

# Sunday Evening News No 349

2023-10-23 – 2023-10-29

Compiled and edited by **BGF** Jany



## Meetings – Conferences / Tagungen - Konferenzen

EU-Kommission-Deutsche Vertretung: **Neue Züchtungstechniken als Beitrag zur Bewältigung multipler Krisen des 21. Jahrhunderts**

Mittwoch, 8. November 2023, 18:00 - 20:30 (CET); Ort Europäisches Haus  
Unter den Linden 78, 10117 Berlin,

[https://germany.representation.ec.europa.eu/events/neue-zuechtungstechniken-als-beitrag-zur-bewaeltigung-multipler-krisen-des-21-jahrhunderts-2023-11-08\\_de](https://germany.representation.ec.europa.eu/events/neue-zuechtungstechniken-als-beitrag-zur-bewaeltigung-multipler-krisen-des-21-jahrhunderts-2023-11-08_de)

EPSO: **Register for the 27th EPSO Plant Science Seminar on 16th November 2023 – the potential of gene editing**

<https://epsoweb.org/epso/register-for-the-27th-epso-plant-science-seminar-on-16th-november-2023-the-potential-of-gene-editing/2023/10/26/>

BMEL: **Fachtagung: “Transformation der Pflanzenproduktion”**

23. November 2023 - 24. November 2023; Berlin

<https://gpz-online.de/events/fachtagung-transformation-der-pflanzenproduktion/>

## Press Releases -Media / Presse- und Medienberichte

Kranz B.: **Gentechnik: Ministerium fördert Pflanzenforschung massiv**

50 Millionen Euro vom Forschungsministerium für neue Gentechnik-Projekte: Warum das in der Ampel-Koalition für Streit sorgen könnte.

<https://www.morgenpost.de/wirtschaft/article239886137/Gentechnik-Ministerium-foerdert-Pflanzenforschung-massiv.html>

ZKBS: **Stellungnahme der ZKBS zum Vorschlag der Europäischen Kommission zur Neuregulierung von Pflanzen, die mit "Neuen Genomischen Techniken (NGT)" gezüchtet wurden**

[https://www.zkbs-online.de/ZKBS/SharedDocs/Downloads/Kommentare%20als%20PDF/Stell%20zu%20NGT,%20EU%20Vorschlag.pdf?\\_\\_blob=publicationFile&v=2](https://www.zkbs-online.de/ZKBS/SharedDocs/Downloads/Kommentare%20als%20PDF/Stell%20zu%20NGT,%20EU%20Vorschlag.pdf?__blob=publicationFile&v=2)

COPA-COGECA: **Position Paper on the Commission’s proposal on plants obtained by certain new genomic techniques and their food and feed, and amending Regulation (EU) 2017/625 (COM (2023)411final)**

<https://www.publicnow.com/view/8A1A6D6881CA39865C600F733135DB471F54024B?1698241653>

Jorasch P.: **Resurrection of Plant Breeding Innovation in the EU?**

<https://european-seed.com/2023/10/resurrection-of-plant-breeding-innovation-in-the-eu/>

Royal Society: **Evidence-led GM crop regulation could help UK lead on tackling global food security and climate change risks, says Royal Society**

<https://royalsociety.org/news/2023/10/gm-crops/>

Miller H.: **Happy 41st birthday, genetically-engineered insulin. Your approval by the FDA in 1982 took 5 months. How many years would it take now?**

<https://geneticliteracyproject.org/2023/10/24/happy-41st-birthday-genetically-engineered-insulin-your-approval-by-the-fda-in-1982-took-5-months-how-many-years-would-it-take-now/>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): October week 43

## Publications – Publikationen

Vighi G. and De Storme N. (2023): **Mind the (CRISPR) gaps**

The European Commission's proposal for the use of NGTs in the EU  
EMBO Reports e58109 | <https://doi.org/10.15252/embr.202358109>

General Secretariat of the Council (2023): **Regulation on new genomic techniques (NGT) – Technical paper on the rationale for the equivalence criteria in Annex I**

[https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CONSIL:ST\\_14204\\_2023\\_INIT](https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CONSIL:ST_14204_2023_INIT)

**COM (2023) 411: Proposal for a REGULATION OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL on plants obtained by certain new genomic techniques and their food and feed, and amending Regulation (EU) 2017/625**

[https://eur-lex.europa.eu/procedure/EN/2023\\_226](https://eur-lex.europa.eu/procedure/EN/2023_226)

The Royal Society (2023): **Enabling genetic technologies for food security: Policy briefing**

<https://royalsociety.org/-/media/policy/projects/gene-tech/genetically-modified-organisms-regulation-policy-briefing.pdf?la=en-GB&hash=CDCA44BD52AD8AC48E80CA44A21852DF>

Ahmad A., Jamil A., Munawar N. (2023): **GMOs or non-GMOs? The CRISPR Conundrum**

Front. Plant Sci., Sec. Plant Biotechnology 14 | <https://doi.org/10.3389/fpls.2023.1232938>

CRISPR-Cas9, the “genetic scissors”, is being presaged as a revolutionary technology, having tremendous potential to create designer crops by introducing precise and targeted modifications in the genome to achieve global food security in the face of climate change and increasing population. Traditional genetic engineering relies on random and unpredictable insertion of isolated genes or foreign DNA elements into the plant genome. However, CRISPR-Cas based gene editing does not necessarily involve inserting a foreign DNA element into the plant genome from different species but introducing new traits by precisely altering the existing genes. CRISPR edited crops are touching markets, however, the world community is divided over whether these crops should be considered genetically modified (GM) or non-GM. Classification of CRISPR edited crops, especially transgene free crops as traditional GM crops, will significantly affect their future and public acceptance in some regions. Therefore, the future of the CRISPR edited crops is depending upon their regulation as GM or non-GMs, and their public perception. Here we briefly discuss how CRISPR edited crops are different from traditional genetically modified crops. In addition, we discuss different CRISPR reagents and their delivery tools to produce transgene-free CRISPR edited crops. Moreover, we also summarize the regulatory classification of CRISPR modifications and how different countries are regulating CRISPR edited crops. We summarize that the controversy of CRISPR-edited plants as GM or non-GM will continue until a universal, transparent, and scalable regulatory framework for CRISPR-edited plants will be introduced worldwide, with increased public awareness by involving all stakeholders.

<https://www.frontiersin.org/articles/10.3389/fpls.2023.1232938/full>

Bartlett M.E., Moyers B.T., Man J., Subramaniam B., Makunga N.P. (2023): **The Power and Perils of De Novo Domestication Using Genome Editing**. *Annu. Rev. Plant Biol.* 74, 727–750

| <https://doi.org/10.1146/annurev-arplant-053122-030653>

There is intense interest in using genome editing technologies to domesticate wild plants, or accelerate the improvement of weakly domesticated crops, in de novo domestication. Here, we discuss promising genetic strategies, with a focus on plant development. Importantly, genome editing releases us from dependence on random mutagenesis or intraspecific diversity, allowing us to draw solutions more broadly from diversity. However, sparse understanding of the complex genetics of diversity limits innovation. Beyond genetics, we urge the ethical use of indigenous knowledge, indigenous plants, and ethnobotany. De novo domestication still requires conventional breeding by phenotypic selection, especially in the development of crops for diverse environments and cultures. Indeed, uniting genome editing with selective breeding could facilitate faster and better outcomes than either technology alone. Domestication is complex and incompletely understood, involving changes to many aspects of plant biology and human culture. Success in de novo domestication requires careful attention to history and collaboration across traditional boundaries.

<https://www.annualreviews.org/doi/abs/10.1146/annurev-arplant-053122-030653>

Pandita, D. (2023). **CRISPR/Cas Mediated Genome Editing for Improving Stress Resilience in Plants**. In: Aftab, T. (eds) *New Frontiers in Plant-Environment Interactions*. Environmental Science and Engineering. Springer, Cham. [https://doi.org/10.1007/978-3-031-43729-8\\_7](https://doi.org/10.1007/978-3-031-43729-8_7)

In nature, the plants have to face and fight both the abiotic (cold, heat, drought, salinity, and heavy metals) and biotic stressors (pathogens, including bacteria, fungi, and viruses and insect pests) with colossal effects respectively of 50% and 20% to 40% of global yield loss in agriculture. Clustered Regularly Interspaced Short Palindromic Repeat/Cas (CRISPR/Cas) system has emerged as a pioneering genome editing toolbox due to its simplicity, versatility and adequacy to accomplish transgene free gene manipulations. CRISPR/Cas can be easily programmed to target specific DNA sequences, and it is much quicker and extra efficient than previous

gene-editing technologies. One of the most promising applications of CRISPR/Cas in plants is the creation of crops with improved resistance to pests, pathogens, and environmental stressors. In this chapter, we concentrate on understanding the molecular mechanisms of CRISPR/Cas genome editing system, types and applications of CRISPR/Cas for the refinement of stress-related traits in crop plants.

[https://link.springer.com/chapter/10.1007/978-3-031-43729-8\\_7](https://link.springer.com/chapter/10.1007/978-3-031-43729-8_7)

Li T., Tang S., Li W., +19 , and Cao X. (2023): **Genome evolution and initial breeding of the Triticeae grass *Leymus chinensis* dominating the Eurasian Steppe.** PNAS 120 (44)

e2308984120 | <https://doi.org/10.1073/pnas.2308984120>

*Leymus chinensis*, a dominant perennial grass in the Eurasian Steppe, is well known for its remarkable adaptability and forage quality. Hardly any breeding has been done on the grass, limiting its potential in ecological restoration and forage productivity. To enable genetic improvement of the untapped, important species, we obtained a 7.85-Gb high-quality genome of *L. chinensis* with a particularly long contig N50 (318.49 Mb). Its allotetraploid genome is estimated to originate 5.29 million years ago (MYA) from a cross between the Ns-subgenome relating to *Psathyrostachys* and the unknown Xm-subgenome. Multiple bursts of transposons during 0.433–1.842 MYA after genome allopolyploidization, which involved predominantly the Tekay and Angela of LTR retrotransposons, contributed to its genome expansion and complexity. With the genome resource available, we successfully developed a genetic transformation system as well as the gene-editing pipeline in *L. chinensis*. We knocked out the monocot-specific miR528 using CRISPR/Cas9, resulting in the improvement of yield-related traits with increases in the tiller number and growth rate. Our research provides valuable genomic resources for Triticeae evolutionary studies and presents a conceptual framework illustrating the utilization of genomic information and genome editing to accelerate the improvement of wild *L. chinensis* with features such as polyploidization and self-incompatibility.

<https://www.pnas.org/doi/10.1073/pnas.2308984120>

Pallarz S., Fiedler S., Wahler D., Lämke J., Grohmann L. (2023): **Reproducibility of next-generation-sequencing-based analysis of a CRISPR/ Cas9 genome edited oil seed rape.** Food Chemistry: Molecular Sciences 7, 100182 | <https://doi.org/10.1016/j.fochms.2023.100182>

Next-generation-sequencing (NGS) becomes increasingly important for laboratories tasked with the detection of genetically modified organisms (GMOs) in food, feed and seeds. Its implementation into standardized workflows demands reliable intra- and inter-laboratory reproducibility. Here, we analyze the reproducibility of short- and long-read targeted NGS and long-read whole genome sequencing (WGS) data between three independent laboratories. Replicate samples were submitted for sequencing and comparatively analyzed. The targeted-NGS-samples consisted of oil seed rape (OSR) sampled from a commodity shipment spiked with a genome edited (GE) OSR and the WGS-samples consisted of leaf material from the GMOs' parental line. All laboratories delivered highly reproducible high-quality targeted NGS data with little variation. The detection of GMO-related sequences works well regardless of the facility, while the mapping to the complex genome is superior using long read data. Long read WGS is currently not suitable for routine use in enforcement laboratories, due to a large inter-laboratory variation.

<https://www.sciencedirect.com/science/article/pii/S2666566223000229>

Koller F. and Cieslak M. (2023): **A perspective from the EU: unintended genetic changes in plants caused by NGT—their relevance for a comprehensive molecular characterisation and risk assessment.** Front. Bioeng. Biotechnol. 11: 1276226. | doi:

10.3389/fbioe.2023.1276226

Several regions in the world are currently holding discussions in regard to the regulation of new genomic techniques (NGTs) and their application in agriculture. The European Commission, for instance, is proposing the introduction of specific regulation for NGT plants. Various questions need to be answered including e.g., the extent to which NGT-induced intended and unintended genetic modifications must be subjected to a mandatory risk assessment as part of an approval procedure. This review mostly focuses on findings in regard to unintended genetic changes that can be caused by the application of NGTs. More specifically, the review deals with the application of the nuclease CRISPR/Cas, which is currently the most important tool for developing NGT plants, and its potential to introduce double strand breaks (DSBs) at a targeted DNA sequence. For this purpose, we identified the differences in comparison to non-targeted mutagenesis methods used in conventional breeding. The review concludes that unintended genetic changes caused by NGT processes are relevant to risk assessment. Due to the technical characteristics of NGTs, the sites of the unintended changes, their genomic context and their frequency (in regard to specific sites) mean that the resulting gene combinations (intended or unintended) may be unlikely to occur with conventional methods. This, in turn, implies that the biological effects (phenotypes) can also be different and may cause risks to health and the environment. Therefore, we conclude that the assessment of intended as well as unintended genetic changes should be part of a mandatory comprehensive molecular characterisation and risk assessment of NGT plants that are meant for environmental releases or for market authorisation.

<https://www.frontiersin.org/articles/10.3389/fbioe.2023.1276226/full>

GEBREGZIABHER B. S. et al. (2022): **Natural variations and geographical distributions of seed carotenoids and chlorophylls in 1 167 Chinese soybean accessions,** Journal of Integrative Agriculture 22 (9), 2632-2647 | [DOI: 10.1016/j.jia.2022.10.011](https://doi.org/10.1016/j.jia.2022.10.011)

Understanding the composition and contents of [carotenoids](#) in various soybean seed accessions is important for their nutritional assessment. This study investigated the variability in the concentrations of carotenoids and chlorophylls and revealed their associations with other nutritional quality traits in a genetically diverse set of Chinese soybean accessions comprised of cultivars and [landraces](#). Genotype, planting year, accession type, seed [cotyledon](#) color, and ecoregion of origin significantly influenced the accumulation of carotenoids and chlorophylls. The mean total carotenoid content was in the range of 8.15–14.72  $\mu\text{g g}^{-1}$  across the ecoregions. The total carotenoid content was 1.2-fold higher in the landraces than in the cultivars. Soybeans with green cotyledons had higher contents of carotenoids and chlorophylls than those with yellow cotyledons. Remarkably, [lutein](#) was the most abundant carotenoid in all the [germplasms](#), ranging from 1.35–37.44  $\mu\text{g g}^{-1}$ . Carotenoids and chlorophylls showed significant correlations with other quality traits, which will help to set breeding strategies for enhancing soybean carotenoids without affecting the other components. Collectively, our results demonstrate that carotenoids are adequately accumulated in soybean seeds, however, they are strongly influenced by genetic factors, accession type, and germplasm origin. We identified novel germplasms with the highest total carotenoid contents across the various ecoregions of China that could serve as the genetic materials for soybean carotenoid breeding programs, and thereby as the raw materials for food sectors, pharmaceuticals, and the cosmetic industry.

<https://www.sciencedirect.com/science/article/pii/S2095311922002611?via%3Dihub>

Guo, W., Duan, J., Shi, Z. et al. (2023): **Biodegradation of PET by the membrane-anchored PET esterase from the marine bacterium *Rhodococcus pyridinivorans* P23**. *Commun Biol* 6, 1090 | <https://doi.org/10.1038/s42003-023-05470-1>

Evidence for microbial biodegradation of polyethylene terephthalate (PET) has been reported, but little is known about the PET biodegradation process and molecular mechanism by marine microorganisms. Here, we show the biodegradation of PET by the membrane-anchored PET esterase from the marine bacterium *Rhodococcus pyridinivorans* P23, elucidate the properties of this enzyme, and propose the PET biodegradation by this strain in biofilm. We identify the PET-degrading enzyme dubbed PET esterase through activity tracking. In addition to depolymerizing PET, it hydrolyzes MHET into TPA under acid conditions. We prove that it is a low and constitutively transcribed, membrane-anchored protein displayed on the cell surface. Furthermore, we also investigate the microbial groups possessing PET esterase coupled with the TPA degradation pathway, mainly in the phyla *Proteobacteria* and *Actinobacteriota*. Clarification of the microbial PET biodegradation in the marine environment will contribute to the understanding of bioremediation of marine PET pollution.

<https://www.nature.com/articles/s42003-023-05470-1>

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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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