

# Sunday Evening News No 269

Week 09 (2022-28-02 – 2022-06-03)

Selected and edited by **BGF** Jany

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11 Tage Krieg in der Ukraine – Ein Krieg um territoriale Machansprüche für ein Großreich Russland durchzusetzen.

**Herr Putin stoppen sie diesen Krieg – Zeigen sie moralische Größe und beenden Sie das Leid der Bevölkerung und das Sterben von Zivilisten**

11 days war in Ukraine - A war to assert territorial power claims for a Russian empire.

**Mr. Putin stop this war - show moral greatness and end the suffering of the population and the death of civilians**

**Joint statement of DVGeo, DPG, GDCh and VBIO concerning the war in Ukraine.**

<https://www.vbio.de/aktuelles/details/joint-statement-of-dvgeo-dpg-gdch-and-vbio-concerning-the-war-in-ukraine>

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Eine Publikation der besonderen Art, die mit großer Sorgfalt und Vorsicht gelesen werden sollte. Nur sehr selten werden Publikationen in den Sunday Evening News kommentiert. Aber diese hier forderte es geradezu heraus (Siehe ► [Kommentar zu Shen et al. \(2022\)](#)).

A special kind of publication that should be read with great care and caution. Only very rarely publications are commented on in the Sunday Evening News. But this one was just asking for it. (see ► [Sunday Evening News 269 Supplement](#)).

<sup>s</sup> Shen, C., Yin, XC., Jiao, BY. et al. (2022): **Evaluation of adverse effects/events of genetically modified food consumption: a systematic review of animal and human studies.** *Environ Sci Eur* 34, 8 (2022). <https://doi.org/10.1186/s12302-021-00578-9>

**Conclusion:** Serious adverse events of GM consumption include mortality, tumour or cancer, significant low fertility, decreased learning and reaction abilities, and some organ abnormalities. Further clinical trials and long-term cohort studies in human populations, especially on GM food-related adverse events and the corresponding GM events, are still warranted. It suggests the necessity of labelling GM food so that consumers can make their own choice.

<https://enveurope.springeropen.com/articles/10.1186/s12302-021-00578-9>

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## Press Releases – Media Reports / Pressemeldungen und Medienberichte

Grossniklaus U: **Die Genomeditierung im Rahmen des Gentechnikgesetzes zu regeln, ist falsch**

<https://www.nzz.ch/meinung/die-genomeditierung-im-rahmen-des-gentechnikgesetzes-zu-regeln-ist-falsch-ld.1671138>

Global 2000: **Neue Gentechnik - NGO-Petition zur Regulierung von Gen-Food startet**

<https://amp.kleinezeitung.at/6105697>

Max Planck Institute for Plant Breeding Research. **"Potato genome decoded: The complete sequencing of the genetic material facilitates the breeding of new varieties."** ScienceDaily.

<https://www.sciencedaily.com/releases/2022/03/220303112155.htm>

University of Texas at Austin: **Gene editing gets safer thanks to redesigned Cas9 protein**  
[https://phys.org/news/2022-03-gene-safer-redesigned-cas9-protein.html?utm\\_source=nwletter&utm\\_medium=email&utm\\_campaign=daily-nwletter](https://phys.org/news/2022-03-gene-safer-redesigned-cas9-protein.html?utm_source=nwletter&utm_medium=email&utm_campaign=daily-nwletter)

**Testbiotech: No deregulation of CRISPR/Cas organisms in the EU through the backdoor!**  
<https://nextcloud.bauernstimme.de/index.php/s/Mffoxjt577Y4Yjg>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): March week 09)

### **Publications – Publikationen**

Puchta H., Jiang J., Wang K., Zhao Y. (2022): **Updates on gene editing and its applications**  
Plant Physiology, kiac032, <https://doi.org/10.1093/plphys/kiac032>  
<https://academic.oup.com/plphys/advance-article/doi/10.1093/plphys/kiac032/6539691>

Bravo, J.P.K., Liu, MS., Hibshman, G.N. et al. (2022): **Structural basis for mismatch surveillance by CRISPR–Cas9**. Nature | <https://doi.org/10.1038/s41586-022-04470-1>  
CRISPR–Cas9 as a programmable genome editing tool is hindered by off-target DNA cleavage<sup>1,2,3,4</sup>, and the underlying mechanisms by which Cas9 recognizes mismatches are poorly understood<sup>5,6,7</sup>. Although Cas9 variants with greater discrimination against mismatches have been designed<sup>8,9,10</sup>, these suffer from substantially reduced rates of on-target DNA cleavage<sup>5,11</sup>. Here we used kinetics-guided cryo-electron microscopy to determine the structure of Cas9 at different stages of mismatch cleavage. We observed a distinct, linear conformation of the guide RNA–DNA duplex formed in the presence of mismatches, which prevents Cas9 activation. Although the canonical kinked guide RNA–DNA duplex conformation facilitates DNA cleavage, we observe that substrates that contain mismatches distal to the protospacer adjacent motif are stabilized by reorganization of a loop in the RuvC domain. Mutagenesis of mismatch-stabilizing residues reduces off-target DNA cleavage but maintains rapid on-target DNA cleavage. By targeting regions that are exclusively involved in mismatch tolerance, we provide a proof of concept for the design of next-generation high-fidelity Cas9 variants.  
<https://www.nature.com/articles/s41586-022-04470-1>  
<https://www.nature.com/articles/s41586-022-04470-1.pdf>

Camerlengo, F.; Frittelli, A.; Pagliarello, R. (2022): **CRISPR towards a Sustainable Agriculture**. Encyclopedia 2, 538–558 | <https://doi.org/10.3390/encyclopedia2010036>  
Definition: Climate change and the need to feed an increasing population undermines food production and safety, representing the reasons behind the development of a new agriculture that is much more sustainable, productive and accessible worldwide. Genome editing and, in particular, clustered regularly interspaced palindromic repeats/CRISPR-associated protein (CRISPR/Cas) tools will play a major role in plant breeding to address these concerns. CRISPR/Cas includes a series of genome editing tools relying on the recognition and cleavage of target DNA/RNA sequences to introduce specific mutations.  
<https://www.mdpi.com/2673-8392/2/1/36>

Scholz, A.H., Freitag, J., Lyal, C.H.C. et al.(2022): **Multilateral benefit-sharing from digital sequence information will support both science and biodiversity conservation**. Nat Commun 13, 1086 | <https://doi.org/10.1038/s41467-022-28594-0>  
Open access to sequence data is a cornerstone of biology and biodiversity research, but has created tension under the United Nations Convention on Biological Diversity (CBD). Policy decisions could compromise research and development, unless a practical multilateral solution is implemented.  
<https://www.nature.com/articles/s41467-022-28594-0.pdf>

Ma J., Wang S., Zhu X. et.al. (2022): **Major episodes of horizontal gene transfer drove the evolution of land plants**. Molecular Plant | [doi: 10.1016/j.molp.2022.02.001](https://doi.org/10.1016/j.molp.2022.02.001)  
How horizontal gene transfer (HGT) has contributed to the evolution of animals and plants remains a major puzzle. Despite recent progress, defining the overall scale and pattern of HGT events in land plants has been largely elusive. In this study, we performed systematic analyses for acquired genes in different plant groups and throughout land plant evolution. We found that relatively recent HGT events occurred in charophytes and all major land plant groups, but their frequency declined rapidly in seed plants. Two major episodes of HGT events occurred in land plant evolution, corresponding to the early evolution of streptophytes and the origin of land plants, respectively. Importantly, a vast majority of the genes acquired in the two episodes have been retained in descendant groups, affecting numerous activities and processes of land plants. We analyzed some of the acquired genes involved in stress responses, ion and metabolite transport, growth and development, and specialized metabolism, and further assessed the cumulative effects of HGT in land plants.  
[https://www.cell.com/molecular-plant/fulltext/S1674-2052\(22\)00049-1](https://www.cell.com/molecular-plant/fulltext/S1674-2052(22)00049-1)  
<https://www.cell.com/action/showPdf?pii=S1674-2052%2822%2900049-1>

Sorbo A., Pucci E., Nobili C., Taglieri I., Passeri D., Zoani C. (2022): **Food Safety Assessment: Overview of Metrological Issues and Regulatory Aspects in the European Union.** Separations 9 (2), 53 | <https://doi.org/10.3390/separations9020053>

The safety of the food we consume has a direct impact on individual and population health and affects the economic growth of the region where food safety is practised and enhanced. The central goal of the European Commission's Food Safety policy is to ensure a high level of protection of human health covering the whole supply chain. In recent years, great attention has been paid to food testing and the application of metrological tools to support food safety. The global food market and national and international food safety regulations have created a huge demand for the measurement traceability and comparability of analytical results that are independent of time or space boundaries. This review provides an overview of the European food safety policy and regulation, with a focus on the measurement-related elements of the European Union (EU) food law. It also highlights how the application of analytical techniques, with particular reference to separation approaches, and metrological tools can ensure the control of certain contaminants that nowadays represent the main challenges for food safety (e.g., mycotoxins, nanoparticles, emerging and process contaminants). METROFOOD-RI-Infrastructure for promoting metrology in food and nutrition is therefore described in this context. This European research infrastructure has been developed and is being implemented in the frame of the European Strategy Forum on Research Infrastructures (ESFRI) to support metrology in food and nutrition and establish a strategy allowing reliable and comparable analytical measurements in food across the entire process line, from primary producers to consumers, and making data findable, accessible, interoperable, and reusable (FAIR).

<https://www.mdpi.com/2297-8739/9/2/53>

Benevenuto R.F., Venter H.J., Zanatta C.B., Nodari R.O., Agapito-Tenfen S.Z. (2022): **Alterations in genetically modified crops assessed by omics studies: Systematic review and meta-analysis,** Trends in Food Science & Technology, 120, 325-337 |

<https://doi.org/10.1016/j.tifs.2022.01.002>.

Background: International agreements and domestic legislation regulate genetically modified (GM) crops for environmental release, recognizing that genetic engineering could result in unintended genotypic and phenotypic effects. In that context, omics technologies, which allow comprehensive characterization of the molecular profile of GM crops at all levels, may be used to assess alterations or effects of genetic engineering. Objective: To determine whether omics techniques are suitable tools to comprehensively screen for metabolic changes due to [genetic modification](#) in plants.

Approaches: A literature search was conducted in four online scientific databases for relevant publications. After removal of duplicates, we retained only studies that included *cry*, *epsps* and *pat/bar* transgenes. We evaluated the full texts of the remaining papers and performed data extraction. We placed the extracted outcomes into an evidence table, which comprised six major categories, including an analysis of altered metabolic pathways based on the KEGG pathway database.

Main findings: Sixty articles were included in this review. We found a high proportion of publicly funded studies (86.7%) compared to just three with industry financial support. We found that 40% of the plant material analyzed was produced in the field, 26.7% in growth chambers, and 18.3% in greenhouse experiments, although this information could not be extracted from all studies. More than one third (38.4%) of the studies did not use a non-GM near-isogenic line as a comparator, and half did not specify the number of plants used per sample in their reports. All the studies (except three that did not perform a comparative analysis) reported statistical differences in GM versus non-GM omic profiles. A heatmap analysis showed that the most frequently affected metabolic pathways were related to metabolism of carbohydrates, energy, lipids, and amino acids, as well as genetic information processing and environmental information processing.

Conclusion: This review shows that omics techniques can profile different levels of genetic information and metabolism and can be useful tools in assessing alterations in [genetically modified plants](#). In recent years, there have been intensive efforts to harmonize omics methods. Consistent guidelines with standardized frameworks are needed to capitalize on the unquestionable potential of implementing untargeted omics analyses in the risk assessment process. Finally, there is a need to build an assessment framework connecting omics results to biologically relevant changes in the [GM organism](#), and this framework to be operable for the risk assessment process.

<https://www.sciencedirect.com/science/article/pii/S0924224422000024>

MacIntosh S.C., Shaw M., Connelly M., Yao Z.J. (2021): **Food and Feed Safety of NS-B5ØØ27-4 Omega-3 Canola (*Brassica napus*): A New Source of Long-Chain Omega-3 Fatty Acids.** Front. Nutr., | <https://doi.org/10.3389/fnut.2021.716659>

DHA canola, a genetically engineered *Brassica napus* (OECD Unique Identifier NS-B5ØØ27-4), has been developed as one of the first land-based production systems for omega-3 long-chain polyunsaturated fatty acids (LCPUFA), whose health benefits are well-established. Yet, the marine sources of these nutrients are under high pressures due to over-fishing and increasing demand. DHA canola is a plant-based source for these essential fatty acids that produces a high level of docosahexaenoic acid (DHA). This terrestrial system allows for sustainable, scalable and stable production of omega-3 LCPUFA that addresses not only the increasing market demand, but also the complex interplay of agriculture, aquaculture, and human nutrition. The vector used to produce the desired oil profile in DHA canola contains the expression cassettes of seven genes in the DHA biosynthesis pathway and was specifically designed to convert oleic acid to DHA in canola seed. The characterization and safety evaluation of food and feed produced from DHA canola are described and

supported by a detailed nutritional analysis of the seed, meal, and oil. Aside from the intended changes of the fatty acid profile, none of the other compositional analytes showed biologically meaningful differences when compared to conventional canola varieties. In addition, the meal from DHA canola is compositionally equivalent to conventional canola meal. Further evidence of nutritional value and safety of DHA canola oil have been confirmed in fish feeding studies. Given that most human populations lack sufficient daily intakes of omega-3 LCPUFA, a dietary exposure assessment is also included. In conclusion, the results from these studies demonstrate it is safe to use products derived from DHA canola in human foods, nutraceuticals, or animal feeds.

<https://www.frontiersin.org/articles/10.3389/fnut.2021.716659/full>

Lin H-Y. , Liao J-W., Chen R.-S., Chang C-H. et al. (2022): **Food Safety Assessment of Commercial Genetically Modified Soybeans in Rats.** *Foods*, 11(4), 496 |

<https://doi.org/10.3390/foods11040496>

Although the safety of commercial genetically modified (GM) soybeans has been well evaluated and GM soybeans are legally sold under government management, some consumers still have concerns about their safety. The objective of this study was to evaluate the safety of commercial GM soybeans sold in markets as a food source. In the present study, two commercial GM (GM-1 and -2) soybeans and one non-GM soybean were randomly purchased and subjected to a whole food toxicity assessment. Rats (SD), male and female, were divided into six groups (10/sex/group). Two dosages of 1 g/kg/day and 5 g/kg/day of soybeans were selected for the low- and high-dose groups. Rats were administered the soybeans via daily oral fed for 90 days. The results indicate that the body weight, organ weight, biochemistry, hematology, and urology showed no biologically adverse effects. At necropsy, no significant differences between organ weights were noted between the non-GM- and GM soybeans-treated groups. Moreover, no gross or histopathological lesions were observed in the high-dosage (5 g/kg/day) fed groups of the non-GM and GM soybean fed rats. In conclusion, this food safety assessment revealed that commercial GM soybeans are substantially equivalent to non-GM soybeans in rats.

<https://www.mdpi.com/2304-8158/11/4/496>

Roberts A.J. and Thizy D. (2022): **Articulating ethical principles guiding Target Malaria's engagement strategy.** *Malaria Journal* 21:35 |

<https://doi.org/10.1186/s12936-022-04062-4>

Progress in gene drive research has engendered a lively discussion about community engagement and the ethical standards the work hinges on. While there is broad agreement regarding ethical principles and established best practices for conducting clinical public health research, projects developing area-wide vector control technologies and initiating ambitious engagement strategies raise specific questions: who to engage, when to engage, and how? When responding to these fundamental questions, with few best practices available for guidance, projects need to reflect on and articulate the ethical principles that motivate and justify their approach. Target Malaria is a not-for-profit research consortium that aims to develop and share malaria control and elimination technology. The consortium is currently investigating the potential of a genetic technique called gene drive to control populations of malaria vectoring mosquito species *Anopheles gambiae*. Due to the potentially broad geographical, environmental impact of gene drive technology, Target Malaria has committed to a robust form of tailored engagement with the local communities in Burkina Faso, Mali, and Uganda, where research activities are currently taking place. This paper presents the principles guiding Target Malaria's engagement strategy. Herein the authors (i) articulate the principles; (ii) explain the rationale for selecting them; (iii) share early lessons about the application of the principles. Since gene drive technology is an emerging technology, with few best practices available for guidance, the authors hope by sharing these lessons, to add to the growing literature regarding engagement strategies and practices for area-wide vector control, and more specifically, for gene drive research.

<https://malariajournal.biomedcentral.com/track/pdf/10.1186/s12936-022-04062-4.pdf>

Mallapaty S.: **How to protect the first 'CRISPR babies' prompts ethical debate**

Fears of excessive interference cloud proposal for protecting children whose genomes were edited, as He Jiankui's release from jail looks imminent.

Nature (2022) | doi: <https://doi.org/10.1038/d41586-022-00512-w>

<https://www.nature.com/articles/d41586-022-00512-w>

**EFSA:**

Lambre C, Barat Baviera JM, Bolognesi C, Coconcelli PS, Crebelli R, Gott DM, Grob K, Lampi E, Mengelers M, Mortensen A, Riviere G, Steffensen I-L, Tlustos C, Van Loveren H, Vernis L, Zorn H, Glandorf B, Herman L, Andryszkiewicz M, Gomes A, Liu Y, Rainieri S and Chesson A, 2022. **Safety evaluation of the food enzyme glucose oxidase from the genetically modified *Aspergillus niger* strain DP-Aze23.** *EFSA Journal* 2022;20(3):7181, 18 pp. <https://doi.org/10.2903/j.efsa.2022.7181>

<https://www.efsa.europa.eu/de/efsajournal/pub/7181>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2022.7181>

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](http://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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