

# Sunday Evening News No 323

2023-04-17 – 2023-04-23

Compiled and edited by **BGF** Jany



## Meetings -Conferences / Tagungen - Konferenzen

**National Associations Council Spanish Presidency Summit: A global Europe - the role of transformative legislation**

22.Juni 2023 14:00

[https://us06web.zoom.us/webinar/register/WN\\_bBV8xqXASHeIP5SCZSh3qQ#/registration](https://us06web.zoom.us/webinar/register/WN_bBV8xqXASHeIP5SCZSh3qQ#/registration)

## Press Releases -Media / Presse- und Medienberichte

Wess L. (2023): **Zucht und Angst** Cicero 4-2023

Pdf-file available

Table-Media: **Grüne Gentechnik: Lemke und andere Gegner bremsen**

<https://table.media/europe/news/gruene-gentechnik-lemke-und-andere-gegner-bremsen/>

[https://table.media/berlin/wp-content/uploads/sites/21/2023/04/Brief\\_Gewessler\\_Rauch.pdf](https://table.media/berlin/wp-content/uploads/sites/21/2023/04/Brief_Gewessler_Rauch.pdf)

Aktion-Agrar: **Saatgut ohne Gentechnik – Gentechnikfreiheit in Europa!**

<https://www.aktion-agrar.de/saatgut-ohne-gentechnik/petition/>

Petition / Unterschriftenaktion an die Umweltministerin Lembke

EU-Commission: **LISTE DES POINTS PRÉVUS POUR FIGURER A L'ORDRE DU JOUR DES PROCHAINES RÉUNIONS DE LA COMMISSION**

Agenda / Tagesordnung

<https://www.politico.eu/wp-content/uploads/2023/04/18/document.pdf>

Riskmonger: **NGO Science: Inside the Mind of a Cult Eco-Warrior**

<https://risk-monger.com/2023/04/18/ngo-science-inside-the-mind-of-a-cult-eco-warrior/>

pdf-Datei auf Deutsch vorhanden- dasOriginal: **Demokratie achten – Wahlfreiheit erhalten**

Keine Gentechnik ohne Risikoprüfung und Kennzeichnung auf unseren Äckern und Teller  
Eine gemeinsame Framing für eine gemeinsame Plattform

FAO: **Food Safety of Gene-Editing “Not Much Different” than Traditional Breeding Techniques**

<https://www.food-safety.com/articles/8522-fao-food-safety-of-gene-editing-not-much-different-than-traditional-breeding-techniques>

Der Report: <https://www.fao.org/3/cc5136en/cc5136en.pdf>

Institute of Development Studies: **New research casts doubt on GM crops as solution for global food crisis**

<https://www.ids.ac.uk/news/new-research-casts-doubt-on-gm-crops-as-solution-for-global-food-crisis/>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): April week 16.

## Publications – Publikationen

Rathenau Instituut (2023). **Editing under provision – Dutch citizens’ views on new genomic techniques in food crops**. Den Haag. Authors: Habets, M., I. Pirson, P. Macnaghten and P. Verhoef

<https://www.rathenau.nl/sites/default/files/2023-04/Rapport%20Editing%20under%20provision.pdf>

Montoliu, L. (2023): **Transgenesis and Genome Engineering: A Historical Review**. In: Saunders, T.L. (eds) Transgenesis. Methods in Molecular Biology, vol 2631. Humana, New York, NY. [https://doi.org/10.1007/978-1-0716-2990-1\\_1](https://doi.org/10.1007/978-1-0716-2990-1_1)

Our ability to modify DNA molecules and to introduce them into mammalian cells or embryos almost appears in parallel, starting from the 1970s of the last century. Genetic engineering techniques rapidly developed between 1970 and 1980. In contrast, robust procedures to microinject or introduce DNA constructs into individuals did not take off until 1980 and evolved during the following two decades. For some years, it was only possible to add transgenes, de novo, of different formats, including artificial chromosomes, in a variety of vertebrate species or to introduce specific mutations essentially in mice, thanks to the gene-targeting methods by homologous recombination approaches using mouse embryonic stem (ES) cells. Eventually, genome-editing tools brought the possibility to add or inactivate DNA sequences, at specific sites, at will, irrespective of the animal species involved. Together with a variety of additional techniques, this chapter will summarize the milestones in the transgenesis and genome engineering fields from the 1970s to date.

[https://link.springer.com/protocol/10.1007/978-1-0716-2990-1\\_1](https://link.springer.com/protocol/10.1007/978-1-0716-2990-1_1)

Latorre S.M, Were V.M., Foster A.J., Langner T. et al. (2023): **Genomic surveillance uncovers a pandemic clonal lineage of the wheat blast fungus.** PLoS Biol 21(4): e3002052 |

<https://doi.org/10.1371/journal.pbio.3002052>

Wheat, one of the most important food crops, is threatened by a blast disease pandemic. Here, we show that a clonal lineage of the wheat blast fungus recently spread to Asia and Africa following two independent introductions from South America. Through a combination of genome analyses and laboratory experiments, we show that the decade-old blast pandemic lineage can be controlled by the Rmg8 disease resistance gene and is sensitive to strobilurin fungicides. However, we also highlight the potential of the pandemic clone to evolve fungicide-insensitive variants and sexually recombine with African lineages. This underscores the urgent need for genomic surveillance to track and mitigate the spread of wheat blast outside of South America and to guide preemptive wheat breeding for blast resistance.

<https://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.3002052>

Singh C., Kumar R., Sehgal H., Bhati S. et al. (2023): **Unclasp potentials of genomics and gene editing in chickpea to fight climate change and global hunger threat.** Front. Genet.14 |

<https://doi.org/10.3389/fgene.2023.1085024>

Genomics and genome editing promise enormous opportunities for crop improvement and elementary research. Precise modification in the specific targeted location of a genome has profited over the unplanned insertional events which are generally accomplished employing unadventurous means of genetic modifications. The advent of new genome editing procedures viz; zinc finger nucleases (ZFNs), homing endonucleases, transcription activator like effector nucleases (TALENs), Base Editors (BEs), and Primer Editors (PEs) enable molecular scientists to modulate gene expressions or create novel genes with high precision and efficiency. However, all these techniques are exorbitant and tedious since their prerequisites are difficult processes that necessitate protein engineering. Contrary to first generation genome modifying methods, CRISPR/Cas9 is simple to construct, and clones can hypothetically target several locations in the genome with different guide RNAs. Following the model of the application in crop with the help of the CRISPR/Cas9 module, various customized Cas9 cassettes have been cast off to advance mark discrimination and diminish random cuts. The present study discusses the progression in genome editing apparatuses, and their applications in chickpea crop development, scientific limitations, and future perspectives for biofortifying cytokinin dehydrogenase, nitrate reductase, superoxide dismutase to induce drought resistance, heat tolerance and higher yield in chickpea to encounter global climate change, hunger and nutritional threats.

<https://www.frontiersin.org/articles/10.3389/fgene.2023.1085024/full>

Marin A., Stubrin L., Patrick van Zwanenberg P. (2023): **Technological lock-in in action: Appraisal and policy commitment in Argentina's seed sector** Research Policy 52 (2): 104678 |

<https://doi.org/10.1016/j.respol.2022.104678>

This paper uses novel empirical evidence to analyse critically the widely held view that genetic engineering technology played a pivotal role in explaining the rapid expansion and increase in productivity of soy production in Argentina over the period from 1995 to 2015. We estimate the relative contribution of different approaches to seed innovation on soy performance over that period. We show how previous analyses have ignored the performance gains from plant breeding or misattributed them to genetic engineering. In our disaggregated assessment, seed innovations based on breeding techniques provide just as plausible an explanation for the expansion and performance gains of soy production. We illustrate how policy support to the seed [industry](#) is consistent with and is justified by mainstream narratives about the central role played by plant genetic engineering technology, and how the asymmetries created by these policy responses are contributing to the crowding out of plant breeding. This evidence, in our view, illustrates an important cognitive mechanism of lock-in to what may be a sub-optimal technology.

<https://www.sciencedirect.com/science/article/abs/pii/S0048733322001998?dgcid=author>

Essa Ali and Kewei Zhang (2023): **CRISPR-mediated technology for seed oil improvement in rapeseed: Challenges and future perspectives.** Front. Plant Sci. 14 |

<https://doi.org/10.3389/fpls.2023.1086847>

Rapeseed not only provide considerable amount of edible oil with high nutritional properties but can also be used as a raw material for biofuel production in many industries. It is therefore in high demand to bring genetic changes in order to fulfill the need of human and of industries. Though traditional breeding techniques such as hybridization and mutagenesis remained the top methods for long time to create improved varieties in oilseed

rape. Clustered regularly interspaced short palindromic repeats (CRISPR) is becoming one of the most valuable gene editing technologies that allow precise genome engineering, and open new ways for research in plant functional genomics. Though CRISPR has been used in many other crops for genetic improvement it is expected to be an effective tool for genome editing and molecular design in oilseed rape for seed oil improvement. This mini review will discuss and summarize the past and ongoing research and development in rapeseed in terms of seed oil improvement and fatty acid composition using CRISPR technology. In addition, the factors that hinder the efficiency of this tool and how to eliminate those factors will be briefly summarized. The improvement of CRISPR technology for getting better results in oilseed rape will also be considered here. This minireview will open new windows for researchers in *Brassica napus* oil improvement research and genetic improvement using CRISPR technology.

<https://www.frontiersin.org/articles/10.3389/fpls.2023.1086847/full>

Sahu, A., Verma, R., Gupta, U. et al. (2023): **An Overview of Targeted Genome Editing Strategies for Reducing the Biosynthesis of Phytic Acid: an Anti-nutrient in Crop Plants.** Mol Biotechnol | <https://doi.org/10.1007/s12033-023-00722-1>

Anti-nutrients are substances either found naturally or are of synthetic origin, which leads to the inactivation of nutrients and limits their utilization in metabolic processes. Phytic acid is classified as an anti-nutrient, as it has a strong binding affinity with most minerals like Fe, Zn, Mg, Ca, Mn, and Cd and impairs their proper metabolism. Removing anti-nutrients from cereal grains may enable the bioavailability of both macro- and micronutrients which is the desired goal of genetic engineering tools for the betterment of agronomic traits. Several strategies have been adopted to minimize phytic acid content in plants. Pursuing the molecular strategies, there are several studies, which result in the decrement of the total phytic acid content in grains of major as well as minor crops. Biosynthesis of phytic acid mainly takes place in the seed comprising lipid-dependent and lipid-independent pathways, involving various enzymes. Furthermore, some studies show that interruption of these enzymes may involve the pleiotropic effect. However, using modern biotechnological approaches, undesirable agronomic traits can be removed. This review presents an overview of different genes encoding the various enzymes involved in the biosynthetic pathway of phytic acid which is being targeted for its reduction. It also, highlights and enumerates the variety of potential applications of genome editing tools such as TALEN, ZFN, and CRISPR/Cas9 to knock out the desired genes, and RNAi for their silencing.

<https://link.springer.com/article/10.1007/s12033-023-00722-1#Ack1>

Haas J., Beck E. , Troczka B.J., Hayward A. et al. (2023): **A conserved hymenopteran-specific family of cytochrome P450s protects bee pollinators from toxic nectar alkaloids.** Science Advances 9, Issue 15 | DOI: [10.1126/sciadv.adg0885](https://doi.org/10.1126/sciadv.adg0885)

Many plants produce chemical defense compounds as protection against antagonistic herbivores. However, how beneficial insects such as pollinators deal with the presence of these potentially toxic chemicals in nectar and pollen is poorly understood. Here, we characterize a conserved mechanism of plant secondary metabolite detoxification in the Hymenoptera, an order that contains numerous highly beneficial insects. Using phylogenetic and functional approaches, we show that the CYP336 family of cytochrome P450 enzymes detoxifies alkaloids, a group of potent natural insecticides, in honeybees and other hymenopteran species that diverged over 281 million years. We linked this function to an aspartic acid residue within the main access channel of CYP336 enzymes that is highly conserved within this P450 family. Together, these results provide detailed insights into the evolution of P450s as a key component of detoxification systems in hymenopteran species and reveal the molecular basis of adaptations arising from interactions between plants and beneficial insects.

<https://www.science.org/doi/10.1126/sciadv.adg0885>

Barreto, H.C., Gordo, I. (2023): **Intrahost evolution of the gut microbiota.** Nat Rev Microbiol | <https://doi.org/10.1038/s41579-023-00890-6>

A massive number of microorganisms, belonging to different species, continuously divide inside the guts of animals and humans. The large size of these communities and their rapid division times imply that we should be able to watch microbial evolution in the gut in real time, in a similar manner to what has been done in vitro. Here, we review recent findings on how natural selection shapes intrahost evolution (also known as within-host evolution), with a focus on the intestines of mice and humans. The microbiota of a healthy host is not as static as initially thought from the information measured at only one genomic marker. Rather, the genomes of each gut-colonizing species can be highly dynamic, and such dynamism seems to be related to the microbiota species diversity. Genetic and bioinformatic tools, and analysis of time series data, allow quantification of the selection strength on emerging mutations and horizontal transfer events in gut ecosystems. The drivers and functional consequences of gut evolution can now begin to be grasped. The rules of this intrahost microbiota evolution, and how they depend on the biology of each species, need to be understood for more effective development of microbiota therapies to help maintain or restore host health.

<https://www.nature.com/articles/s41579-023-00890-6>

Graham, A.E., Ledesma-Amaro, R. (2023): **The microbial food revolution.** Nat Commun 14, 2231 | <https://doi.org/10.1038/s41467-023-37891-1>

Our current food system relies on unsustainable practices, which often fail to provide healthy diets to a growing population. Therefore, there is an urgent demand for new sustainable nutrition sources and processes. Microorganisms have gained attention as a new food source solution, due to their low carbon footprint, low

reliance on land, water and seasonal variations coupled with a favourable nutritional profile. Furthermore, with the emergence and use of new tools, specifically in synthetic biology, the uses of microorganisms have expanded showing great potential to fulfil many of our dietary needs. In this review, we look at the different applications of microorganisms in food, and examine the history, state-of-the-art and potential to disrupt current foods systems. We cover both the use of microbes to produce whole foods out of their biomass and as cell factories to make highly functional and nutritional ingredients. The technical, economical, and societal limitations are also discussed together with the current and future perspectives.

<https://www.nature.com/articles/s41467-023-37891-1>

## EFSA

GMO Panel (2023): **Statement on the risk assessment of additional information on maize MIR162**. EFSA Journal 21( 4): 7935, 8 pp. | <https://doi.org/10.2903/j.efsa.2023.7935>  
<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.7935>

CEP Panel (2023): **Scientific Opinion on the safety evaluation of the food enzyme phospholipase A2 from porcine pancreas**. EFSA Journal 21 ( 4): 7913, 11 pp. | <https://doi.org/10.2903/j.efsa.2023.7913>

Aufgrund zahlreich fehlender Daten konnte keine Bewertung durchgeführt werden – Der Ausschuss kann keine Aussage zur Sicherheit des Lebensmittelenzyms machen.

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.7913>

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

*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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