

# Sunday Evening News No 353

2023-11-20 – 2023-11-26

Compiled and edited by **BGF** Jany



Wissenschaftskreis  
Genomik und  
Gentechnik e.V.

## Meetings – Conferences / Tagungen – Konferenzen

**EFSA: Webinar on protein safety assessment in GMOs – save the date or register now!**

<https://www.efsa.europa.eu/de/events/webinar-protein-safety-assessment-gmos-save-date-or-register-now>

**ALLEA: Towards Sustainable Food Consumption in Europe: The Role of Informal Food Chains**

6 December 2023

<https://allea.org/6-december-2023-towards-sustainable-food-consumption-in-europe-the-role-of-informal-food-chains/>

## Press Releases -Media / Presse- und Medienberichte

**Verbände fordern strikte Regulierung von Gentechnik - Offener Brief an Bundesminister Özdemir**

<https://www.presseportal.de/pm/7666/5653018>

**EINE DEREGULIERUNG NEUER GENTECHNIK-VERFAHREN!**

[https://www.dnr.de/sites/default/files/2023-11/Positionspapier\\_NGT.pdf](https://www.dnr.de/sites/default/files/2023-11/Positionspapier_NGT.pdf)

**Koch J.: Gentechniknovelle: EU-Agrarminister sind sich nicht grün**

<https://www.wochenblatt-dlv.de/politik/gentechniknovelle-eu-agrarminister-gruen-574837><https://www.wochenblatt-dlv.de/politik/gentechniknovelle-eu-agrarminister-gruen-574837>

**Noisette C.: GMOs/NGTs: consumers want a choice**

<https://www.infogm.org/7925-gmos-ntgs-consumers-want-a-choice?lang=fr>

**GM Watch: Academics, scientists call to scrap gene-editing proposal**

<https://gmwatch.org/en/106-news/latest-news/20328>

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 week 47

## Publications – Publikationen

Ahmar S., Usman B., Hensel G., Jung K.-H., Gruszka D. (2023): **CRISPR enables sustainable cereal production for a greener future.** Trends in Plant Science |

<https://doi.org/10.1016/j.tplants.2023.10.016> (Special issue: 21st century tools in plant science)

The clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 (Cas9) system has become the most important tool for targeted genome editing in many plant and animal species over the past decade. The CRISPR/Cas9 technology has also sparked a flood of applications and technical advancements in genome editing in the key cereal crops, including rice, wheat, maize, and barley. Here, we review advanced uses of CRISPR/Cas9 and derived systems in genome editing of cereal crops to enhance a variety of agronomically important features. We also highlight new technological advances for delivering preassembled Cas9-gRNA ribonucleoprotein (RNP)-editing systems, multiplex editing, gain-of-function strategies, the use of artificial intelligence (AI)-based tools, and combining CRISPR with novel speed breeding (SB) and vernalization strategies.

<https://www.sciencedirect.com/science/article/pii/S1360138523003588>

Vora, Z., Pandya, J., Sangh, C. et al. (2023): **The evolving landscape of global regulations on genome-edited crops.** J. Plant Biochem. Biotechnol. | <https://doi.org/10.1007/s13562-023-00863-z>

The creators of CRISPR/Cas have been awarded the 2020 Nobel Prize in Chemistry for their ground-breaking technology and its exceptional potential to address fundamental issues in the field of biological sciences. This revolutionary tool has accelerated the development of novel crop varieties with enhanced features in agriculture, all without the need for transgenes. However, in order for this technology to reach its full potential, the establishment of a precise and comprehensive global regulatory framework for these crops is crucial. Despite the absence of foreign genetic material in crops developed through CRISPR/Cas mediated genome editing, there is an ongoing and intense debate surrounding the regulation of these crops prior to their release

into the market. While certain CRISPR-edited crops have already been introduced in Japan, their legal status remains a point of contention in several nations, including the EU and New Zealand. This review paper serves as a comprehensive guide to the worldwide regulatory framework for CRISPR-edited crops, as well as provide insights into the future prospects of this transformative technology. By examining the current landscape of regulations and exploring potential avenues for harmonization, we can better understand the challenges and opportunities that lie ahead for CRISPR-edited crops.

<https://link.springer.com/article/10.1007/s13562-023-00863-z>

Vives Vallés J.A. (2023): **The new EC proposal for a regulation on the production and marketing of plant reproductive material: upgrade or regression? An intellectual property perspective.** *Journal of Intellectual Property Law & Practice* 18 (11) 774–778 |

<https://doi.org/10.1093/jiplp/jpad085>

With the proposed EC reform, Value for Cultivation and Use (VCU) trials will include sustainability as a driver, broadening their scope from agricultural varieties to horticultural and fruit on ,s, and a plethora of derogations to variety registration and seed certification standards will be added or deepened; however, it is unlikely that the EU and Member States' plant variety protection schemes, farmers, or end consumers will truly benefit from it.

<https://academic.oup.com/jiplp/article-abstract/18/11/774/7331469?redirectedFrom=fulltext>

[https://academic.oup.com/jiplp/article/18/11/774/7331469?guestAccessKey=dbeba2b1-4021-4378-bbe7-d26f820fdfe9&utm\\_source=authorollfreelink&utm\\_campaign=jiplp&utm\\_medium=email](https://academic.oup.com/jiplp/article/18/11/774/7331469?guestAccessKey=dbeba2b1-4021-4378-bbe7-d26f820fdfe9&utm_source=authorollfreelink&utm_campaign=jiplp&utm_medium=email)

Wang Y, Mu Y, Yan L, Tang B, Jiang F. (2023): **Regulatory Policies of Genome Editing Products around the World.** *J Biomed Res Environ Sci.* 4 (10): 1447-1454. doi: 10.37871/jbres1817, Article ID: JBRES1817,

Genome editing is one of the powerful tools that has been applied to the improvement of plants, animals and microorganisms, and human therapy. The regulation of genome editing products vary among nations. Here we summarize the legislation of genome editing in different nations to let people know how genome editing products have been regulated in different nations. Additionally, the departments responsible for genome editing regulation in each nation are provided in this review.

<https://www.ielsciences.com/articles/jbres1817.pdf>

Zaman O.U., Raza A., Lozano-Juste J., Li Chao L. et al. (2023): **Engineering plants using diverse CRISPR-associated proteins and deregulation of genome-edited crops. Trends in Biotechnology** | <https://doi.org/10.1016/j.tibtech.2023.10.007>

The CRISPR/Cas system comprises RNA-guided [nucleases](#), the target specificity of which is directed by Watson–Crick base pairing of target loci with single guide (sg)RNA to induce the desired edits. CRISPR-associated proteins and other engineered nucleases are opening new avenues of research in crops to induce heritable mutations. Here, we review the diversity of CRISPR-associated proteins and strategies to deregulate genome-edited (GEd) crops by considering them to be close to natural processes. This technology ensures yield without penalties, advances plant breeding, and guarantees manipulation of the genome for desirable traits. DNA-free and off-target-free GEd crops with defined characteristics can help to achieve sustainable global food security under a changing climate, but need alignment of international regulations to operate in existing supply chains.

<https://www.sciencedirect.com/science/article/abs/pii/S016779923002986>

Dassler, T., Myhr, A.I., Lalyer, C.R. et al. (2023): **Structured analysis of broader GMO impacts inspired by technology assessment to inform policy decisions.** *Agric Hum Values* |

<https://doi.org/10.1007/s10460-023-10519-2>

If genetically modified organisms (GMOs) are approved in the EU for experimental release or marketing authorization (placing on the market), a risk assessment (RA) is carried out beforehand to determine whether this may be associated with negative effects on human health, nature or the environment. Applications are reviewed by the European Food Safety Authority (EFSA) and the national Competent Authorities of the Member States. However, the potential ramifications of the GMOs that are systematically addressed in the current RA context are limited. Broader consideration can include environmental and health aspects beyond the scope of the statutory RA, as well as societal, ethical and cultural impacts. These other levels of impact may be considered during the comitology process of authorisation, but how this is done is typically not made explicit in a systematic way. However, with the dynamic developments of new kinds of GMOs, these considerations as well as transparency regarding the role of broader considerations in political decision-making become more and more relevant. Against this backdrop, we identified the requirements and suggest the main elements for such a broader assessment. We use insights from the field of Technology Assessment (TA) to explore the requirements for operationalising a rapid but still systematic, transparent and broad case-by-case GMO assessment compatible with the existing legislative framework.

<https://link.springer.com/article/10.1007/s10460-023-10519-2>

Gupta , R., Verma , A., Yadav, H., Gupta, A. K., Srivastava , A. et al. (2023):. **Genome Sequencing in Field Crops: Unlocking Agricultural Potential.** *International Journal of*

Environment and Climate Change, 13 (11), 3669–3677 |

<https://doi.org/10.9734/ijecc/2023/v13i113544>

Genome sequencing has revolutionized agriculture by providing crucial insights into the genetic make-up of field crops. This paper explores the importance of genome sequencing in unlocking the agricultural potential of various field crops. By sequencing the DNA of crops such as wheat, maize, rice, and soybean researchers are gain a comprehensive understanding of their genetic diversity, disease resistance and yield-enhancing traits. This knowledge enables the development of precision breeding strategies, leading to the creation of high-yielding, stress-tolerant and nutritionally enhanced crop varieties. In addition, genome sequencing is facilitating the identification of key genes involved in plant-microbe interactions and adaptation to environmental stressors. Such knowledge can inform sustainable agricultural practices, reduce chemical inputs and increase crop resilience in the face of climate change. This paper highlights the transformative impact of genome sequencing on crop improvement, food security and global agricultural sustainability.

<https://journalijecc.com/index.php/IJECC/article/view/3544>

Joshi A., Yang S.-Y., Song H.-G., Min J., Lee J.-H. (2023): **Genetic Databases and Gene Editing Tools for Enhancing Crop Resistance against Abiotic Stress**. *Biology* 12 (11), 1400 |

<https://doi.org/10.3390/biology12111400>

Abiotic stresses extensively reduce agricultural crop production globally. Traditional breeding technology has been the fundamental approach used to cope with abiotic stresses. The development of gene editing technology for modifying genes responsible for the stresses and the related genetic networks has established the foundation for sustainable agriculture against environmental stress. Integrated approaches based on functional genomics and transcriptomics are now expanding the opportunities to elucidate the molecular mechanisms underlying abiotic stress responses. This review summarizes some of the features and weblinks of plant genome databases related to abiotic stress genes utilized for improving crops. The gene-editing tool based on clustered, regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 (Cas9) has revolutionized stress tolerance research due to its simplicity, versatility, adaptability, flexibility, and broader applications. However, off-target and low cleavage efficiency hinder the successful application of CRISPR/Cas systems. Computational tools have been developed for designing highly competent gRNA with better cleavage efficiency. This powerful genome editing tool offers tremendous crop improvement opportunities, overcoming conventional breeding techniques' shortcomings. Furthermore, we also discuss the mechanistic insights of the CRISPR/Cas9-based genome editing technology. This review focused on the current advances in understanding plant species' abiotic stress response mechanism and applying the CRISPR/Cas system genome editing technology to develop crop resilience against drought, salinity, temperature, heavy metals, and herbicides.

<https://www.mdpi.com/2079-7737/12/11/1400>

Altae-Tran H., Shmakov, S.A., Makarova K.S. et al. (2023): **Diversity, evolution, and classification of the RNA-guided nucleases TnpB and Cas12**. *PNAS* 120 (48) e2308224120 |

<https://doi.org/10.1073/pnas.2308224120>

The TnpB proteins are transposon-associated RNA-guided nucleases that are among the most abundant proteins encoded in bacterial and archaeal genomes, but whose functions in the transposon life cycle remain unknown. TnpB appears to be the evolutionary ancestor of Cas12, the effector nuclease of type V CRISPR-Cas systems. We performed a comprehensive census of TnpBs in archaeal and bacterial genomes and constructed a phylogenetic tree on which we mapped various features of these proteins. In multiple branches of the tree, the catalytic site of the TnpB nuclease is rearranged, demonstrating structural and probably biochemical malleability of this enzyme. We identified numerous cases of apparent recruitment of TnpB for other functions of which the most common is the evolution of type V CRISPR-Cas effectors on about 50 independent occasions. In many other cases of more radical exaptation, the catalytic site of the TnpB nuclease is apparently inactivated, suggesting a regulatory function, whereas in others, the activity appears to be retained, indicating that the recruited TnpB functions as a nuclease, for example, as a toxin. These findings demonstrate remarkable evolutionary malleability of the TnpB scaffold and provide extensive opportunities for further exploration of RNA-guided biological systems as well as multiple applications.

<https://www.pnas.org/doi/10.1073/pnas.2308224120>

## EFSA

CEP Panel (2023): Safety evaluation of the food enzyme subtilisin from the non-genetically modified *Bacillus licheniformis* strain NZYM-CX. *EFSA Journal*, 21(11), e8406.

<https://doi.org/10.2903/j.efsa.2023.8406>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8406>

CEP Panel (2023): Safety evaluation of the food enzyme glucan 1,4- $\alpha$ -maltohydrolase from the genetically modified *Bacillus subtilis* strain MAMDSM. *EFSA Journal*, 21(11), e8410.

<https://doi.org/10.2903/j.efsa.2023.8410>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8410>

CEP Panel (2023). Safety evaluation of the food enzyme glucan 1,4- $\alpha$ -maltohydrolase from the genetically modified *Bacillus subtilis* strain AR-513. *EFSA Journal*, 21(11), e8389.

<https://doi.org/10.2903/j.efsa.2023.8389>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8389>

CEP Panel (2023). Safety evaluation of the food enzyme endo-polygalacturonase from the non-genetically modified *Aspergillus tubingensis* strain MUCL 55013. *EFSA Journal*, 21(11), e8389. <https://doi.org/10.2903/j.efsa.2023.8397>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8397>

CEP Panel (2023): Safety evaluation of the food enzyme phospholipase A<sub>2</sub> from the genetically modified *Aspergillus niger* strain PLA. *EFSA Journal*, 21(11), e8400.

<https://doi.org/10.2903/j.efsa.2023.8400>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8400>

CEP Panel (2023): Safety evaluation of the food enzyme  $\alpha$ -amylase from the genetically modified *Bacillus licheniformis* strain NZYM-AC. *EFSA Journal*, 21(11), e8393.

<https://doi.org/10.2903/j.efsa.2023.8393>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8393>

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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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