

Sunday Evening News No 324

2023-04-24 – 2023-04-30

Compiled and edited by **BGF** Jany



Meetings – Conferences / Veranstaltungen - Konferenzen

Labvolution 2023: Die ganze Welt des Labors

09. – 10. Mai 2023 in Hannover

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

Wissenschaftskreis Genomik und Gentechnik e.V. (WGG)

Genome Editing: Potentiale neuer genomischer Techniken für eine nachhaltige Landwirtschaft und Lebensmittelproduktion.

10. Mai 2023 | 10.00 – 11.45 Uhr | INDUSTRY FORUM Halle 20 Stand D18

<https://www.labvolution.de/de/rahmenprogramm/genome-editing/>

oder

<https://www.labvolution.de/veranstaltung/genome-editing/for/103823>

VLOG: „International Non-GMO Summit“

09.-10. Mai 2023 Frankfurt/Main

Am 9. und 10. Mai findet in Frankfurt am Main der erste „International Non-GMO Summit“ statt. Erstmals treffen sich Unternehmen und Expert:innen aus der gesamten „Ohne Gentechnik“-Wertschöpfungskette zu einer hochkarätigen internationalen Konferenz

<https://www.ohnegentechnik.org/ueber-uns/presse/artikel/international-non-gmo-summit-am-9-und-10-mai-2023-in-frankfurt>

Zukunftsdialog Agrar und Ernährung 2023

11. Mai 2023

Alte Münze, Berlin

<https://dfvcg-events.de/zdae/>

ENSSER: The integrity of science

A conference about the conflict between public policy and independent science, in honour of Dr. Árpád Pusztai (1930 – 2021)

Edinburgh (UK), 26 – 27 May 2023

open to both on site and online participation

https://ensser.org/events/events_2023/2nd-announcement-the-integrity-of-science/

Press Releases -Media / Presse- und Medienberichte

Müller-Jung J.: **Technologie offen auf dem Feld**, FAZ 28.04.2023 pdf-Datei vorhanden

Quoos J.: **Stark-Watzinger (FDP), Bundesministerin für Bildung und Forschung, spricht sich für neue EU-Regeln bei der Pflanzen-Gentechnik aus**

<https://www.morgenpost.de/politik/article238263261/stark-watzinger-eu-gentechnik-regeln-lockerung.html>

<https://california18.com/eu-genetic-engineering-rules-stark-watzinger-fdp-calls-for-relaxation/10617932023/>

Informationsdienst Gentechnik: **Neues Gentechnikrecht erst nach Europawahl?**

<https://www.keine-gentechnik.de/nachricht/34757?cHash=8ab956aaafcd5a131f81991c91ce3f16>

POINT NEWSLETTER NR. 250 – APRIL 2023 - **Aktuelle Biotechnologie**

[https://www.scienceindustries.ch/file/33813/point-2023-04-250-](https://www.scienceindustries.ch/file/33813/point-2023-04-250-d.pdf?utm_source=POINT+Newsletter&utm_campaign=342b05159e-)

[d.pdf?utm_source=POINT+Newsletter&utm_campaign=342b05159e-](https://www.scienceindustries.ch/file/33813/point-2023-04-250-d.pdf?utm_source=POINT+Newsletter&utm_campaign=342b05159e-)

[POINT_250_Live&utm_medium=email&utm_term=0_19eef28c92-342b05159e-1210937714](https://www.scienceindustries.ch/file/33813/point-2023-04-250-d.pdf?utm_source=POINT+Newsletter&utm_campaign=342b05159e-1210937714)

Cerier S.: **Germany is the major obstacle to the adoption of gene editing and other crop biotechnology innovations in the EU. When might that change?**

<https://geneticliteracyproject.org/2023/04/26/germany-is-the-major-obstacle-to-the-adoption-of-gene-editing-and-other-crop-biotechnology-innovations-in-the-eu-when-might-that-change/>

Ministerial lunch – New genomic techniques for plants

https://table.media/berlin/wp-content/uploads/sites/21/2023/04/Council_SE_NGT_Note_Agricouncil_2023-04-25.pdf

Contreras A.: Writ of kalikasan and science: Is the risk from GMOs or from judicial activism?

<https://www.manilatimes.net/2023/04/29/opinion/columns/writ-of-kalikasan-and-science-is-the-risk-from-gmos-or-from-judicial-activism/1889176>

Beda M. Stadler: Wir zwei für die Zukunft

<https://cameo-verlag.com/product/wir-zwei-fuer-die-zukunft/>

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 17

Publications – Publikationen

Calabrese, C., Albarracín, D. (2023): **Bypassing misinformation without confrontation improves policy support as much as correcting it.** *Sci Rep* 13, 6005 |

<https://doi.org/10.1038/s41598-023-33299-5>

Curbing the negative impact of misinformation is typically assumed to require correcting misconceptions. Conceivably, however, bypassing the misinformation through alternate beliefs of opposite implications may reduce the attitudinal impact of the misinformation. Three experiments, one preregistered with a sample representative of the United States population, examined the impact of (a) directly correcting prior misinformation offered in support of restricting Genetically Modified (GM) foods (i.e., the correction strategy) and (b) discussing information in support of GM foods (i.e., the bypassing strategy), compared to a misinformation-only control condition. Findings consistently revealed that bolstering beliefs with opposite implications is just as effective at reducing opposition to GM foods as is correcting misinformation about GM foods. Thus, bypassing should be added to our arsenal of methods to curb the impact of misinformation.

<https://www.nature.com/articles/s41598-023-33299-5>

Hirt H., Al-Babili S, Almeida-Trapp M., Martin A. et al. (2023): **PlantACT! – how to tackle the climate crisis.** Special issue: Food security:

Greenhouse gas (GHG) emissions have created a global climate crisis which requires immediate interventions to mitigate the negative effects on all aspects of life on this planet. As current agriculture and land use contributes up to 25% of total GHG emissions, plant scientists take center stage in finding possible solutions for a transition to sustainable agriculture and land use. In this article, the PlantACT! (Plants for climate ACTION!) initiative of plant scientists lays out a road map of how and in which areas plant scientists can contribute to finding immediate, mid-term, and long-term solutions, and what changes are necessary to implement these solutions at the personal, institutional, and funding levels.

<https://www.sciencedirect.com/science/article/pii/S1360138523000249>

Hodge R, on behalf of the *PLOS Biology* staff editors (2023): **The future is bright, the future is biotechnology.** *PLoS Biol* 21(4): e3002135. <https://doi.org/10.1371/journal.pbio.3002135>

Zhou Z., Liu Y, Feng Y., Klepin S., Tsimring L.S. et al. (2023): **Engineering longevity—design of a synthetic gene oscillator to slow cellular aging.** *Science* 380 (6643), 376-381 | [DOI: 10.1126/science.add7631](https://doi.org/10.1126/science.add7631)

Synthetic biology enables the design of gene networks to confer specific biological functions, yet it remains a challenge to rationally engineer a biological trait as complex as longevity. A naturally occurring toggle switch underlies fate decisions toward either nucleolar or mitochondrial decline during the aging of yeast cells. We rewired this endogenous toggle to engineer an autonomous genetic clock that generates sustained oscillations between the nucleolar and mitochondrial aging processes in individual cells. These oscillations increased cellular life span through the delay of the commitment to aging that resulted from either the loss of chromatin silencing or the depletion of heme. Our results establish a connection between gene network architecture and cellular longevity that could lead to rationally designed gene circuits that slow aging.

<https://www.science.org/doi/10.1126/science.add7631>

Eckerstorfer M.F., Dolezel M., Engelhard M., Giovannelli V. et I. (2023): **Recommendations for the Assessment of Potential Environmental Effects of Genome-Editing Applications in Plants in the EU.** *Plants* 12 (9), 1764; <https://doi.org/10.3390/plants12091764>

The current initiative of the European Commission (EC) concerning plants produced using certain new genomic techniques, in particular, targeted mutagenesis and cisgenesis, underlines that a high level of protection for human and animal health and the environment needs to be maintained when using such applications. The current EU biosafety regulation framework ensures a high level of protection with a mandatory environmental risk assessment (ERA) of genetically modified (GM) products prior to the authorization of individual GMOs for

environmental release or marketing. However, the guidance available from the European Food Safety Authority (EFSA) for conducting such an ERA is not specific enough regarding the techniques under discussion and needs to be further developed to support the policy goals towards ERA, i.e., a case-by-case assessment approach proportionate to the respective risks, currently put forward by the EC. This review identifies important elements for the case-by-case approach for the ERA that need to be taken into account in the framework for a risk-oriented regulatory approach. We also discuss that the comparison of genome-edited plants with plants developed using conventional breeding methods should be conducted at the level of a scientific case-by-case assessment of individual applications rather than at a general, technology-based level. Our considerations aim to support the development of further specific guidance for the ERA of genome-edited plants.

<https://www.mdpi.com/2223-7747/12/9/1764>

Koller, F., Schulz, M., Juhas, M. et al. (2023): **The need for assessment of risks arising from interactions between NGT organisms from an EU perspective.** *Environ Sci Eur* 35, 27 (2023).

<https://doi.org/10.1186/s12302-023-00734-3>

Background: New genomic techniques (NGTs) allow new genotypes and traits to be developed in different ways and with different outcomes compared to previous genetic engineering methods or conventional breeding (including non-targeted mutagenesis). EU GMO regulation requires an assessment of their direct and indirect effects that may be immediate, delayed or cumulative. Such effects may also result from the interactions of NGT organisms simultaneously present in a shared receiving environment or emerge from a combination of their traits. This review elaborates such potential interactions based on a literature review and reasoned scenarios to identify possible pathways to harm.

Main findings: NGT organisms might be introduced into the environment and food chains on a large-scale, involving many traits, across a broad range of species and within short periods of time. Unavoidably, this would increase the likelihood that direct or indirect effects will occur through interactions between NGT organisms that are, for example simultaneously present within a shared environment. It has to be assumed that the cumulative effects of these NGT organisms may exceed the sum of risks identified in the distinct 'events'. Consequently, risk assessors and risk managers not only need to consider the risks associated with individual NGT organisms ('events'), but should also take account of risks resulting from their potential interactions and combinatorial effects. In addition, a prospective technology assessment could help the risk manager in defining criteria to minimize potential unintended interactions between NGT organisms through limiting the scale of releases.

Conclusions: If genetically engineered (GE) organisms derived from NGTs are released into the environment, their potentially negative impacts need to be minimized. As with all GE organisms, it is, therefore, crucial to not only assess the risks of the individual events, but also their potential interactions which can trigger direct and indirect effects with adverse impacts. It is necessary to develop hypotheses and specific scenarios to explore interactions between NGT organisms and possible pathways to harm from the perspective of the precautionary principle. In addition, the introduction prospective technology assessment could provide an instrument for the risk manager to control the scale of releases of NGT organisms.

<https://enveurope.springeropen.com/articles/10.1186/s12302-023-00734-3>

Kulishova, L.M., Vokhtantsev, I.P., Kim, D.V. et al. (2023): **Mechanisms of the Specificity of the CRISPR/Cas9 System in Genome Editing.** *Mol Biol* 57, 258–271 |

<https://doi.org/10.1134/S0026893323020139>

The CRISPR/Cas9 system, which was discovered recently, utilizes nucleases targeted by sequence complementarity and is originally intended to protect bacteria from foreign genetic elements. The system provided a convenient tool for manipulating the genomes of living cells. The CRISPR/Cas9 genomic editing technology moved beyond the laboratory and already found application in biotechnology and agriculture. However, off-target activity of the CRISPR/Cas9 system can cause oncogenic mutations and thus limits its use for genome editing in human cells for medical purposes. Many studies are therefore aimed at developing variants of the CRISPR/Cas9 system with improved accuracy. The review considers the mechanisms of precise and erroneous actions of Cas9 RNA-guided nuclease, natural and artificial variants of RNA-targeted nucleases, possibilities to modulate their specificity through guide RNA modifications, and other approaches to increasing the accuracy of the CRISPR/Cas9 system in genome editing.

<https://link.springer.com/article/10.1134/S0026893323020139>

Sun, C., Lei, Y., Li, B. et al. (2023): **Precise integration of large DNA sequences in plant genomes using PrimeRoot editors.** *Nat Biotechnol* | <https://doi.org/10.1038/s41587-023-01769-w>

A technique for chromosomal insertion of large DNA segments is much needed in plant breeding and synthetic biology to facilitate the introduction of desired agronomic traits and signaling and metabolic pathways. Here we describe PrimeRoot, a genome editing approach to generate targeted precise large DNA insertions in plants. Third-generation PrimeRoot editors employ optimized prime editing guide RNA designs, an enhanced plant prime editor and superior recombinases to enable precise large DNA insertions of up to 11.1 kilobases into plant genomes. We demonstrate the use of PrimeRoot to accurately introduce gene regulatory elements in rice. In this study, we also integrated a gene cassette comprising *PigmR*, which confers rice blast resistance driven by an Act1 promoter, into a predicted genomic safe harbor site of Kitaake rice and obtain edited plants harboring the expected insertion with an efficiency of 6.3%. We found that these rice plants have increased blast resistance. These results establish PrimeRoot as a promising approach to precisely insert large segments of DNA in plants.

<https://www.nature.com/articles/s41587-023-01769-w>

Laloum T., Carvalho S.D., Martín, G., Richardson D.N. et al. (2023): **The SCL30a SR protein regulates ABA-dependent seed traits and germination under stress**, *Plant, Cell & Environment* | DOI: [10.1111/pce.14593](https://doi.org/10.1111/pce.14593)

SR proteins are conserved RNA-binding proteins best known as splicing regulators that have also been implicated in other steps of gene expression. Despite mounting evidence for a role in plant development and stress responses, the molecular pathways underlying SR protein regulation of these processes remain poorly understood. Here we show that the plant-specific SCL30a SR protein negatively regulates ABA signaling to control seed traits and stress responses during germination in *Arabidopsis*. Transcriptome-wide analyses revealed that loss of *SCL30a* function barely affects splicing, but largely induces ABA-responsive gene expression and genes repressed during germination. Accordingly, *scl30a* mutant seeds display delayed germination and hypersensitivity to ABA and high salinity, while transgenic plants overexpressing *SCL30a* exhibit reduced ABA and salt stress sensitivity. An ABA biosynthesis inhibitor rescues the enhanced mutant seed stress sensitivity, and epistatic analyses confirm that this hypersensitivity requires a functional ABA pathway. Finally, seed ABA levels are unchanged by altered *SCL30a* expression, indicating that the gene promotes seed germination under stress by reducing sensitivity to the phytohormone. Our results reveal a new player in ABA-mediated control of early development and stress response.

<https://onlinelibrary.wiley.com/doi/10.1111/pce.14593>

Liu W., Mei Z., Yu L., Gu T. et al. (2023): **The ABA-induced NAC transcription factor MdNAC1 interacts with a bZIP-type transcription factor to promote anthocyanin synthesis in red-fleshed apples**, *Horticulture Research* uhad049 . DOI: [10.1093/hr/uhad049](https://doi.org/10.1093/hr/uhad049)

Anthocyanins are valuable compounds in red-fleshed apples. The MdMYB10 transcription factor is an important regulator of the anthocyanin synthesis pathway. However, other transcription factors are key components of the complex network controlling anthocyanin synthesis and should be more thoroughly characterized. In this study, we used a yeast-based screening technology to identify MdNAC1 as a transcription factor that positively regulates anthocyanin synthesis. The overexpression of *MdNAC1* in apple fruits and calli significantly promoted the accumulation of anthocyanins. In binding experiments, we demonstrated that MdNAC1 combines with the bZIP-type transcription factor *MdbZIP23* to activate the transcription of *MdMYB10* and *MdUFGT*. Our analyses also indicated that the expression of *MdNAC1* is strongly induced by ABA because of the presence of an ABRE cis-acting element in its promoter. Additionally, the accumulation of anthocyanins in apple calli co-transformed with *MdNAC1* and *MdbZIP23* increased in the presence of ABA. Therefore, we revealed a novel anthocyanin synthesis mechanism involving the ABA-induced transcription factor MdNAC1 in red-fleshed apples.

<https://academic.oup.com/hr/advance-article/doi/10.1093/hr/uhad049/7077840>

Tabashnik B.E., Fabrick J.A., Carrière Y.(2023): **Global Patterns of Insect Resistance to Transgenic Bt Crops: The First 25 Years**. *Journal of Economic Entomology*, 116 (2), 297–309 | <https://doi.org/10.1093/jee/toac183>

A correction has been published: *Journal of Economic Entomology*, 648,

<https://doi.org/10.1093/jee/toad013>

Crops genetically engineered to produce insecticidal proteins from the bacterium *Bacillus thuringiensis* (Bt) have improved pest management and reduced reliance on insecticide sprays. However, evolution of practical resistance by some pests has reduced the efficacy of Bt crops. We analyzed global resistance monitoring data for 24 pest species based on the first 25 yr of cultivation of Bt crops including corn, cotton, soybean, and sugarcane. Each of the 73 cases examined represents the response of one pest species in one country to one Bt toxin produced by one or more Bt crops. The cases of practical resistance rose from 3 in 2005 to 26 in 2020. Practical resistance has been documented in some populations of 11 pest species (nine lepidopterans and two coleopterans), collectively affecting nine widely used crystalline (Cry) Bt toxins in seven countries. Conversely, 30 cases reflect no decrease in susceptibility to Bt crops in populations of 16 pest species in 10 countries. The remaining 17 cases provide early warnings of resistance, which entail genetically based decreases in susceptibility without evidence of reduced field efficacy. The early warnings involve four Cry toxins and the Bt vegetative insecticidal protein Vip3Aa. Factors expected to favor sustained susceptibility include abundant refuges of non-Bt host plants, recessive inheritance of resistance, low resistance allele frequency, fitness costs, incomplete resistance, and redundant killing by multi-toxin Bt crops. Also, sufficiently abundant refuges can overcome some unfavorable conditions for other factors. These insights may help to increase the sustainability of current and future transgenic insecticidal crops.

<https://academic.oup.com/jee/article/116/2/297/6968925?login=false>

Woike S., Eustermann S., Jung J., Wenzl S.J. et al. (2023): **Structural basis for TBP displacement from TATA box DNA by the Swi2/Snf2 ATPase Mot1**. *Nature Structural & Molecular Biology* | DOI: [10.1038/s41594-023-00966-0](https://doi.org/10.1038/s41594-023-00966-0)

The Swi2/Snf2 family transcription regulator Modifier of Transcription 1 (Mot1) uses adenosine triphosphate (ATP) to dissociate and reallocate the TATA box-binding protein (TBP) from and between promoters. To reveal how Mot1 removes TBP from TATA box DNA, we determined cryogenic electron microscopy structures that capture different states of the remodeling reaction. The resulting molecular video reveals how Mot1 dissociates TBP in a process that, intriguingly, does not require DNA groove tracking. Instead, the motor grips DNA in the

presence of ATP and swings back after ATP hydrolysis, moving TBP to a thermodynamically less stable position on DNA. Dislodged TBP is trapped by a chaperone element that blocks TBP's DNA binding site. Our results show how Swi2/Snf2 proteins can remodel protein–DNA complexes through DNA bending without processive DNA tracking and reveal mechanistic similarities to RNA gripping DEAD box helicases and RIG-I-like immune sensors. <https://www.nature.com/articles/s41594-023-00966-0>

Hu Y., Liu Y., Tao J.-J., Lu L. et al. (2023): **GmJAZ3 interacts with GmRR18a and GmMYC2a to regulate seed traits in soybean.** *Journal of Integrative Plant Biology* | DOI: [10.1111/jipb.13494](https://doi.org/10.1111/jipb.13494)

Seed weight is usually associated with seed size and is one of the important agronomic traits that determine yield. Understanding of seed weight control is limited especially in soybean plants. Here we show that *GmJAZ3*, a gene identified through gene co-expression network analysis, regulates seed-related traits in soybean. Overexpression of *GmJAZ3* promotes seed size/weight and other organ size in stable transgenic soybean plants likely by increasing cell proliferation. *GmJAZ3* interacted with both *GmRR18a* and *GmMYC2a* to inhibit their transcriptional activation of cytokinin oxidase gene *GmCKX3-4*, which usually affects seed traits. Meanwhile, the *GmRR18a* binds to the promoter of *GmMYC2a* and activates *GmMYC2a* gene expression. In *GmJAZ3*-overexpressing soybean seeds, the protein contents were increased while the fatty acid contents were reduced compared to those in the control seeds, indicating that the *GmJAZ3* affects seed size/weight and compositions. Natural variation in *JAZ3* promoter region was further analyzed and Hap3 promoter correlates with higher promoter activity, higher gene expression and higher seed weight. The Hap3 promoter may be selected and fixed during soybean domestication. *JAZ3* orthologues from other plants/crops may also control seed size and weight. Taken together, our study reveals a novel molecular module *GmJAZ3*-*GmRR18a*/*GmMYC2a*-*GmCKXs* for seed size and weight control, providing promising targets during soybean molecular breeding for better seed traits.

<https://onlinelibrary.wiley.com/doi/10.1111/jipb.13494>

Tetreault H. et al. (2022): **A power analysis for detecting aging of dry-stored soybean seeds: Germination versus RNA integrity assessments.** *Crop Science* | DOI: [10.1002/csc2.20821](https://doi.org/10.1002/csc2.20821)

Deterioration of seed during dry storage is a major problem for genebanks and seed companies. Germination tests are the gold standard to monitor seed viability; however, these prove to be insensitive during the early stage of storage when viability changes are subtle. Recent findings demonstrate that decline in RNA integrity may be an early indicator of seed longevity during dry storage. The goal of this study was to determine the sensitivity of RNA integrity, measured as RNA integrity number (RIN), regarding how soon changes can be detected and how many seeds are required. We compared the statistical power of germination and RIN assays using a well-characterized collection of 'Williams 82' soybean seeds, with cohorts harvested between 1989 and 2019 and stored at 5 °C. Germination was monitored in 1- to 3-yr intervals since 1989, and RIN was monitored in 1- to 2-yr intervals since 2016 providing an extensive dataset to conduct statistical power analyses. Decline in RIN can be detected in soybean seeds within 10 yr with a RNA monitor test that consumes approximately 30 seeds. In contrast, a germination test detects deterioration in 16 yr using approximately 50 seeds, and by this time, the seed lot is near the limit of longevity and has entered the phase of rapid mortality. Work from this study indicates that early detection of aging using RIN decline can be used to predict the longevity threshold to optimize viability monitoring and regeneration times, preventing loss of valuable samples by overtesting or missing the longevity threshold.

<https://access.onlinelibrary.wiley.com/doi/10.1002/csc2.20821>

Smith, W.P.J., Wucher, B.R., Nadell, C.D. et al. Bacterial defences: mechanisms, evolution and antimicrobial resistance. *Nat Rev Microbiol* (2023). <https://doi.org/10.1038/s41579-023-00877-3>

Throughout their evolutionary history, bacteria have faced diverse threats from other microorganisms, including competing bacteria, bacteriophages and predators. In response to these threats, they have evolved sophisticated defence mechanisms that today also protect bacteria against antibiotics and other therapies. In this Review, we explore the protective strategies of bacteria, including the mechanisms, evolution and clinical implications of these ancient defences. We also review the countermeasures that attackers have evolved to overcome bacterial defences. We argue that understanding how bacteria defend themselves in nature is important for the development of new therapies and for minimizing resistance evolution.

<https://www.nature.com/articles/s41579-023-00877-3>

EFSA:

GMO Panel (2023): Scientific Opinion on the assessment of genetically modified oilseed rape MS8, RF3 and MS8 × RF3 for renewal authorisation under Regulation (EC) No 1829/2003 (application EFSA-GMO-RX-024). *EFSA Journal* 21 (4):7934, 14 pp.

<https://www.efsa.europa.eu/de/efsajournal/pub/7934>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.7934>

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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