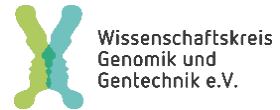


Sunday Evening News No 358

2024-01-01 – 2024-02-07

Compiled and edited by **BGF** Jany



EU-Authorisation of GM plants for import as food and feed in 2023

The Commission has authorised 13 genetically modified plants for import as food and feed. 7 GM plants were authorised for the first time and authorisation was renewed for 6 ones. The average time taken to process applications - from receipt by EFSA to authorisation by the Commission - was 51.2 months for new authorisations and 28.1 months for the renewal of authorisations ([▶ Authorisations 2023](#))

EFSA received applications for the safety assessment of six GM plants in 2023. The safety assessments for maize MON 810 and DP-023211-2 have been completed, but the opinions were no longer published in 2023. For five other GM plants, the opinions were still published in 2023, with two (maize GA21xT25 and maize 87419) still being authorised in 2023.

Food Biotechnology / white genetic engineering - enzymes

In 2023, the CEP Panel completed the safety assessment for a total of 71 food enzymes. The opinions for 61 food enzymes were published in 2023 ([▶ Safety assessments completed in 2023](#)). Of the 61 food enzymes, 23 were obtained from GM microorganisms.

In 2023, EFSA received 101 applications for the safety assessment of food enzymes ([▶ pending safety assessments](#), Table, only).

With regard to the publication of a "Union List" for marketable food enzymes, a total of 67 food enzymes from the list of applications submitted by the deadline of 11 March 2015 still need to be assessed, whereby the applications for 7 have not yet been submitted to the Panel for assessment ([▶ deadline list](#), Table, only). As the period for the safety assessment is not prescribed for the food enzymes from the reference date list, but the Union list should (can) only be drawn up after the assessment of all food enzymes from the reference date list, the Union list is probably not expected before the end of 2026.

Meetings – Conferences / Veranstaltungen - Konferenzen

Save the date:

Volkswagen-Stiftung: **Grüne Gentechnik – Allheilmittel oder versteckte Gefahr?**

04. Apr. 2024, 19:00 Uhr - 21:00 Uhr

<https://www.volkswagenstiftung.de/de/veranstaltungen/gruene-gentechnik-allheilmittel-oder-versteckte-gefahr>

Press Releases -Media / Presse- und Medienberichte

Newsdesk: **Shaping the Future, Belgium's Agenda for the EU Presidency**

<https://europeantimes.news/2024/01/shaping-the-future-belgiums-agenda-for-the-eu-presidency/>

Hodgson R.: **EU Policy. Belgium in eight-week sprint to close deals on emissions, packaging waste legislation**

<https://www.euronews.com/green/2024/01/05/belgium-in-eight-week-sprint-to-close-deals-on-emissions-packaging-waste-legislation>

Dahm J. und Arboleas M.S.: **2023 in der EU-Agrarpolitik: Ein Jahr der Hindernisse und Blockaden**

<https://www.euractiv.de/section/farm-to-fork-strategie/news/2023-in-der-eu-agrarpolitik-ein-jahr-der-hindernisse-und-blockaden/>

Karberg S: **Landwirtschaft in Europa tabu bleibt?**

<https://www.tagesspiegel.de/wissen/was-passiert-wenn-gentechnik-in-der-landwirtschaft-in-europa-tabu-bleibt-10979026.html>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): January week 01-2024

Publications – Publikationen

European Network of GMO Laboratories (ENGL) (2023): ***Detection of food and feed plant products obtained by targeted mutagenesis and cisgenesis***

The current EU legislation on GMOs and GM food and feed requires analytical testing to support traceability of these products on the market. The European Network of GMO Laboratories has reviewed the implications of the analytical requirements when they are applied to plant products developed with the use of new genomic techniques, i.e. targeted mutagenesis and cisgenesis. This review concluded that analytical testing to support traceability is not considered feasible for all products obtained by targeted mutagenesis and cisgenesis, both due to technical restrictions and because of implementation issues.

https://gmo-crl.jrc.ec.europa.eu/doc/JRC133689_kjna31521enn.pdf

Tagliabue G.M. (2023): **Genetically Modified Organisms: A Scientific-Political Dialogue on a Meaningless Meme**. Cambridge Scholars Publishing 2023:

Due to an intricate web of psychological, socio-political and economic factors, an alliance of ill-advised forces of radical activism and powerful commercial interests encourage the rejection of so-called “genetically modified organisms” (GMOs), that is agri-food products whose DNA has been directly retouched, or “recombined” (rDNA).

While the pseudo-concept has no scientific meaning, the opponents of the agro-industry insist on attacking it as an alleged symbol of the exploitation of nature for greed and profit: this socio-political struggle, in itself legitimate, but directed at the wrong target, fosters doubts and fears about the supposed negative effects of GMOs on the environment and health. Instead, scientists recommend carefully checking new individual plant varieties or animal breeds, regardless of how they are obtained (through rDNA or other processes). Similarly, the important socio-economic pros and cons of the cultivation and consumption of agri-food novelties, in richer or poorer countries as well, should be assessed independently of the developers’ biotech methods. The book explains this contemporary taboo and calls for a well-regulated use of all biotechnological innovations, ending the decades-long quagmire which stymies public research and its philanthropic repercussions.

www.cambridgescholars.com/product/978-1-5275-0522-3

Park J.-C. and Bae S. (2023): **Current status of genome editing technologies: special issue of BMB Reports in 2024**

Since the identification of DNA as a genetic material, manipulating DNA in various organisms has been a long standing dream of humanity. In pursuit of this objective, technologies to edit genome have been extensively developed over the recent decades. The emergence of zinc finger nuclease (ZFN), transcription activator-like effector nuclease (TALEN), and clustered regularly interspaced short palindromic repeats (CRISPR) and CRISPR-associated (Cas) systems enabled site-specific DNA cleavage in a programmable manner. Furthermore, the advent of base editors (BEs) and prime editors (PEs) has enabled base conversion and insertion/deletion with a high accuracy. In addition to the editing of genomic DNA in the nucleus, attempts to manipulate circular DNAs in organelle are currently ongoing. These technologies are bringing major progress in diverse fields including the engineering of cells, livestock, and plants as well as therapeutic gene correction in humans. In this special issue, we aim to cover the recent advances in genome editing technology and its applications in therapeutics, breed improvement in plants and livestock, RNA recording, and protein evolution.

<https://pubmed.ncbi.nlm.nih.gov/38178650/>

Regnault-Roger, C. (2023): **What Regulation for NGTs in the EU?** In: Biotech Challenges.

Springer, Cham. https://doi.org/10.1007/978-3-031-38237-6_8

Should the regulations applied to first-generation GMOs in the European Union be applied to NGTs? This regulation, undoubtedly one of the most demanding and restrictive in the world, has strongly limited the development of transgenic plants in this part of the world. Today, faced with the generalization of commercial circuits of goods and food freight, the regulation that will be granted to agricultural products derived from NGTs has become a major political issue for the European Union as well as a strategic development choice.

https://link.springer.com/chapter/10.1007/978-3-031-38237-6_8

Regnault-Roger, C. (2023): **GMOs: A Regulatory Concept**. In: Biotech Challenges. Springer, Cham. https://doi.org/10.1007/978-3-031-38237-6_6

For many people, GMOs have become synonymous with monstrosity, whereas, as we have seen in the previous chapters, research after the creation of genetically modified organisms in laboratories by genetic engineering techniques and the establishment of specific regulations in many countries have demonstrated that organisms resulting from mutagenesis or transgenesis exist spontaneously in nature. So why have we created this concept of GMO and what does it cover?

https://link.springer.com/chapter/10.1007/978-3-031-38237-6_6

Vora, Z., Pandya, J., Sangh, C. et al. (2023): **The evolving landscape of global regulations on genome-edited crops.** J. Plant Biochem. Biotechnol. **32**, 831–845 | <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>

Demaria, F.; D'Annolfo, R.; Sardone, R. (2023): **Consumer Evaluations of and Attitudes towards New Genome Editing Techniques: An Italian Case Study.** Agriculture 2024, 14, 51. <https://doi.org/10.3390/agriculture14010051>

The ever-increasing development of assisted evolution technologies (AETs) in agriculture has boosted crop improvement. The commercialization of improved biotech crops can be promoted by modern gene editing instead of conventional genetic modification, which is a cheaper and faster approach that can help address future agriculture challenges, such as food security, environmental sustainability, and climate change. However, the use of these technologies is still sensitive and debated in many countries. Each region promotes a different approach, depending on regulatory policies, and adopting these technologies requires knowledge of consumer views and stakeholder acceptance. For this purpose, we conducted a survey of 564 Italians regarding their knowledge of genetic techniques, informational tools, purchase preferences, environmental sustainability, and food safety issues. The research aims are twofold: (a) to assess the level of knowledge and (b) to determine how consumer background, including social and demographic characteristics, affects their level of knowledge. Our findings emphasize the importance of communication and dissemination activities, in which clarity and a broad appeal are key.

<https://www.mdpi.com/2077-0472/14/1/51>

Muha-Ud-Din G., Ali F., Hameed A., Naqvi S.A.H. et al. (2023): **CRISPR/Cas9-based genome editing: A revolutionary approach for crop improvement and global food security.** Physiological and Molecular Plant Pathology 129, 102191 |

<https://doi.org/10.1016/j.pmpp.2023.102191>

In the face of a growing global population, climate change, and limited [arable land](#), the need for resilient, high-yielding crops is pressing. Traditional [breeding methods](#) have struggled to meet these demands, but CRISPR/Cas9-based genome editing offers a groundbreaking solution. This article provides an in-depth overview of CRISPR/Cas9's role in enhancing crop traits to ensure global food security. By harnessing modern sequencing technologies, researchers can precisely edit genes in crop plants especially major crops like [Triticum aestivum](#), [Oryza sativa](#), [Zea mays](#), and [Solanum tuberosum](#) etc., imparting traits such as disease resistance and stress tolerance. The technology is pivotal to producing next-generation crops (NGC's) capable of adapting to changing climates and delivering higher yields and product quality. Ethical and regulatory considerations are important, but responsible governance of genome editing promises significant advancements in [agriculture](#). This review highlights CRISPR/Cas9's transformative potential in crop improvement and its pivotal role in shaping the future of food production.

<https://www.sciencedirect.com/science/article/pii/S0885576523002461?via%3Dihub>

Ji, N., Liang, D., Clark, L.V. et al. (2023): **Host genetic variation drives the differentiation in the ecological role of the native *Miscanthus* root-associated microbiome.** Microbiome 11, 216 | <https://doi.org/10.1186/s40168-023-01646-3>

Background: Microbiome recruitment is influenced by plant host, but how host plant impacts the assembly, functions, and interactions of perennial plant root microbiomes is poorly understood. Here we examined prokaryotic and fungal communities between rhizosphere soils and the root endophytic compartment in two native *Miscanthus* species (*Miscanthus sinensis* and *Miscanthus floridulus*) of Taiwan and further explored the roles of host plant on root-associated microbiomes.

Results: Our results suggest that host plant genetic variation, edaphic factors, and site had effects on the root endophytic and rhizosphere soil microbial community compositions in both *Miscanthus sinensis* and *Miscanthus floridulus*, with a greater effect of plant genetic variation observed for the root endophytic communities. Host plant genetic variation also exerted a stronger effect on core prokaryotic communities than on non-core prokaryotic communities in each microhabitat of two *Miscanthus* species. From rhizosphere soils to root endophytes, prokaryotic co-occurrence network stability increased, but fungal co-occurrence network stability decreased. Furthermore, we found root endophytic microbial communities in two *Miscanthus* species were more strongly driven by deterministic processes rather than stochastic processes. Root-enriched

prokaryotic OTUs belong to Gammaproteobacteria, Alphaproteobacteria, Betaproteobacteria, Sphingobacteriia, and [Saprosirae] both in two *Miscanthus* species, while prokaryotic taxa enriched in the rhizosphere soil are widely distributed among different phyla.

Conclusions: We provide empirical evidence that host genetic variation plays important roles in root-associated microbiome in *Miscanthus*. The results of this study have implications for future bioenergy crop management by providing baseline data to inform translational research to harness the plant microbiome to sustainably increase agriculture productivity.

<https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168-023-01646-3>

Zargar M. et al. (2023), **Microsatellite-Based Genetic Diversity Analysis and Population Structure of Proso Millet (*Panicum miliaceum* L.) in Kazakhstan**, *Agronomy* | DOI: [10.3390/agronomy13102514](https://doi.org/10.3390/agronomy13102514)

Proso millet is an important allotetraploid cereal crop; however, it is the least studied species of the Poaceae family, as it is an under-utilized crop. Genomic resources for proso millet are very limited compared to major crops. An understanding of the genetic relationships among germplasm resources is important for future breeding endeavors. In the present study, simple sequence repeat (SSR) markers were employed to assess the polymorphism and genetic diversity of 100 millet accessions from different countries, which were tested in the dry steppe zone conditions of the Akmola region from 2020 to 2022. The use of 20 SSR markers detected a total of 47 alleles, with an average allele number of 2.35 per locus among these proso accessions. Nine of them were polymorphic among the genotypes, which suggests that these SSR markers can be used for genetic studies. The results showed a moderate level of polymorphism information content (PIC) that averaged at 0.424, ranging from 0.125 to 0.795. The markers SSR-67, SSR-82, SSR-85 and SSR-109 showed high PIC values of 0.536, 0.756, 0.795 and 0.758, respectively. Markers SSR 85 and SSR 86 significantly correlated to agronomic traits, such as productive tillering (PT) and grain yield (GY). The genetic structure, UPGMA cluster and PCoA assay indicated that the accessions that originated from Central Asia had higher genetic diversity. Based on structure (K = 3), all the accessions were divided into three groups, where the gene pool that originated from Central Asia was detected in all three clusters. Based on a principal component analysis (PCA), the accessions of Central Asian origin were genetically closer to the North Asian group.

<https://www.mdpi.com/2073-4395/13/10/2514>

Santó-Pastor, A., Kajala, K., Shaar-Moshe, L. et al. (2024): **A suberized exodermis is required for tomato drought tolerance**. *Nat. Plants* | <https://doi.org/10.1038/s41477-023-01567-x>

Plant roots integrate environmental signals with development using exquisite spatiotemporal control. This is apparent in the deposition of suberin, an apoplastic diffusion barrier, which regulates flow of water, solutes and gases, and is environmentally plastic. Suberin is considered a hallmark of endodermal differentiation but is absent in the tomato endodermis. Instead, suberin is present in the exodermis, a cell type that is absent in the model organism *Arabidopsis thaliana*. Here we demonstrate that the suberin regulatory network has the same parts driving suberin production in the tomato exodermis and the *Arabidopsis* endodermis. Despite this co-option of network components, the network has undergone rewiring to drive distinct spatial expression and with distinct contributions of specific genes. Functional genetic analyses of the tomato MYB92 transcription factor and ASFT enzyme demonstrate the importance of exodermal suberin for a plant water-deficit response and that the exodermal barrier serves an equivalent function to that of the endodermis and can act in its place.

<https://www.nature.com/articles/s41477-023-01567-x>

Westbrook A.S., DiTommaso A. (2023); **Hybridization in agricultural weeds: A review from ecological, evolutionary, and management perspectives**. *Am J Bot.* 2023; e16258. |

<https://doi.org/10.1002/ajb2.16258>

Agricultural weeds frequently hybridize with each other or with related crop species. Some hybrid weeds exhibit heterosis (hybrid vigor), which may be stabilized through mechanisms like genome duplication or vegetative reproduction. Even when heterosis is not stabilized, hybridization events diversify weed gene pools and often enable adaptive introgression. Consequently, hybridization may promote weed evolution and exacerbate weed-crop competition. However, hybridization does not always increase weediness. Even when viable and fertile, hybrid weeds sometimes prove unsuccessful in crop fields. This review provides an overview of weed hybridization and its management implications. We describe intrinsic and extrinsic factors that influence hybrid fitness in agroecosystems. We also survey the rapidly growing literature on crop-weed hybridization and the link between hybridization and invasiveness. These topics are increasingly relevant in this era of genetic tools for crop improvement, intensive and simplified cropping systems, and globalized trade. The review concludes with suggested research priorities, including hybridization in the context of climate change, plant-insect interactions, and redesigned weed management programs. From a weed management perspective, hybridization is one of many reasons that

researchers and land managers must diversify their weed control toolkits.

<https://bsapubs.onlinelibrary.wiley.com/doi/epdf/10.1002/ajb2.16258>

Nicola Schmidt N., Sielemann K., Breitenbach S. Fuchs J. et al. (2023): **Repeat turnover meets stable chromosomes: repetitive sequences mark speciation and gene pool boundaries in sugar beet and wild beets**. *The Plant Journal* (2023) | doi: 10.1111/tpj.16599

Sugar beet and its wild relatives share a base chromosome number of nine and similar chromosome morphologies. Yet, interspecific breeding is impeded by chromosome and sequence divergence that is still not

fully understood. Since repetitive DNAs are among the fastest evolving parts of the genome, we investigated, if repeatome innovations and losses are linked to chromosomal differentiation and speciation. We traced genome and chromosome-wide evolution across 13 beet species comprising all sections of the genera Beta and Patellifolia. For this, we combined short and long read sequencing, flow cytometry, and cytogenetics to build a comprehensive framework that spans the complete scale from DNA to chromosome to genome. Genome sizes and repeat profiles reflect the separation into three gene pools with contrasting evolutionary patterns. Among all repeats, satellite DNAs harbor most genomic variability, leading to fundamentally different centromere architectures, ranging from chromosomal uniformity in Beta and Patellifolia to the formation of patchwork chromosomes in Corollinae/Nanae. We show that repetitive DNAs are causal for the genome expansions and contractions across the beet genera, providing insights into the genomic underpinnings of beet speciation. Satellite DNAs in particular vary considerably between beet genomes, leading to the evolution of distinct chromosomal setups in the three gene pools, likely contributing to the barriers in beet breeding. Thus, with their isokaryotypic chromosome sets, beet genomes present an ideal system for studying the link between repeats, genomic variability, and chromosomal differentiation and provide a theoretical fundament for understanding barriers in any crop breeding effort.

<https://pubmed.ncbi.nlm.nih.gov/38128038/>

Chen F., Pu A., Luo J., Wang Z. et al. (2024): **Pathways to Ensuring Food Security in the Context of the Chinese Bioeconomy Landscape**. ACS Agric. Sci. Technol. XXXX, XXX, XXX-XXX |

<https://doi.org/10.1021/acsagscitech.3c00423>

Recently, China released its first 5-year plan for bioeconomy development, in which bioagriculture was identified as one of the five key development areas. It not only aims to cultivate new momentum for ensuring food security in China but also outlines a new direction for agro-biotechnology innovation and the development of the bioindustry. This paper elaborates on the significance of agriculture as a crucial application scenario in the future bioeconomy and analyzes the demand for agricultural biotechnology in the context of China's food security. Additionally, it summarizes the development experiences of countries and regions, such as the United States and the European Union in the field of bioeconomy, including their strategic policies, leading technologies, and policy impacts. The paper further proposes specific ways to fully leverage the supportive role of bioeconomy in ensuring China's food security. These methods encompass the enhancement of agricultural biotechnology innovation capabilities, the application of biotechnological achievements in agriculture, and the refinement of the regulatory framework for biotechnology.

<https://pubs.acs.org/doi/10.1021/acsagscitech.3c00423>

Li, J., Martin, C. & Fernie, A. **Biofortification's contribution to mitigating micronutrient deficiencies**. *Nat Food* (2024). <https://doi.org/10.1038/s43016-023-00905-8>

Biofortification was first proposed in the early 1990s as a low-cost, sustainable strategy to enhance the mineral and vitamin contents of staple food crops to address micronutrient malnutrition. Since then, the concept and remit of biofortification has burgeoned beyond staples and solutions for low- and middle-income economies. Here we discuss what biofortification has achieved in its original manifestation and the main factors limiting the ability of biofortified crops to improve micronutrient status. We highlight the case for biofortified crops with key micronutrients, such as provitamin D₃/vitamin D₃, vitamin B₁₂ and iron, for recognition of new demographics of need. Finally, we examine where and how biofortification can be integrated into the global food system to help overcome hidden hunger, improve nutrition and achieve sustainable agriculture.

<https://www.nature.com/articles/s43016-023-00905-8>

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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