

# Sunday Evening News

Week 06 (2018-02-05 / 02-11)

Selected and edited by **BGF** Jany

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Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter, und hier wieder meine sicherlich etwas subjektive Zusammenstellung der Ereignisse aus Woche 06.

Dear all,

and here again my certainly subjective compilation of events from week 06.

## [Koalitionsvertrag zwischen CDU, CSU und SPD](#)

### **Ein neuer Aufbruch für Europa**

### **Eine neue Dynamik für Deutschland**

### **Ein neuer Zusammenhalt für unser Land**

Der Koalitionsvertrag wurde zwar ausgehandelt, aber ob es tatsächlich zu einer neuen Regierung kommt entscheidet sich erst über den Mitgliederentscheid. Das Ergebnis liegt wahrscheinlich bis zum 3./4. März vor.

Das Thema „Gentechnik“ wird in den Zeilen 472 und 3915-3922 abgehandelt.

„Patente auf Pflanzen und Tiere lehnen wir ab. Ebensodas Klonen von Tieren zur Lebensmittelerzeugung. Wir halten an der Saatgutreinheit fest. Ein Gentechnikanbau-Verbot werden wir bundesweit einheitlich regeln (Opt-Out-Richtlinie der EU). Im Anschluss an die noch ausstehende Entscheidung des Europäischen Gerichtshofes (EuGH) zu den neuen molekularbiologischen Züchtungstechnologien werden wir auf europäischer oder gegebenenfalls nationaler Ebene Regelungen vornehmen, die das **Vorsorgeprinzip** und die **Wahlfreiheit** gewährleisten.“

Hier kommt zum Ausdruck:

- a) Ein generelles Anbauverbot von gentechnisch veränderten Pflanzen in Deutschland wird kommen. (Wunderlich, dass das Anbauverbot nicht auch im Grundgesetz verankert werden soll!)
- b) Gleichgültig wie Teile der neuen Züchtungsmethoden vom EuGH rechtlich eingeordnet werden, soll das Vorsorgeprinzip und die Wahlfreiheit durch eine Kennzeichnung genutzt werden, um Anwendungen aus den neuen Züchtungsmethoden zu erschweren oder zu verhindern.

## Glyphosat unter Biodiversität abgehandelt (Zeilen 6727 -6733)

Wir werden mit einer systematischen Minderungsstrategie den Einsatz von glyphosathaltigen Pflanzenschutzmitteln deutlich einschränken mit dem Ziel, die Anwendung so schnell wie möglich grundsätzlich zu beenden. Dazu werden wir gemeinsam mit der Landwirtschaft Alternativen im Rahmen einer Ackerbaustrategie entwickeln und u.a. umwelt- und naturverträgliche Anwendungen von Pflanzenschutzmitteln regeln. Die dazu notwendigen rechtlichen Maßnahmen werden wir in einem EU-konformen Rahmen verankern.

Das Wort „Biotechnologie“ kommt im Vertrag nicht vor und „Bioökonomie“ einmal. Das Wort „Innovation“ wird sehr häufig und in den unterschiedlichsten Zusammenhängen genutzt. Ob mit der modernen Biotechnologie und aus der Bioökonomie Innovationen geschaffen werden können (sollen), bleibt offen. Eine Förderung der Wissenschaften im Bereich der Biotechnologie wird nicht erwähnt.

Elbing K. *Geschäftsstelle Berlin – VBIO*

„**Von der Biologie zur Innovation**“ - Biologenverband zum Koalitionsvertrag 2018

<https://idw-online.de/de/news688932>

Reuters Staff

German coalition deal sets no timetable to end glyphosate use

<https://uk.reuters.com/article/uk-germany-politics-glyphosate/german-coalition-deal-sets-no-timetable-to-end-glyphosate-use-idUKKBN1FR2GF?il=0>

Kuntz M.

### **Glyphosate: The Triumph of Post-Truth in Europe**

<https://www.acsh.org/news/2018/02/08/glyphosate-triumph-post-truth-europe-12544>

Brilliant talk by Deborah Piován (Confagricoltura) on **farmers and innovation** for TED

<https://youtu.be/EWXCebuRIEM>

Some of the main key messages in her talk are:

The history of agriculture is a history of continuous innovation: to ignore this is to condemn our traditions.

Sustainability in agriculture means low environmental impact, adequate remuneration for farmers, a general acceptance of the process by society.

To reach this goal farmers and researchers must work together, and together communicate their work to the public."

Thanks to Fabio

White S. – Euractiv

### **De Castro MEP: New plant breeding techniques are nothing like 'Frankenstein' GMOs**

The vice-chair of the European Parliament's agriculture committee has argued that Europe should embrace innovative biotechnologies to boost food production while cutting the environmental impact of farming.

<https://www.euractiv.com/section/agriculture-food/news/mep-new-plant-breeding-techniques-are-nothing-like-frankenstein-gmos/>

Schmitz A.M. – Cornell University

### **New 'Tomato Expression Atlas' dives deep into the fruit's flesh**

<http://news.cornell.edu/stories/2018/02/new-tomato-expression-atlas-dives-deep-fruits-flesh>

Adenle A.A. et al. (2018): **Rationalizing governance of genetically modified products in developing countries**. NATURE BIOTECHNOLOGY 36 (2), 137-139

<https://www.nature.com/articles/nbt.4069> pdf-file available

Strassheim S., Schenkel W. (2018): Correspondence: **Existing rules cover gene-drive usage**. Nature 554, 169

<https://www.nature.com/articles/d41586-018-01623-z>

Case P. - Farmers Weekly

### **GM crops area rises by 20% in Spain**

Four countries in the EU grew commercial genetically modified (GM) maize in 2016, with Spain adopting the largest area.

<http://www.fwi.co.uk/arable/gm-crops-area-rises-by-20-in-spain.htm>

The daily press releases and media reports in German and English languages can be found at

<https://www.biotech-gm-food.com/press>

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## **Scientific Issues**

Saraswathi M.S., Kalaiponmani K., Uma S and Backiyarani S. (2018): Chapter 14–**Critical Evaluation of the Benefits and Risks of Genetically Modified Horticultural Crops**. *Genetic Engineering of Horticultural Crops*. 2018, 315–351; <https://doi.org/10.1016/B978-0-12-810439-2.00014-3>

Crop improvement in terms of high yield and tolerance to biotic and abiotic stresses can be easily achieved by supplementing conventional breeding with modern biotechnological techniques such as “transgenics.” Furthermore, generating transgenic crops is a more specific and faster approach for crop improvement. A wide variety of transformation and regeneration protocols are available, which have resulted in engineering a wide array of horticultural crops for pest and disease resistance, enhanced shelf-life, etc. The issues of public concern are use of selectable marker genes, spread of the transgenes through pollen, possibility for the development of resistant lines in case of insect or fungal pests, allergenicity of the introduced proteins in humans, etc. Currently, techniques are available to eliminate the use of selectable markers in genetic transformation. In the recent past, numbers of research groups and reputed organizations have assessed the state-of-the-art with respect to the safety of genetically modified (GM) plants for human consumption and also concluded that transgenic crop varieties are as safe and nutritious as their respective non-GM plants.

Regulatory issues pose a significant obstacle to the development of transgenics and their commercialization. Efforts should be made to hasten the conduct of necessary toxicological studies and issue of necessary clearance to the transgenic crop varieties. Advanced genome editing techniques such as ZFN, TALEN, and CRISPR/Cas9 have opened more avenues for the development of genetically edited isogenic lines, which are both consumer and environmentally friendly. Furthermore, they do not warrant much regulation because they are near-isogenic lines of the parental types.

<https://www.sciencedirect.com/science/article/pii/B9780128104392000143> have also a look on the book!

**Aldemita R.R. and Hautea R.A. (2018): Biotech crop planting resumes high adoption in 2016. GM Crops & Food Biotechnology in Agriculture and the Food Chain.**

<https://doi.org/10.1080/21645698.2018.1428166>

The global area of biotech crops in 2016 increased from 179.7 million hectares to 185.1 million hectares, a 3% increase equivalent to 5.4 million hectares. Some 26 countries planted biotech crops, 19 of which were developing countries and seven were industrial. Information and data collected from various credible sources showed variations from the previous year. Fluctuations in biotech crop area (both increases and decreases) are influenced by factors including, among others, acceptance and commercialization of new products, demand for meat and livestock feeds, weather conditions, global market price, disease/pest pressure, and government's enabling policies. Countries which have increased biotech crop area in decreasing order in 2016 were Brazil, United States of America, Canada, South Africa, Australia, Bolivia, Philippines, Spain, Vietnam, Bangladesh, Colombia, Honduras, Chile, Sudan, Slovakia, and Costa Rica. Countries with decreased biotech area in decreasing order were China, India, Argentina, Paraguay, Uruguay, Mexico, Portugal, and Czech Republic, in decreasing incremental decrease in biotech area. Pakistan and Myanmar were the only countries with no change in biotech crop (cotton) planted. Information detailed in the paper including future crops and traits in each country could guide stakeholders in informed crafting of strategies and policies for increased adoption of biotech crops in the country.

<http://www.tandfonline.com/doi/full/10.1080/21645698.2018.1428166> file available

**Lewis C.M. et al. (2018): Potential for re-emergence of wheat stem rust in the United Kingdom.**

Communications Biology Article number: 13 [DOI: 10.1038/s42003-018-0013-y](https://doi.org/10.1038/s42003-018-0013-y)

Wheat stem rust, a devastating disease of wheat and barley caused by the fungal pathogen *Puccinia graminis* f. sp. *tritici*, was largely eradicated in Western Europe during the mid-to-late twentieth century. However, isolated outbreaks have occurred in recent years. Here we investigate whether a lack of resistance in modern European varieties, increased presence of its alternate host barberry and changes in climatic conditions could be facilitating its resurgence. We report the first wheat stem rust occurrence in the United Kingdom in nearly 60 years, with only 20% of UK wheat varieties resistant to this strain. Climate changes over the past 25 years also suggest increasingly conducive conditions for infection. Furthermore, we document the first occurrence in decades of *P. graminis* on barberry in the UK. Our data illustrate that wheat stem rust does occur in the UK and, when climatic conditions are conducive, could severely harm wheat and barley production.

<https://www.nature.com/articles/s42003-018-0013-y> ; <https://www.nature.com/articles/s42003-018-0013-y.pdf>

and [John Innes Centre](#)

First report in decades of a forgotten crop pathogen calls for critical close monitoring

<https://phys.org/news/2018-02-decades-forgotten-crop-pathogen-critical.html#jCp>

**Monteiro F., Frese L., Castro S., Duarte M.C., Paulo O.S., Loureiro J. and Romeiras M.M. (2018): Genetic and Genomic Tools to Assist Sugar Beet Improvement: The Value of the Crop Wild Relatives.** *Front. Plant Sci.* 9:74. doi: 10.3389/fpls.2018.00074

Sugar beet (*Beta vulgaris* L. ssp. *vulgaris*) is one of the most important European crops for both food and sugar production. Crop improvement has been developed to enhance productivity, sugar content or other breeder's desirable traits. The introgression of traits from Crop Wild Relatives (CWR) has been done essentially for lessening biotic stresses constraints, namely using Beta and Patellifolia species which exhibit disease resistance characteristics. Several studies have addressed crop-to-wild gene flow, yet, for breeding programs genetic variability associated with agronomically important traits remains unexplored regarding abiotic factors. To accomplish such association from phenotype to genotype, screening for wild relatives occurring in habitats where selective pressures are in play (i.e., populations in salt marshes for salinity tolerance; populations subjected to pathogen attacks and likely evolved resistance to pathogens) are the most appropriate streamline to identify causal genetic information. By selecting sugar beet CWR species based on genomic tools, rather than random variations, is a promising but still seldom explored route toward the development of improved crops. In this perspective, a viable streamline for sugar beet improvement is proposed through the use of different genomic tools by recurring to sugar beet CWRs and focusing on agronomic traits associated with abiotic stress tolerance. Overall, identification of genomic and epigenomic landscapes associated to adaptive ecotypes, along with the cytogenetic and habitat characterization of sugar beet CWR, will enable to identify potential hotspots for agrobiodiversity of sugar beet crop improvement toward abiotic stress tolerance

<https://www.frontiersin.org/articles/10.3389/fpls.2018.00074/full>

Moises Zotti et al. (2018): **RNA interference technology in crop protection against arthropod pests, pathogens and nematodes.** *Pest Manag Sci* (2018); DOI 10.1002/ps.4813

Scientists have made significant progress in understanding and unraveling several aspects of double-stranded RNA (dsRNA)-mediated gene silencing during the last two decades. Now that the RNA interference (RNAi) mechanism is well understood, it is time to consider how to apply the acquired knowledge to agriculture and crop protection. Some RNAi-based products are already available for farmers and more are expected to reach the market soon. Tailor-made dsRNA as an active ingredient for biopesticide formulations is considered a raw material that can be used for diverse purposes, from pest control and bee protection against viruses to pesticide resistance management. The RNAi mechanism works at the messenger RNA (mRNA) level, exploiting a sequence-dependent mode of action, which makes it unique in potency and selectivity compared with conventional agrochemicals. Furthermore, the use of RNAi in crop protection can be achieved by employing plant-incorporated protectants through plant transformation, but also by non-transformative strategies such as the use of formulations of sprayable RNAs as direct control agents, resistance factor repressors or developmental disruptors. In this review, RNAi is presented in an agricultural context (discussing products that have been launched on the market or will soon be available), and we go beyond the classical presentation of successful examples of RNAi in pest-insect control and comprehensively explore its potential for the control of plant pathogens, nematodes and mites, and to fight against diseases and parasites in beneficial insects. Moreover, we also discuss its use as a repressor for the management of pesticide-resistant weeds and insects. Finally, this review reports on the advances in non-transformative dsRNA delivery and the production costs of dsRNA, and discusses environmental considerations.

<http://onlinelibrary.wiley.com/doi/10.1002/ps.4813/abstract>

Schmierer, B., Botla, S. K., Zhang, J., Turunen, M., Kivioja, T. and Taipale, J. (2017): **CRISPR/Cas9 screening using unique molecular identifiers.** *Molecular Systems Biology* 13, 10;

<http://msb.embopress.org/content/msb/13/10/945.full.pdf>  
<http://www.ask-force.org/web/Genomics/Schmierer-CRISPR-Cas-screening-using-unique-molecular-identifiers-2017.pdf> open access

Liang, Y. et al. ***Arabidopsis glutamate:glyoxylate aminotransferase 1 (Ler) mutants generated by CRISPR/Cas9 and their characteristics.*** *Transgenic Res* (2018).

<https://doi.org/10.1007/s11248-017-0052-z>

Clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated 9 (CRISPR/Cas9) technology provides an efficient tool for editing the genomes of plants, animals and microorganisms. Glutamate:glyoxylate aminotransferase 1 (GGAT1) is a key enzyme in the photorespiration pathway; however, its regulation mechanism is largely unknown. Given that EMS-mutagenized *ggat1* (Col-0 background) M2 pools have been generated, *ggat1* (Ler background) should be very useful in the positional cloning of suppressor and/or enhancer genes of *GGAT1*. Unfortunately, such *ggat1* (Ler) mutants are not currently available. In this study, CRISPR/Cas9 was used to generate *ggat1* (Ler) mutants. Two *GGAT1* target single-guide RNAs (sgRNAs) were constructed into pYLCRISPR/Cas9P<sub>35S</sub>-N, and flowering *Arabidopsis* (Ler) plants were transformed using an *Agrobacterium tumefaciens*-mediated floral dip protocol. Eleven chimeric and two heterozygous *GGAT1*-edited T1 lines of target 1 were separately screened from positive transgenic lines. Two *ggat1* homozygous mutants, CTC-deletion and T-deletion at target 1, were generated from T2 generations of the 13 T1 lines. The edited mutation sites were found to be stable through generations regardless of whether the T-DNA was present. In addition, the genetic segregation of the mutation sites obeyed the Mendelian single gene segregation rule, and no mutations were detected at the possible off-target site. Also, the two independent *ggat1* mutants had similar photorespiration phenotypes and down-regulated GGAT enzyme activity. Together, these results indicate that genetically stable *ggat1* (Ler) mutants were generated by CRISPR/Cas9 genome editing, and these mutants will be used to promote the positional cloning of suppressor and/or enhancer genes of *GGAT1* in our subsequent study.

<https://link.springer.com/article/10.1007%2Fs11248-017-0052-z>

Masahiko Yoshimura M. et al. (2018): **Discovery of Shoot Branching Regulator Targeting Strigolactone Receptor DWARF14.** *ACS Cent. Sci.*, Article ASAP DOI: 10.1021/acscentsci.7b00554

DWARF14 (D14) is a strigolactone receptor that plays a central role in suppression of shoot branching, and hence is a potential target to increase crop productions and biomass. Recently, we reported a fluorescence turn-on probe, Yoshimulactone Green (YLG), which generates a strong fluorescence upon the hydrolysis by D14-type strigolactone receptors. Herein, we applied a YLG-based in vitro assay to a high-throughput chemical screening and identified a novel small molecule DL1 as a potent inhibitor of D14. DL1 competes with endogenous strigolactones, thereby increasing the number of shoot branching in a model plant *Arabidopsis* as well as in rice. Thus, DL1 is expected to be useful not only as a tool to understand the biological roles of D14 receptors in plant growth and development, but also as a potent agrochemical to improve the crop yield.

<https://pubs.acs.org/doi/pdf/10.1021/acscentsci.7b00554>

**Shu Y., Romeis J. and Meissle M. (2018) : No Interactions of Stacked Bt Maize with the Non-target Aphid *Rhopalosiphum padi* and the Spider Mite *Tetranychus urticae*.** *Front. Plant Sci.* 9:39. doi: 10.3389/fpls.2018.00039

In the agroecosystem, genetically engineered plants producing insecticidal Cry proteins from *Bacillus thuringiensis* (Bt) interact with non-target herbivores and other elements of the food web. Stacked Bt crops expose herbivores to multiple Cry proteins simultaneously. In this study, the direct interactions between SmartStaxR Bt maize producing six different Cry proteins and two herbivores with different feeding modes were investigated. Feeding on leaves of Bt maize had no effects on development time, fecundity, or longevity of the aphid *Rhopalosiphum padi* (Hemiptera: Aphididae), and no effects on the egg hatching time, development time, sex ratio, fecundity, and survival of the spider mite *Tetranychus urticae* (Acari: Tetranychidae). The results thus confirm the lack of effects on those species reported previously for some of the individual Cry proteins. In the Bt maize leaves, herbivore infestation did not result in a consistent change of Cry protein concentrations. However, occasional statistical differences between infested and non-infested leaves were observed for some Cry proteins and experimental repetitions. Overall, the study provides evidence that the Cry proteins in stacked Bt maize do not interact with two common non-target herbivores.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.00039/full>

**Yang Y, Zhang B, Zhou X, Romeis J, Peng Y and Li Y (2018): Toxicological and Biochemical Analyses Demonstrate the Absence of Lethal or Sublethal Effects of cry1C- or cry2A- Expressing Bt Rice on the Collembolan *Folsomia candida*.** *Front. Plant Sci.* 9:131. doi: 10.3389/fpls.2018.00131

Assessing the potential effects of insect-resistant genetically engineered (GE) plants on collembolans is important because these common soil arthropods may be exposed to insecticidal proteins produced in GE plants by ingestion of plant residues, crop pollen, or root exudates. Laboratory studies were conducted to evaluate the potential effects of two *Bacillus thuringiensis* (Bt)-rice lines expressing Cry1C and Cry2A in pollen and leaves and of their non-Bt conventional isolines on the fitness of the collembolan *Folsomia candida* and on the activities of its antioxidant-related enzymes, superoxide dismutase and peroxidase, and of its detoxification-related enzymes, glutathione reductase and glutathione S-transferase. Survival, development, reproduction, and the intrinsic rate of increase (*r<sub>m</sub>*) were not significantly reduced when *F. candida* fed on the Bt rice pollen or leaf powder than on the non-Bt rice materials; these parameters, however, were significantly reduced when *F. candida* fed on non-Bt rice pollen or non-Bt leaf-based diets containing the protease inhibitor E-64 at 75 µg/g. The activities of the antioxidant-related and detoxification-related enzymes in *F. candida* were not significantly affected when *F. candida* fed on the Bt rice materials, but were significantly increased when *F. candida* fed on the non-Bt rice materials containing E-64. The results demonstrate that Cry1C and Cry2A are not toxic to *F. candida*, and also indicate the absence of unintended effects on the collembolan caused by any change in plant tissue nutritional composition due to foreign gene transformation.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.00131/full>

**Gutekunst J. et al. (2018): Clonal genome evolution and rapid invasive spread of the marbled crayfish.** *Nature Ecology & Evolution*; doi:10.1038/s41559-018-0467-9

The marbled crayfish *Procambarus virginalis* is a unique freshwater crayfish characterized by very recent speciation and parthenogenetic reproduction. Marbled crayfish also represent an emerging invasive species and have formed wild populations in diverse freshwater habitats. However, our understanding of marbled crayfish biology, evolution and invasive spread has been hampered by the lack of freshwater crayfish genome sequences. We have now established a de novo draft assembly of the marbled crayfish genome. We determined the genome size at approximately 3.5 gigabase pairs and identified >21,000 genes. Further analysis confirmed the close relationship to the genome of the slough crayfish, *Procambarus fallax*, and also established a triploid AA'B genotype with a high level of heterozygosity. Systematic fieldwork and genotyping demonstrated the rapid expansion of marbled crayfish on Madagascar and established the marbled crayfish as a potent invader of freshwater ecosystems. Furthermore, comparative whole-genome sequencing demonstrated the clonality of the population and their genetic identity with the oldest known stock from the German aquarium trade. Our study closes an important gap in the phylogenetic analysis of animal genomes and uncovers the unique evolutionary history of an emerging invasive species.

<https://www.nature.com/articles/s41559-018-0467-9>

**Stein J.C. et al. (2018): Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus *Oryza*.** *Nature Genetics* 50, 285–296 doi:10.1038/s41588-018-0040-0 -

The genus *Oryza* is a model system for the study of molecular evolution over time scales ranging from a few thousand to 15 million years. Using 13 reference genomes spanning the *Oryza* species tree, we show that despite few large-scale chromosomal rearrangements rapid species diversification is mirrored by lineage-specific emergence and turnover of many novel elements, including transposons, and potential new coding and noncoding genes. Our study resolves controversial areas of the *Oryza* phylogeny, showing a complex history of

introgression among different chromosomes in the young 'AA' subclade containing the two domesticated species. This study highlights the prevalence of functionally coupled disease resistance genes and identifies many new haplotypes of potential use for future crop protection. Finally, this study marks a milestone in modern rice research with the release of a complete long-read assembly of IR 8 'Miracle Rice', which relieved famine and drove the Green Revolution in Asia 50 years ago.  
<https://www.nature.com/articles/s41588-018-0040-0>

Barba-Montoya J. et al. (2018): **Constraining uncertainty in the timescale of angiosperm evolution and the veracity of a Cretaceous Terrestrial Revolution**, *New Phytologist* (2018). DOI: [10.1111/nph.15011](https://doi.org/10.1111/nph.15011)

Through the lens of the fossil record, angiosperm diversification precipitated a Cretaceous Terrestrial Revolution (KTR) in which pollinators, herbivores and predators underwent explosive co-diversification. Molecular dating studies imply that early angiosperm evolution is not documented in the fossil record. This mismatch remains controversial.

We used a Bayesian molecular dating method to analyse a dataset of 83 genes from 644 taxa and 52 fossil calibrations to explore the effect of different interpretations of the fossil record, molecular clock models, data partitioning, among other factors, on angiosperm divergence time estimation.

Controlling for different sources of uncertainty indicates that the timescale of angiosperm diversification is much less certain than previous molecular dating studies have suggested. Discord between molecular clock and purely fossil-based interpretations of angiosperm diversification may be a consequence of false precision on both sides.

We reject a post-Jurassic origin of angiosperms, supporting the notion of a cryptic early history of angiosperms, but this history may be as much as 121 Myr, or as little as 23 Myr. These conclusions remain compatible with palaeobotanical evidence and a more general KTR in which major groups of angiosperms diverged later within the Cretaceous, alongside the diversification of pollinators, herbivores and their predators.

<http://onlinelibrary.wiley.com/doi/10.1111/nph.15011/abstract;jsessionid=506478EC2F8A2D1F706FC7FC315E811A.f01t04>

<http://onlinelibrary.wiley.com/doi/10.1111/nph.15011/epdf>

and [University College London](#)

**When did flowers originate?**

<https://phys.org/news/2018-02-when-did-flowers-originate.html#jCp>

Kazuhiro Nakajima K. et al. (2018): **Precise and efficient nucleotide substitution near genomic nick via noncanonical homology-directed repair**. *Genome Research*, 2017; DOI: [10.1101/gr.226027.117](https://doi.org/10.1101/gr.226027.117)

CRISPR/Cas9, which generates DNA double-strand breaks (DSBs) at target loci, is a powerful tool for editing genomes when codelivered with a donor DNA template. However, DSBs, which are the most deleterious type of DNA damage, often result in unintended nucleotide insertions/deletions (indels) via mutagenic nonhomologous end joining. We developed a strategy for precise gene editing that does not generate DSBs. We show that a combination of single nicks in the target gene and donor plasmid (SNGD) using Cas9D10A nickase promotes efficient nucleotide substitution by gene editing. Nicking the target gene alone did not facilitate efficient gene editing. However, an additional nick in the donor plasmid backbone markedly improved the gene-editing efficiency. SNGD-mediated gene editing led to a markedly lower indel frequency than that by the DSB-mediated approach. We also show that SNGD promotes gene editing at endogenous loci in human cells. Mechanistically, SNGD-mediated gene editing requires long-sequence homology between the target gene and repair template, but does not require CtIP, RAD51, or RAD52. Thus, it is considered that noncanonical homology-directed repair regulates the SNGD-mediated gene editing. In summary, SNGD promotes precise and efficient gene editing and may be a promising strategy for the development of a novel gene therapy approach.

<http://genome.cshlp.org/content/28/2/223>

and Osaka University

New genome-editing method 'cuts back' on unwanted genetic mutations

Researchers develop novel method that can introduce precise modifications to defective genes with fewer safety drawbacks

<https://www.sciencedaily.com/releases/2018/02/180205092918.htm>

Messer K.D., Costanigro M. and Kaiser H.M. (2017): **Labeling Food Processes: The Good, the Bad and the Ugly**. *Applied Economic Perspectives and Policy*, Volume 39, Issue 3, 1 September 2017, Pages 407–427, <https://doi.org/10.1093/aep/ppx028>

Consumers are increasingly exposed to labels communicating specific processing aspects of food production, and recent state and federal legislation in the United States has called for making some of these labels mandatory. This article reviews the literature in this area and identifies the positive and negative aspects of labeling food processes. The good parts are that, under appropriate third-party or governmental oversight, process labels can effectively bridge the informational gap between producers and consumers, satisfy consumer demand for broader and more stringent quality assurance criteria, and ultimately create value for

both consumers and producers. Despite the appeal of the “Consumer Right to Know” slogan, process labeling also can have serious unintentional consequences. The bad parts are that consumers can misinterpret these labels and thus misalign their personal preferences and their actual food purchases. The ugly parts are that these labels can stigmatize food produced with conventional processes even when there is no scientific evidence that they cause harm, or even that it is compositionally any different. Based on this review of the literature, we provide three policy recommendations: (i) mandatory labeling of food processes should occur only in situations in which the product has been scientifically demonstrated to harm human health; (ii) governments should not impose bans on process labels because this approach goes against the general desire of consumers to know about and have control over the food they are eating, and it can undermine consumer trust of the agricultural sector; and (iii) a prudent policy approach is to encourage voluntary process labeling, perhaps using smart phone technology similar to that proposed in 2016 federal legislation related to foods containing ingredients that were genetically engineered.

<https://academic.oup.com/aep/article/39/3/407/4085217#96234080>

### **Mold infestation and aflatoxins production in traditionally processed spices and aromatic herbs powder mostly used in West Africa.** Food Science & Nutrition, DOI: 10.1002/fsn3.579

Mold infestation and occurrence of aflatoxins were investigated in 66 samples of dried spices and aromatic herbs powder (SAH) as commercialized in Benin and its neighboring countries. The samples were randomly collected from markets, supermarkets, and processing sites. Mold counts were enumerated according to standard method and aflatoxins levels were assessed using high-performance liquid chromatography coupled with fluorescence detection (HPLC-FLD). The results revealed that mold counts of samples ranged between 2.62 and 4.34 LogCFU/g. Aflatoxin B<sub>1</sub> contents were between 0.46 µg/kg and 84.84 µg/kg with 40% of samples exceeding the recommended limit of 5 µg/kg. Aflatoxins G<sub>1</sub> and G<sub>2</sub> levels were low in general with means values varying from 0.24 to 8.56 µg/kg, and 0.11 to 3.68 µg/kg, respectively. Fifty-two percent (52%) of samples analyzed contained total aflatoxins levels lower than the stipulated limit of 10 µg/kg, whereas 92% of them were contaminated at various levels with one type aflatoxin, B<sub>1</sub> or B<sub>2</sub>, G<sub>1</sub> or G<sub>2</sub>. This study provides the first information about the occurrence of aflatoxins in the common spices used in West Africa.

<http://onlinelibrary.wiley.com/doi/10.1002/fsn3.579/full>

### **Cook Q.S. and Burks W.A. (2018): Peptide and Recombinant Allergen Vaccines for Food Allergy.**

Clinic Rev Allerg Immunol; <https://doi.org/10.1007/s12016-018-8673-4>

Food allergy is a significant public health problem, with no suitable treatments available for patients. Currently, patients are limited to avoidance and the use of readily available emergency medications. Immunotherapy is an appealing therapeutic strategy for inducing tolerance. Studies with whole native allergens have demonstrated the efficacy of immunotherapy for food allergy; however, the risk of IgE-mediated reactions with such treatment is significant. Advances in molecular biology techniques, including purification, sequencing, and cloning, have allowed researchers to identify specific allergen components and T cell binding epitopes. Support for the use of recombinant and peptide vaccines for food allergy comes from prior studies involving aeroallergens and hymenoptera venom. By manipulating allergen structure and IgE binding, allergenicity can be reduced, thereby reducing systemic reactions, making recombinant and peptide vaccines a safe and effective form of immunotherapy. Pre-clinical studies using in vitro and murine models demonstrated a more tolerant state following the use of these therapies. Studies with human subjects will be necessary to characterize the effects of recombinant and peptide food allergy vaccines and to demonstrate a safe treatment option for patients.

<https://link.springer.com/article/10.1007/s12016-018-8673-4#citeas>

## **Tagungen – Meetings**

### **Genome Editing**

23.03.2018 Anuga FoodTech 2018 Messe Köln  
Wissenschaftlerkreis Grüne Gentechnik e.V. (WGG)

<http://www.anugafoodtec.de/aft/die-messe/events-und-veranstaltungen/veranstaltungssuche/index.php?tab=1&art=754&ort=27880&stichwort=trends>  
Programm als pdf-Datei angehängt.

### **7. Jahrestreffen der Seniorenexperten Chemie**

02.-04.05.2018 in Weimar

Allgemeine Informationen einschließlich Rahmenprogramm

<https://www.gdch.de/weimar2018>

Detailliertes Programm

<https://veranstaltungen.gdch.de/tms/frontend/index.cfm?l=8084&modus>

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

Bitte besuchen sie auch die Webseite des Wissenschaftlerkreis Grüne Gentechnik e.V. (WGG): [www.wgg-ev.de](http://www.wgg-ev.de) . Sie finden hier 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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