

# Sunday Evening News No 354

2023-11-27 – 2023-12-03

Compiled and edited by **BGF** Jany



Wissenschaftskreis  
Genomik und  
Gentechnik e.V.

## Meetings – Conferences / Tagungen – Konferenzen

Lebensmittelverband Deutschland: **Tagung "Grüner Deal und Vom-Hof-auf-den-Tisch-Strategie: Zwischenbilanz und Ausblick" am 13. Dezember 2023 ab 10:00 Uhr**

Anmeldung bis 08.12.2023 unter:

<https://www.lebensmittelverband.de/de/verband/veranstaltungen/tagung-gruener-deal-und-vom-hof-auf-den-tisch-strategie-zwischenbilanz-und-ausblick>

## Press Releases -Media / Presse- und Medienberichte

Bockholt K.: **Gentechnik: Darum rät dieser bekannte Bio-Pionier zu Crispr/Cas9**

<https://www.agrarheute.com/pflanze/getreide/gentechnik-raet-bekannte-bio-pionier-crisprcas9-613669>

Grünes Netzwerk Evidenzbasierte Politik: **Bericht von der Bundesdelegiertenkonferenz 2023**

[https://evidenzbasierte-politik.de/2023/11/28/bericht-von-der-bundesdelegiertenkonferenz-2023/?fbclid=IwAR0bi9Rnh2xVfK6uUUgW1k0iM7L6j-GFlv11Y6Rf8Y3Z6xrWrYfv\\_PyW1RA](https://evidenzbasierte-politik.de/2023/11/28/bericht-von-der-bundesdelegiertenkonferenz-2023/?fbclid=IwAR0bi9Rnh2xVfK6uUUgW1k0iM7L6j-GFlv11Y6Rf8Y3Z6xrWrYfv_PyW1RA)

immer wieder lesenswert!

**Grünes Netzwerk Evidenzbasierte Politik Wissenschaft und Politik im Dialog**

<https://evidenzbasierte-politik.de/>

Stahmann F.: **EU-Novelle gefährdet Marktsegment mit gentechnikfreien Lebensmitteln**

<https://background.tagesspiegel.de/agrar-ernaehrung/eu-novelle-gefaehrdet-marktsegment-mit-gentechnikfreien-lebensmitteln>

Informationsdienst Gentechnik: **Handel kritisiert übereilte Gentechnik-Verordnung**

<https://www.keine-gentechnik.de/nachricht/34863?cHash=8e2f77e9350219bbfc57ee0ef6bdbb0e>

GM Watch: **Eight major German and Austrian supermarkets say consumer choice, organic must be protected from new GMOs**

<https://www.gmwatch.org/en/106-news/latest-news/20336-eight-major-german-and-austrian-supermarkets-say-consumer-choice-organic-must-be-protected-in-new-gmo-deregulation>

Leading representatives of the food retail industry: Proposed EU legislation on new genomic techniques must not jeopardize consumer choice, organic farming, and food price stability.

[https://www.enga.org/fileadmin/user\\_upload/LEH-Brief\\_KOM\\_MEPs\\_NGT\\_END\\_final\\_28112023.pdf](https://www.enga.org/fileadmin/user_upload/LEH-Brief_KOM_MEPs_NGT_END_final_28112023.pdf)

**Agricultural and environmental organisations protest against new GMO legislation in Europe**

<https://gmwatch.org/en/106-news/latest-news/20337>

**New GMOs: 13 organisations alert the French President and Prime Minister to EU deregulation project**

<https://gmwatch.org/en/106-news/latest-news/20338>

**The letter:** [https://www.pollinis.org/admin/wp-content/uploads/2023/11/13-organisations-demandent-un-rendez-vous-avec-monsieur-le-president-de-la-republique-et-madame-la-premiere-ministre---nouveaux-ogm---28.11.pdf?utm\\_source=brevo&utm\\_campaign=CP%20Lettre%20Prsident%20nouveaux%20OGM&utm\\_medium=email](https://www.pollinis.org/admin/wp-content/uploads/2023/11/13-organisations-demandent-un-rendez-vous-avec-monsieur-le-president-de-la-republique-et-madame-la-premiere-ministre---nouveaux-ogm---28.11.pdf?utm_source=brevo&utm_campaign=CP%20Lettre%20Prsident%20nouveaux%20OGM&utm_medium=email)

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): November / December week 48

## Publications – Publikationen

Wijerathna-Yapa A., Henry R.J., Dunn, M. Beveridge C.A. (2023): **Science and opinion in decision making: A case study of the food security collapse in Sri Lanka.** Modern Agriculture | <https://doi.org/10.1002/moda.18>

Making decisions related to security, whether at the community, national, or regional level, is a highly intricate task. This requires a multi-criteria decision-making approach that incorporates inputs from various perspectives, including those of science, culture, economics, sustainability, and climate change. In order to make successful decisions, it is imperative to compare alternatives and rank the consequences and relative impacts associated with each option. Such comparisons and rankings require a careful balance of evidence-based scientific data and diverse opinions. The recent scenario of the food security collapse in Sri Lanka provides a poignant reminder of the importance of this decision-making process and the consequences of unacknowledged or unidentified misinformation. Sri Lanka responded to an unexplained health condition and a desire to enter a new sales market by swiftly transitioning to organic farming. However, this abrupt change led to the rapid collapse of Sri Lanka's food supply, a significant decline in GDP, and hardships for both rural and urban communities. While the government eventually reversed its policy, Sri Lanka faced challenges in recovery. It is evident that disinformation and misinformation played a role in this unfortunate situation. This paper offers an in-depth exploration of the events, underlining the necessity to distinguish between disinformation and misinformation in policy development.

<https://onlinelibrary.wiley.com/doi/10.1002/moda.18>

Wilcks A. and Quemada H. (2023): **Editorial: Policy and regulation in bioengineering and biotechnology.** Front. Bioeng. Biotechnol., Sec. Biosafety and Biosecurity, 11 - 2023 |

<https://doi.org/10.3389/fbioe.2023.1337663>

All Articles: <https://www.frontiersin.org/research-topics/45536/policy-and-regulation-in-bioengineering-and-biotechnology>

Bi, W., Liu, J., Li, Y., He, Z. et al. (2023): **CRISPR/Cas9-guided editing of a novel susceptibility gene in potato improves Phytophthora resistance without growth penalty.** Plant Biotechnol. J., <https://doi.org/10.1111/pbi.14175>.

<https://onlinelibrary.wiley.com/doi/10.1111/pbi.14175>

Tan J., Shen M., Chai, N., Lui, N., Lui, Y.-G., Zhu Q. (2023): **Genome editing for plant synthetic metabolic engineering and developmental regulation.** Journal of Plant Physiology 291:154141 | DOI:[10.1016/j.jplph.2023.154141](https://doi.org/10.1016/j.jplph.2023.154141)

Plant metabolism and development are a reflection of the orderly expression of [genetic](#) information intertwined with the environment interactions. Genome editing is the cornerstone for scientists to modify endogenous genes or introduce exogenous functional genes and metabolic pathways, holding immense potential applications in [molecular breeding](#) and [biosynthesis](#). Over the course of nearly a decade of development, genome editing has advanced significantly beyond the simple cutting of double-stranded [DNA](#), now enabling precise base and fragment replacements, regulation of gene expression and translation, as well as [epigenetic modifications](#). However, the utilization of genome editing in plant synthetic [metabolic engineering](#) and developmental regulation remains exploratory. Here, we provide an introduction and a comprehensive overview of the editing attributes associated with various CRISPR/Cas tools, along with diverse strategies for the meticulous control of plant metabolic pathways and developments. Furthermore, we discuss the limitations of current approaches and future prospects for genome editing-driven [plant breeding](#).

<https://www.sciencedirect.com/science/article/abs/pii/S0176161723002353?via%3Dihub>

Sharma, D., Kumari, A., Sharma, P. et al. (2023): **Meta-QTL analysis in wheat: progress, challenges and opportunities.** Theor Appl Genet 136, 247 | <https://doi.org/10.1007/s00122-023-04490-z>

Wheat, an important cereal crop globally, faces major challenges due to increasing global population and changing climates. The production and productivity are challenged by several biotic and abiotic stresses. There is also a pressing demand to enhance grain yield and quality/nutrition to ensure global food and nutritional security. To address these multifaceted concerns, researchers have conducted numerous meta-QTL (MQTL) studies in wheat, resulting in the identification of candidate genes that govern these complex quantitative traits. MQTL analysis has successfully unraveled the complex genetic architecture of polygenic quantitative traits in wheat. Candidate genes associated with stress adaptation have been pinpointed for abiotic and biotic traits, facilitating targeted breeding efforts to enhance stress tolerance. Furthermore, high-confidence candidate genes (CGs) and flanking markers to MQTLs will help in marker-assisted breeding programs aimed at enhancing stress tolerance, yield, quality and nutrition. Functional analysis of these CGs can enhance our understanding of intricate trait-related genetics. The discovery of orthologous MQTLs shared between wheat and other crops sheds light on common evolutionary pathways governing these traits. Breeders can leverage the most promising MQTLs and CGs associated with multiple traits to develop superior next-generation wheat cultivars with improved trait performance. This review provides a comprehensive overview of MQTL analysis in

wheat, highlighting progress, challenges, validation methods and future opportunities in wheat genetics and breeding, contributing to global food security and sustainable agriculture.  
<https://link.springer.com/article/10.1007/s00122-023-04490-z>

Chen, S., Wang, P., Kong, W. et al. (2023): **Gene mining and genomics-assisted breeding empowered by the pangenome of tea plant *Camellia sinensis***. *Nat. Plants* | <https://doi.org/10.1038/s41477-023-01565-z>

Tea is one of the world's oldest crops and is cultivated to produce beverages with various flavours. Despite advances in sequencing technologies, the genetic mechanisms underlying key agronomic traits of tea remain unclear. In this study, we present a high-quality pangenome of 22 elite cultivars, representing broad genetic diversity in the species. Our analysis reveals that a recent long terminal repeat burst contributed nearly 20% of gene copies, introducing functional genetic variants that affect phenotypes such as leaf colour. Our graphical pangenome improves the efficiency of genome-wide association studies and allows the identification of key genes controlling bud flush timing. We also identified strong correlations between allelic variants and flavour-related chemistries. These findings deepen our understanding of the genetic basis of tea quality and provide valuable genomic resources to facilitate its genomics-assisted breeding.  
<https://www.nature.com/articles/s41477-023-01565-z>

Zanatta C.B., Hoepers A.M., Rubens O.O.N., Agapito-Tenfen S.Z. (2023): **Specificity Testing for NGT PCR-Based Detection Methods in the Context of the EU GMO Regulations**. *Foods* 12 (23) | 4298; <https://doi.org/10.3390/foods12234298>

The term new genomic techniques (NGTs) is an umbrella term used to describe a variety of techniques that can alter the genetic material of an organism and that have emerged or have been developed since 2001, when the existing genetically modified organism (GMO) legislation was adopted. The analytical framework used to detect GMOs in Europe is an established single harmonized procedure that is mandatory for the authorization of GM food and feed, thus generating a reliable, transparent, and effective labeling scheme for GMO products. However, NGT products can challenge the implementation and enforcement of the current regulatory system in the EU, relating in particular to the detection of NGT products that contain no foreign genetic material. Consequently, the current detection methods might fail to meet the minimum performance requirements. Although existing detection methods may be able to detect and quantify even small alterations in the genome, this does not necessarily confirm the distinction between products resulting from NGTs subject to the GMO legislation and other products. Therefore, this study provides a stepwise approach for the in silico prediction of PCR systems' specificity by testing a bioinformatics pipeline for amplicon and primer set searches in current genomic databases. In addition, it also empirically tested the PCR system evaluated during the in silico analysis. Two mutant genotypes produced by CRISPR-Cas9 in *Arabidopsis thaliana* were used as a case study. Overall, our results demonstrate that the single PCR system developed for identifying a nucleotide insertion in the *grf1-3* genotype has multiple matches in the databases, which do not enable the discrimination of this mutated event. Empirical assays further support this demonstration. In contrast, the second mutated genotype, *grf8-61*, which contains a -3 bp deletion, did not yield any matches in the sequence variant database. However, the primer sequences were not efficient during the empirical assay. Our approach represents a first step in decision making for analytical methods for NGT detection, identification, and quantification in light of the European labeling regulations.

<https://www.mdpi.com/2304-8158/12/23/4298>

Otto M., Papastefanou P., Fahse L. (2023): **Pressure from insect-resistant maize on protected butterflies and moths**. *Conservation Biology* | <https://doi.org/10.1111/cobi.14222>

Intensification in agriculture affects many insect species, including butterflies. Insect resistant crops, such as Bt (*Bacillus thuringiensis*) maize, which produces a toxin active against Lepidoptera, are an alternative to insecticide sprays. Genetically modified (GM) crops are regulated in most countries and require an environmental risk assessment. In the European Union (EU), such assessments include use of simulation models to predict the effects on nontarget Lepidoptera (NTL). To support the assessment of protected NTL, we extended an individual-based, stochastic, spatially explicit mathematical model (LepiX) to include a wider range of exposure scenarios, a species-sensitivity distribution, and an option for repeated exposure of individuals. We applied the model to transgenic maize DAS-1507, which expresses a high concentration of Bt toxin in pollen that may be consumed by NTL larvae on their host plants nearby. Even in the most conservative scenario without repeated exposure, mortality estimates for highly sensitive species ranged from 41% to 6% at distances of 10–1000 m from the nearest maize field. Repeated exposure can cause additional mortality and thus is relevant for the overall risk assessment. Uncertainties in both exposure and ecotoxicity estimates strongly influenced the predicted mortalities. Care should be taken to include these uncertainties in the model scenarios used for decision-making. In accordance with other modeling results, our simulations demonstrated that mean mortality may not be safe for protected species. With its high pollen expression, Bt maize may pose risks to sensitive and protected butterfly and moth species that may be difficult to manage. High expression of Bt toxin in pollen is unnecessary for controlling target pests. Consequently, we suggest that Bt maize with high pollen expression not be cultivated in regions where protected butterflies are to be conserved.

<https://conbio.onlinelibrary.wiley.com/doi/abs/10.1111/cobi.14222>

Ellis L.B., Molina K., C.R., Freisthler M. et al. (2023): **Adult Organophosphate and Carbamate Insecticide Exposure and Sperm Concentration: A Systematic Review and Meta-Analysis of**

**the Epidemiological Evidence.** Environmental Health Perspectives 131(11) | <https://doi.org/10.1289/EHP12678>

Background: Evidence of the negative impacts of contemporary use insecticides on sperm concentration has increased over the last few decades; however, meta-analyses on this topic are rare.

Objectives: This investigation assessed the qualitative and quantitative strength of epidemiological evidence regarding adult exposure to two classes of contemporary use insecticides—organophosphates (OPs) and methyl carbamates (NMCs)—and sperm concentration using robust and reproducible systematic review and meta-analysis methods.

Methods: Three scientific databases (PubMed, Scopus, and Web of Science), two U.S. government databases (NIOSH TIC-2 and Science.gov), and five nongovernmental organization websites were searched for relevant primary epidemiological studies published in any language through 11 August 2022. Risk of bias and strength of evidence were evaluated according to Navigation Guide systematic review methodology. Bias-adjusted standardized mean difference effect sizes were calculated and pooled using a three-level, multivariate random-effect meta-analysis model with cluster-robust variance estimation.

Results: Across 20 studies, 21 study populations, 42 effect sizes, and 1,774 adult men, the pooled bias-adjusted standardized mean difference in sperm concentration between adult men more- and less-exposed to OP and NMC insecticides was (95% CI: , ; ). Sensitivity and subgroup analyses explored statistical heterogeneity and validated the model robustness. Although the pooled effect estimate was modified by risk of bias, insecticide class, exposure setting, and recruitment setting, it remained negative in direction across all meta-analyses. The body of evidence was rated to be of moderate quality, with sufficient evidence of an association between higher adult OP and NMC insecticide exposure and lower sperm concentration.

Discussion: This comprehensive investigation found sufficient evidence of an association between higher OP and NMC insecticide exposure and lower sperm concentration in adults. Although additional cohort studies can be beneficial to fill data gaps, the strength of evidence warrants reducing exposure to OP and NMC insecticides now to prevent continued male reproductive harm.

<https://ehp.niehs.nih.gov/doi/10.1289/EHP12678>

Xu P., Cao T., Fan Q., +2, Eiser E. (2023): **Whole-genome detection using multivalent DNA-coated colloids.** PNAS 120 (37) e2305995120 | <https://doi.org/10.1073/pnas.2305995120>

To minimize the incorrect use of antibiotics, there is a great need for rapid and inexpensive tests to identify the pathogens that cause an infection. The gold standard of pathogen identification is based on the recognition of DNA sequences that are unique for a given pathogen. Here, we propose and test a strategy to develop simple, fast, and highly sensitive biosensors that make use of multivalency. Our approach uses DNA-functionalized polystyrene colloids that distinguish pathogens on the basis of the frequency of selected short DNA sequences in their genome. Importantly, our method uses entire genomes and does not require nucleic acid amplification. Polystyrene colloids grafted with specially designed surface DNA probes can bind cooperatively to frequently repeated sequences along the entire genome of the target bacteria, resulting in the formation of large and easily detectable colloidal aggregates. Our detection strategy allows “mix and read” detection of the target analyte; it is robust and highly sensitive over a wide concentration range covering, in the case of our test target genome *Escherichia coli* bl21-de3, 10 orders of magnitude from to copies/mL. The sensitivity compares well with state-of-the-art sensing techniques and has excellent specificity against nontarget bacteria. When applied to real samples, the proposed technique shows an excellent recovery rate. Our detection strategy opens the way to developing a robust platform for pathogen detection in the fields of food safety, disease control, and environmental monitoring.

<https://www.pnas.org/doi/10.1073/pnas.2305995120>

## EFSA

CEP Panel (2023): Safety evaluation of the food enzyme endo-1,4- $\beta$ -xylanase from the non-genetically modified *Trichoderma citrinoviride* strain 278

<https://www.efsa.europa.eu/it/efsajournal/pub/8399>

CEP Panel (2023): Safety evaluation of the food enzyme bacillolysin from the non-genetically modified *Bacillus amyloliquefaciens* strain AGS 430

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8392>

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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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