore, predatory and parasitic arthropod taxa within the commercial maize agroecosystem are highly similar indicating that relevant data generated in one ecoregion can be transportable for the risk assessment of the same or similar GM crop in another ecoregion.
<http://onlinelibrary.wiley.com/doi/10.1111/jen.12499/epdf>

Alsaïari S.K. et al. (2018): **Endosomal Escape and Delivery of CRISPR/Cas9 Genome Editing Machinery Enabled by Nanoscale Zeolitic Imidazolate Framework.** *J. Am. Chem. Soc.*, 2018, 140 (1), pp 143–146, DOI: 10.1021/jacs.7b11754

CRISPR/Cas9 is a combined protein (Cas9) and an engineered single guide RNA (sgRNA) genome editing platform that offers revolutionary solutions to genetic diseases. It has, however, a double delivery problem owing to the large protein size and the highly charged RNA component. In this work, we report the first example of CRISPR/Cas9 encapsulated by nanoscale zeolitic imidazole frameworks (ZIFs) with a loading efficiency of 17% and enhanced endosomal escape promoted by the protonated imidazole moieties. The gene editing potential of CRISPR/Cas9 encapsulated by ZIF-8 (CC-ZIFs) is further verified by knocking down the gene expression of green fluorescent protein by 37% over 4 days. The nanoscale CC-ZIFs are biocompatible and easily scaled-up offering excellent loading capacity and controlled codelivery of intact Cas9 protein and sgRNA.

<https://pubs.acs.org/doi/pdf/10.1021/jacs.7b11754>

King Abdullah University of Science and Technology

A delivery platform for gene-editing technology

<https://phys.org/news/2018-02-delivery-platform-gene-editing-technology.html#jCp>

Paul M.J., Michael L. Nuccio M.L., and Basu S.S. (2018): **Are GM Crops for Yield and Resilience Possible?** *Trends in Plant Science* 23, (1)

<http://dx.doi.org/10.1016/j.tplants.2017.09.007>

Crop yield improvements need to accelerate to avoid future food insecurity. Outside Europe, genetically modified (GM) crops for herbicide- and insect-resistance have been transformative in agriculture; other traits have also come to market. However, GM of yield potential and stress resilience has yet to impact on food security. Genes have been identified for yield such as grain number, size, leaf growth, resource allocation, and signaling for drought tolerance, but there is only one commercialized drought-tolerant GM variety. For GM and genome editing to impact on yield and resilience there is a need to understand yield-determining processes in a cell and developmental context combined with evaluation in the grower environment. We highlight a sugar signaling mechanism as a paradigm for this approach.

[http://www.cell.com/trends/plant-science/pdf/S1360-1385\(17\)30203-0.pdf](http://www.cell.com/trends/plant-science/pdf/S1360-1385(17)30203-0.pdf)

Zhu G. et al. (2018): **Rewiring of the Fruit Metabolome in Tomato Breeding.**

Cell, Volume 172, Issue 1, 249 - 261.e12. DOI: <http://dx.doi.org/10.1016/j.cell.2017.12.019>

Humans heavily rely on dozens of domesticated plant species that have been further improved through intensive breeding. To evaluate how breeding changed the tomato fruit metabolome, we have generated and analyzed a dataset encompassing genomes, transcriptomes, and metabolomes from hundreds of tomato genotypes. The combined results illustrate how breeding globally altered fruit metabolite content. Selection for alleles of genes associated with larger fruits altered metabolite profiles as a consequence of linkage with nearby genes. Selection of five major loci reduced the accumulation of anti-nutritional steroidal glycoalkaloids in ripened fruits, rendering the fruit more edible. Breeding for pink tomatoes modified the content of over 100 metabolites. The introgression of resistance genes from wild relatives in cultivars also resulted in major and unexpected metabolic changes. The study reveals a multi-omics view of the metabolic breeding history of tomato, as well as provides insights into metabolome-assisted breeding and plant biology.

Bouwman A.C. et al. (2018): **Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals.** *Nature Genetics* (2018); doi:10.1038/s41588-018-0056-5

Stature is affected by many polymorphisms of small effect in humans¹. In contrast, variation in dogs, even within breeds, has been suggested to be largely due to variants in a small number of genes^{2,3}. Here we use data from cattle to compare the genetic architecture of stature to those in humans and dogs. We conducted a meta-analysis for stature using 58,265 cattle from 17 populations with 25.4 million imputed whole-genome sequence variants. Results showed that the genetic architecture of stature in cattle is similar to that in humans, as the lead variants in 163 significantly associated genomic regions ($P < 5 \times 10^{-8}$) explained at most 13.8% of the phenotypic variance. Most of these variants were noncoding, including variants that were also expression quantitative trait loci (eQTLs) and in ChIP-seq peaks. There was significant overlap in loci for stature with humans and dogs, suggesting that a set of common genes regulates body size in mammals.

<https://www.nature.com/articles/s41588-018-0056-5>

and

<https://phys.org/news/2018-02-genetic-code-complex-traits-cattle.html#jCp>

Dolezel M, Bartel A, Heissenberger A (2018): **Spatial analysis of the occurrence of protected butterflies in six European biogeographic regions as a tool for the environmental risk assessment of Bt maize.** *BioRisk* 13: 31–52. <https://doi.org/10.3897/biorisk.13.20688> (*Environment Agency Austria!*)

In the environmental risk assessment (ERA) of genetically modified plants (GMP), the consideration of the different environments where genetically modified plants (GMP) will be commercially grown (the receiving environments) plays a crucial role. In addition, relevant protection goals which may be adversely affected by the GMP have to be considered during the ERA. Using a literature- and GIS-based approach, distribution data of

protected lepidopteran species listed in Council Directive 92/43/EEC and of maize cultivation was used in order to evaluate potential spatial overlaps between GM maize and protected non-target Lepidoptera in different biogeographical regions (BGR) of the EU. Each BGR has its peculiarity regarding maize cultivation and the distribution of protected butterflies. The lepidopteran fauna of the Pannonian BGR is particularly sensitive due to large maize cultivation shares and wide distribution of protected butterflies within this BGR. For the BGRs evaluated potential, spatial exposures of protected butterflies to GM maize cannot be excluded. This study shows that the suggested approach is a useful tool for the consideration of EU-wide protected species in different receiving environments during the problem formulation of the ERA of GMPs.

<https://biorisk.pensoft.net/articles.php?id=20688>

Miller ME, Zhang Y, Omidvar V, Sperschneider J, Schwessinger B, Raley C, Palmer JM, Garnica D, Upadhyaya N, Rathjen J, Taylor JM, Park RF, Dodds PN, Hirsch CD, Kianian SF, Figueroa M. 2018. **De novo assembly and phasing of dikaryotic genomes from two isolates of *Puccinia coronata* f. sp. *avenae*, the causal agent of oat crown rust.** mBio 9: e01650-17.

<https://doi.org/10.1128/mBio.01650-17>.

Oat crown rust, caused by the fungus *Puccinia coronata* f. sp. *avenae*, is a devastating disease that impacts worldwide oat production. For much of its life cycle, *P. coronata* f. sp. *avenae* is dikaryotic, with two separate haploid nuclei that may vary in virulence genotype, highlighting the importance of understanding haplotype diversity in this species. We generated highly contiguous *de novo* genome assemblies of two *P. coronata* f. sp. *avenae* isolates, 12SD80 and 12NC29, from long-read sequences. In total, we assembled 603 primary contigs for 12SD80, for a total assembly length of 99.16 Mbp, and 777 primary contigs for 12NC29, for a total length of 105.25 Mbp; approximately 52% of each genome was assembled into alternate haplotypes. This revealed structural variation between haplotypes in each isolate equivalent to more than 2% of the genome size, in addition to about 260,000 and 380,000 heterozygous single-nucleotide polymorphisms in 12SD80 and 12NC29, respectively. Transcript-based annotation identified 26,796 and 28,801 coding sequences for isolates 12SD80 and 12NC29, respectively, including about 7,000 allele pairs in haplotype-phased regions. Furthermore, expression profiling revealed clusters of coexpressed secreted effector candidates, and the majority of orthologous effectors between isolates showed conservation of expression patterns. However, a small subset of orthologs showed divergence in expression, which may contribute to differences in virulence between 12SD80 and 12NC29. This study provides the first haplotype-phased reference genome for a dikaryotic rust fungus as a foundation for future studies into virulence mechanisms in *P. coronata* f. sp. *avenae*.

<http://mbio.asm.org/content/9/1/e01650-17>

Schwessinger B, Sperschneider J, Cuddy WS, Garnica DP, Miller ME, Taylor JM, Dodds PN, Figueroa M, Park RF, Rathjen JP. 2018. **A near-complete haplotype-phased genome of the dikaryotic wheat stripe rust fungus *Puccinia striiformis* f. sp. *tritici* reveals high interhaplotype diversity.** mBio 9: e02275-17. <https://doi.org/10.1128/mBio.02275-17>.

A long-standing biological question is how evolution has shaped the genomic architecture of dikaryotic fungi. To answer this, high-quality genomic resources that enable haplotype comparisons are essential. Short-read genome assemblies for dikaryotic fungi are highly fragmented and lack haplotype-specific information due to the high heterozygosity and repeat content of these genomes. Here, we present a diploid-aware assembly of the wheat stripe rust fungus *Puccinia striiformis* f. sp. *tritici* based on long reads using the FALCON-Unzip assembler. Transcriptome sequencing data sets were used to infer high-quality gene models and identify virulence genes involved in plant infection referred to as effectors. This represents the most complete *Puccinia striiformis* f. sp. *tritici* genome assembly to date (83 Mb, 156 contigs, N_{50} of 1.5 Mb) and provides phased haplotype information for over 92% of the genome. Comparisons of the phase blocks revealed high interhaplotype diversity of over 6%. More than 25% of all genes lack a clear allelic counterpart. When we investigated genome features that potentially promote the rapid evolution of virulence, we found that candidate effector genes are spatially associated with conserved genes commonly found in basidiomycetes. Yet, candidate effectors that lack an allelic counterpart are more distant from conserved genes than allelic candidate effectors and are less likely to be evolutionarily conserved within the *P. striiformis* species complex and *Pucciniales*. In summary, this haplotype-phased assembly enabled us to discover novel genome features of a dikaryotic plant-pathogenic fungus previously hidden in collapsed and fragmented genome assemblies.

<http://mbio.asm.org/content/9/1/e02275-17.full.pdf+html>

and

University of Minnesota

Scientists poised to win the race against rust disease and beyond

<https://phys.org/news/2018-02-scientists-poised-rust-disease.html#jCp>

Betto-Colliard, C., Hofmann, Sermier R., Perrin N, Stöck M. (2018): **Profound genetic divergence and asymmetric parental genome contributions as hallmarks of hybrid speciation in polyploid toads**, *Proceedings of the Royal Society B: Biological Sciences* (2018). DOI: [10.1098/rspb.2017.2667](https://doi.org/10.1098/rspb.2017.2667)

The evolutionary causes and consequences of allopolyploidization, an exceptional pathway to instant

hybrid speciation, are poorly investigated in animals. In particular, when and why hybrid polyploids versus diploids are produced, and constraints on sources of paternal and maternal ancestors, remain underexplored. Using the Palearctic green toad radiation (including bisexually reproducing species of three ploidy levels) as model, we generate a range-wide multi-locus phylogeny of 15 taxa and present four new insights: (i) at least five (up to seven) distinct allotriploid and allotetraploid taxa have evolved in the Pleistocene; (ii) all maternal and paternal ancestors of hybrid polyploids stem from two deeply diverged nuclear clades (6 Mya, 3.1–9.6 Mya), with distinctly greater divergence than the parental species of diploid hybrids found at secondary contact zones; (iii) allotriploid taxa possess two conspecific genomes and a deeply diverged allospecific one, suggesting that genomic imbalance and divergence are causal for their partly clonal reproductive mode; (iv) maternal versus paternal genome contributions exhibit asymmetry, with the maternal nuclear (and mitochondrial) genome of polyploids always coming from the same clade, and the paternal genome from the other. We compare our findings with similar patterns in diploid/polyploid vertebrates, and suggest deep ancestral divergence as a precondition for successful allopolyploidization.

<http://rspb.royalsocietypublishing.org/content/royprsb/285/1872/20172667.full.pdf>
and

Forschungsverbund Berlin

Green toads with multiple genomes have ancestors that are only distantly related

<https://phys.org/news/2018-02-green-toads-multiple-genomes-ancestors.html#jCp>

Exposito-Alonso M. et al. (2018): **The rate and potential relevance of new mutations in a colonizing plant lineage**, *PLOS Genetics*. DOI: [10.1371/journal.pgen.1007155](https://doi.org/10.1371/journal.pgen.1007155)

By following the evolution of populations that are initially genetically homogeneous, much can be learned about core biological principles. For example, it allows for detailed studies of the rate of emergence of *de novo* mutations and their change in frequency due to drift and selection. Unfortunately, in multicellular organisms with generation times of months or years, it is difficult to set up and carry out such experiments over many generations. An alternative is provided by “natural evolution experiments” that started from colonizations or invasions of new habitats by selfing lineages. With limited or missing gene flow from other lineages, new mutations and their effects can be easily detected. North America has been colonized in historic times by the plant *Arabidopsis thaliana*, and although multiple intercrossing lineages are found today, many of the individuals belong to a single lineage, HPG1. To determine in this lineage the rate of substitutions—the subset of mutations that survived natural selection and drift—, we have sequenced genomes from plants collected between 1863 and 2006. We identified 73 modern and 27 herbarium specimens that belonged to HPG1. Using the estimated substitution rate, we infer that the last common HPG1 ancestor lived in the early 17th century, when it was most likely introduced by chance from Europe. Mutations in coding regions are depleted in frequency compared to those in other portions of the genome, consistent with purifying selection. Nevertheless, a handful of mutations is found at high frequency in present-day populations. We link these to detectable phenotypic variance in traits of known ecological importance, life history and growth, which could reflect their adaptive value. Our work showcases how, by applying genomics methods to a combination of modern and historic samples from colonizing lineages, we can directly study new mutations and their potential evolutionary relevance.

<http://journals.plos.org/plosgenetics/article/file?id=10.1371/journal.pgen.1007155&type=printable>

Grinberg I. R. et al. (2018): **Novel ATP-cone-driven allosteric regulation of ribonucleotide reductase via the radical-generating subunit**. *eLife*, 2018 DOI: [10.7554/eLife.31529.001](https://doi.org/10.7554/eLife.31529.001)

Ribonucleotide reductases (RNRs) are key enzymes in DNA metabolism, with allosteric mechanisms controlling substrate specificity and overall activity. In RNRs, the activity master-switch, the ATP-cone, has been found exclusively in the catalytic subunit. In two class I RNR subclasses whose catalytic subunit lacks the ATP-cone, we discovered ATP-cones in the radical-generating subunit. The ATP-cone in the *Leeuwenhoekiella blandensis* radical-generating subunit regulates activity via quaternary structure induced by binding of nucleotides. ATP induces enzymatically competent dimers, whereas dATP induces non-productive tetramers, resulting in different holoenzymes. The tetramer forms by interactions between ATP-cones, shown by a 2.45 Å crystal structure. We also present evidence for an Mn^{III}Mn^{IV} metal center. In summary, lack of an ATP-cone domain in the catalytic subunit was compensated by transfer of the domain to the radical-generating subunit. To our knowledge, this represents the first observation of transfer of an allosteric domain between components of the same enzyme complex.

<https://doi.org/10.7554/eLife.31529.001>

Ford E.E. et al. (2018): **Frequent lack of repressive capacity of promoter DNA methylation identified through genome-wide epigenomic manipulation**

It is widely assumed that the addition of DNA methylation at CpG rich gene promoters silences gene transcription. However, this conclusion is largely drawn from the observation that promoter DNA methylation inversely correlates with gene expression. The effect of forced DNA methylation on endogenous promoters has yet to be comprehensively assessed. Here, we conducted artificial methylation of thousands of promoters in

human cells using an artificial zinc finger-DNMT3A fusion protein, enabling assessment of the effect of forced DNA methylation upon transcription and histone modifications, and the durability of DNA methylation after the removal of the fusion protein. We find that DNA methylation is frequently insufficient to transcriptionally repress promoters. Furthermore, DNA methylation deposited at promoter regions associated with H3K4me3 is rapidly erased after removal of the zinc finger-DNMT3A fusion protein. Finally, we demonstrate that induced DNA methylation can exist simultaneously on promoter nucleosomes that possess the active histone modification H3K4me3. These findings suggest that promoter DNA methylation is not generally sufficient for transcriptional inactivation, with implications for the emerging field of epigenome engineering.

<https://www.biorxiv.org/content/early/2017/08/16/170506>

Fiolet T. et al. (2018): **Consumption of ultra-processed foods and cancer risk: results from NutriNet-Santé prospective cohort.** *MJ* 2018; 360 doi: <https://doi.org/10.1136/bmj.k322>

MAIN OUTCOME MEASURES: Associations between ultra-processed food intake and risk of overall, breast, prostate, and colorectal cancer assessed by multivariable Cox proportional hazard models adjusted for known risk factors

CONCLUSIONS: In this large prospective study, a 10% increase in the proportion of ultra-processed foods in the diet was associated with a significant increase of greater than 10% in risks of overall and breast cancer. Further studies are needed to better understand the relative effect of the various dimensions of processing (nutritional composition, food additives, contact materials, and neofomed contaminants) in these associations.

<http://www.bmj.com/content/360/bmj.k322> <http://www.bmj.com/content/bmj/360/bmj.k322.full.pdf>

Gardner C.D., Trepanowski J.F., Del Gobbo L.C., et al. (2018): **Effect of Low-Fat vs Low-Carbohydrate Diet on 12-Month Weight Loss in Overweight Adults and the Association With Genotype Pattern or Insulin Secretion**The DIETFITS Randomized Clinical Trial. *JAMA*. 2018; 319(7):667-679. doi:10.1001/jama.2018.0245

Conclusions and Relevance: In this 12-month weight loss diet study, there was no significant difference in weight change between a healthy low-fat diet vs a healthy low-carbohydrate diet, and neither genotype pattern nor baseline insulin secretion was associated with the dietary effects on weight loss. In the context of these 2 common weight loss diet approaches, neither of the 2 hypothesized predisposing factors was helpful in identifying which diet was better for whom.

<https://jamanetwork.com/journals/jama/article-abstract/2673150?redirect=true><https://jamanetwork.com/journals/jama/article-abstract/2673150?redirect=true>

Séralini G.-E., Douzelet J.(2018): **The Taste of Pesticides in Wines.** *Food & Nutrition Journal* : FDNJ-161. DOI: 10.29011/2575-7091. 100061

A very first description of the tastes of 11 pesticides is proposed. They are detected first in water, diluted freshly at the levels found in wines, by 36 professionals from wine or cooking in 195 blind tests at different periods. They are the most frequently found pesticides in wines in our experiment. Some animals can detect pesticides and change their behaviour in response. In order to find out if humans can also detect pesticides by their taste in wines, a three-step experiment was conducted. First, 16 pairs of organic and non-organic bottles of wine were identified in 7 regions. The same varieties of grapes in each pair were grown on the same soils (in neighbouring vineyards), in the same climate and in the same year. The resulting wines were assessed for over 250 pesticides. Traces were present only in one organic bottle. In contrast, 4686 ppb were detected in total in non-organic bottles, with only 2 samples at 0 and a mean of 293 ± 270 [0-1144] ppb reached by up to 6 pesticides—mostly fungicides and one glyphosate-based herbicide. Secondly, 195 blind tests with 71 different professionals were conducted at different periods. In 77% of the cases, organic wines were preferred. The same pesticides alone or in mixtures were diluted in water at the levels present in wines. At least one pesticide of the mixture was identified as such because it was judged to taste different from water in blind tests: this held true in 85% of cases in which answers (147) were offered by the professionals, and 58% recognized them all. Among the experts who detected pesticides, 57% identified the wine containing them out of the pair of bottles. To our knowledge, this experiment is the first where humans can identify pesticides by taste.

https://gavinpublishers.com/admin/assets/articles_pdf/1515065578article_pdf1909863773.pdf

Wang W. et al. (2014): **A novel 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase transgene for glyphosate resistance stimulates growth and fecundity in weedy rice (*Oryza sativa*) without herbicide.** *New Phytologist* (2014) 202: 679–688; doi: 10.1111/nph.12428

<http://onlinelibrary.wiley.com/doi/10.1111/nph.12428/epdf>

Fang J., Nan P., Gu Z., Ge X, Feng Y.-Q., and Lu B. (2018): **Overexpressing exogenous 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) genes increases fecundity and auxin content of transgenic Arabidopsis plants** *Front. Plant Sci.*; doi: 10.3389/fpls.2018.00233

Transgenic glyphosate-tolerant plants overproducing EPSPS (5-enolpyruvylshikimate-3-phosphate synthase) may exhibit enhanced fitness in glyphosate-free environments. If so, introgression of transgenes overexpressing EPSPS into wild relative species may lead to increased competitiveness of crop-wild hybrids, resulting in unpredicted environmental impact. Assessing fitness effects of transgenes overexpressing EPSPS in a model plant species can help address this question, while elucidating how overproducing EPSPS affects the fitness-related traits of plants. We produced segregating T2 and T3 Arabidopsis thaliana lineages with or without a transgene overexpressing EPSPS isolated from rice or Agrobacterium (CP4). For each of the three transgenes, we compared glyphosate tolerance, some fitness-related traits, and auxin (indole-3-acetic acid) content in transgene-present, transgene-absent, empty vector (EV), and parental lineages in a common-garden experiment. We detected substantially increased glyphosate tolerance in T2 plants of transgene-present lineages that overproduced EPSPS. We also documented significant increases in fecundity, which was associated with increased auxin content in T3 transgene-present lineages containing rice EPSPS genes, compared with their segregating transgene-absent lineages, EV, and parental controls. Our results from Arabidopsis with nine transgenic events provide a strong support to the hypothesis that transgenic plants overproducing EPSPS can benefit from a fecundity advantage in glyphosate-free environments. Stimulated biosynthesis of auxin, an important plant growth hormone, by overproducing EPSPS may play a role in enhanced fecundity of the transgenic Arabidopsis plants. The obtained knowledge is useful for assessing environmental impact caused by introgression of transgenes overproducing EPSPS from any GE crop into populations of its wild relatives.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.00233/abstract>

Veranstaltungen - Meetings

6th Halle Conference on Recombinant Proteins

The Conference will take place on March 8th-9th, 2018 at "Deutsche Akademie der Naturforscher Leopoldina". There is no registration fee charged.

http://www.biochemtech.uni-halle.de/halle_conference/

G-TwYST stakeholder consultation workshop

28-29 MARCH 2018 in Antwerp, Belgium

Deadline for registration is March 14.

<https://www.g-twyst.eu/files/Finalstakeholderconsultations/G-TwYSTStakeholderConsultationPreliminaryagenda.pdf>

EFSA scientific colloquium "Omics in risk assessment: state-of-the-art and next steps"

Berlin, 24 April 2018 to 25 April 2018

http://www.efsa.europa.eu/en/events/event/180424-0?utm_source=EFSA+Newsletters&utm_campaign=9d3eec2bf5-EMAIL_CAMPAIGN_2018_02_07&utm_medium=email&utm_term=0_7ea646dd1d-9d3eec2bf5-59436449

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

Bitte besuchen sie auch die Webseite des Wissenschaftlerkreis Grüne Gentechnik e.V. (WGG): www.wgg-ev.de. Hier finden Sie weitere interessante Informationen.

As always, I thank you all for hints and for publications, especially to Klaus Ammann. Most of the pdf files can be downloaded directly from the links.

This file is saved at <https://www.biotech-gm-food.com/sunday-evening-news/> as well as at <https://www.wgg-ev.de/infos/wgg-nachrichten/>

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