

# Sunday Evening News No 366

2024-02-26 – 2024-03-03

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Wissenschaftskreis  
Genomik und  
Gentechnik e.V.

## Press Releases -Media / Presse- und Medienberichte

### EFI: Innovationen im Pflanzenbau: Präzisionstechnologien und Gentechnik für mehr Nachhaltigkeit

Die Landwirtschaft steht vor großen Herausforderungen – Potenziale durch neue Präzisionstechnologien stärker ausschöpfen - Rechtsrahmen zu Grüner Gentechnik ist überholt

<https://nachrichten.idw-online.de/2024/02/28/innovationen-im-pflanzenbau-praezisionstechnologien-und-gentechnik-fuer-mehr-nachhaltigkeit?groupcolor=6>

### Uni Jena: Forschungsstandort Deutschland ist attraktiver geworden, aber...

<https://www.uni-jena.de/nachrichteneubersicht/forschungsstandort-deutschland-ist-attraktiver-geworden-aber>

### POINT NEWSLETTER NR. 260 – Aktuelle Biotechnologie; Februar 2024

[https://www.scienceindustries.ch/\\_file/35517/point-2024-02-260-d.pdf?utm\\_source=POINT+Newsletter&utm\\_campaign=fd8ef3e418-POINT\\_Januar\\_2024\\_COPY\\_01&utm\\_medium=email&utm\\_term=0\\_19eef28c92-fd8ef3e418-1210937714](https://www.scienceindustries.ch/_file/35517/point-2024-02-260-d.pdf?utm_source=POINT+Newsletter&utm_campaign=fd8ef3e418-POINT_Januar_2024_COPY_01&utm_medium=email&utm_term=0_19eef28c92-fd8ef3e418-1210937714)

### VBIO: Biowissenschaften bestmöglich kommunizieren - VBIO legt Positionspapier „Wissenschaftskommunikation“ vor

<https://www.vbio.de/aktuelles/details/biowissenschaften-bestmoeglich-kommunizieren-vbio-legt-positionspapier-wissenschaftskommunikation-vor-1>

Positionspapier:

[https://www.vbio.de/fileadmin/user\\_upload/verband/Positionen/240226\\_Position\\_WissKomm\\_final.pdf](https://www.vbio.de/fileadmin/user_upload/verband/Positionen/240226_Position_WissKomm_final.pdf)

### Brzeziński B., Andrés P.: Patent war looms over Europe's future supercrops

<https://www.politico.eu/article/gene-edited-seeds-europe-patent-war-supercrops/>

### epi Position Paper on New Genomic Technique (NGT) Plant Patenting Proposal of the European Parliament

<https://patentepi.org/en/epi/library/main/a6777526-35ef-45f4-9418-fea850e93a0f/file>

### MacLennan R.: Broccoli, tomatoes and pepper: Why the EU may block protection of GM plants

<https://www.worldipreview.com/patent/broccoli-tomatoes-and-pepper-why-the-eu-may-block-protection-of-gm-plants>

### Knight P.: Argentina Greenlights Genetically Modified Yeast for Ethanol Manufacturing

<https://www.chemanalyst.com/NewsAndDeals/NewsDetails/argentina-greenlights-genetically-modified-yeasts-for-ethanol-manufacturing-25516>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): February/March 09-2024

## Publications – Publikationen

Ryan, C.D., Henggeler E., Gilbert S., Schaul A.J., Swarthout J.T. (2024): **Exploring the GMO narrative through labeling: strategies, products, and politics**. GM Crops & Food, 15:1, 51-66, DOI: [10.1080/21645698.2024.2318027](https://doi.org/10.1080/21645698.2024.2318027)

Labels are influential signals in the marketplace intended to inform and to eliminate buyer confusion. Despite this, food labels continue to be the subject of debate. None more so than non-GMO (genetically modified organisms) labels. This manuscript provides a timeline of the evolution of GMO labels beginning with the early history of the anti-GMO movement to the current National Bioengineered Food Disclosure Standard in the United States. Using media and market intelligence data collected through Buzzsumo™ and Mintel™, public discourse of GMOs is analyzed in relation to sociopolitical events and the number of new food products with anti-GMO labels, respectively. Policy document and publication data is collected with Overton™ to illustrate the policy landscape for the GMO topic and how it has changed over time. Analysis of the collective data illustrates that while social media and policy engagement around the topic of GMOs has diminished over time, the number of new products with a GMO-free designation continues to grow. While discourse peaked at one point, and has since declined, our results suggest that the legacy of an anti-GMO narrative remains firmly embedded

in the social psyche, evidenced by the continuing rise of products with GMO-free designation. Campaigns for GMO food labels to satisfy consumers' right to know were successful and the perceived need for this information now appears to be self-sustaining.

<https://www.tandfonline.com/doi/full/10.1080/21645698.2024.2318027>

Yuechen Bai Y., Liu X., Baldwin I.T. (2024): **Using Synthetic Biology to Understand the Function of Plant Specialized Metabolites**. Annual Review of Plant Biology 75: 1 |

<https://doi.org/10.1146/annurev-arplant-060223-013842>

Plant specialized metabolites (PSMs) are variably distributed across taxa, tissues, and ecological contexts; this variability has inspired many theories about PSM function, which to-date remain poorly tested because predictions have outpaced the available data. Advances in mass spectrometry-based metabolomics have enabled unbiased PSM profiling, and molecular biology techniques have produced PSM-free plants; the combination of these methods has accelerated our understanding of the complex ecological roles that PSMs play in plants. Synthetic biology techniques and workflows are producing high-value, structurally complex PSMs in quantities and purities sufficient for both medicinal and functional studies. These workflows enable the reengineering of PSM transport, externalization, structural diversity, and production in novel taxa, facilitating rigorous tests of long-standing theoretical predictions about why plants produce so many different PSMs in particular tissues and ecological contexts. Plants use their chemical prowess to solve ecological challenges, and synthetic biology workflows are accelerating our understanding of these evolved functions.

<https://www.annualreviews.org/doi/abs/10.1146/annurev-arplant-060223-013842>

Tachikawa M. and Matsuo M. (2024): **Global regulatory trends of genome editing technology in agriculture and food**. Breeding Science Preview | doi: 10.1270/jsbbs.23046

There is a need to introduce new regulations regarding genome editing technology and its application to agriculture and food. Regulations are different among countries and sometimes inconsistent. Here, we summarize the current regulations regarding the use of genome editing technology in agriculture and food in various countries around the world. We also discuss the main regulatory developments expected to occur in the future.

[https://www.jstage.jst.go.jp/article/jsbbs/advpub/0/advpub\\_23046/\\_pdf](https://www.jstage.jst.go.jp/article/jsbbs/advpub/0/advpub_23046/_pdf)

Guadarrama-Escobar, L.M., Hunt, J., Gurung, A., Zarco-Tejada, P.J., Shabala, S., Camino, C., Hernandez, P. and Pourkheirandish, M. (2024): **Back to the future for drought tolerance**.

New Phytol. <https://doi.org/10.1111/nph.19619>

Global agriculture faces increasing pressure to produce more food with fewer resources. Drought, exacerbated by climate change, is a major agricultural constraint costing the industry an estimated US\$80 billion per year in lost production. Wild relatives of domesticated crops, including wheat (*Triticum* spp.) and barley (*Hordeum vulgare* L.), are an underutilized source of drought tolerance genes. However, managing their undesirable characteristics, assessing drought responses, and selecting lines with heritable traits remains a significant challenge. Here, we propose a novel strategy of using multi-trait selection criteria based on high-throughput spectral images to facilitate the assessment and selection challenge. The importance of measuring plant capacity for sustained carbon fixation under drought stress is explored, and an image-based transpiration efficiency (ITE) index obtained via a combination of hyperspectral and thermal imaging, is proposed. Incorporating ITE along with other drought-related variables in selection criteria will allow the identification of accessions with diverse tolerance mechanisms. A comprehensive approach that merges high-throughput phenotyping and *de novo* domestication is proposed for developing drought-tolerant prebreeding material and providing breeders with access to gene pools containing unexplored drought tolerance mechanisms.

<https://nph.onlinelibrary.wiley.com/doi/full/10.1111/nph.19619>

Nor A'azizam, N.M., Chopra, S., Guleria, P. et al. (2024): **Harnessing the potential of mutation breeding, CRISPR genome editing, and beyond for sustainable agriculture**. Funct Integr Genomics 24, 44 (2024).

<https://doi.org/10.1007/s10142-024-01325-y>

By 2050, the global population is projected to exceed 9.5 billion, posing a formidable challenge to ensure food security worldwide. To address this pressing issue, mutation breeding in horticultural crops, utilizing physical or chemical methods, has emerged as a promising biotechnological strategy. However, the efficacy of these mutagens can be influenced by various factors, including biological and environmental variables, as well as targeted plant materials. This review highlights the global challenges related to food security and explores the potential of mutation breeding as an indispensable biotechnological tool in overcoming food insecurity. This review also covers the emergence of CRISPR-Cas9, a breakthrough technology offering precise genome editing for the development of high-yield, stress-tolerant crops. Together, mutation breeding and CRISPR can potentially address future food demands. This review focuses into these biotechnological advancements, emphasizing their combined potential to fortify global food security in the face of a booming population.

<https://link.springer.com/article/10.1007/s10142-024-01325-y>

Mishra A., Pandey V.P. (2024): **CRISPR/Cas system: A revolutionary tool for crop improvement**. Biotechnology Journal | <https://doi.org/10.1002/biot.202300298>

World's population is elevating at an alarming rate thus, the rising demands of producing crops with better adaptability to biotic and abiotic stresses, superior nutritional as well as morphological qualities, and generation

of high-yielding varieties have led to encourage the development of new plant breeding technologies. The availability and easy accessibility of genome sequences for a number of crop plants as well as the development of various genome editing technologies such as zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs) has opened up possibilities to develop new varieties of crop plants with superior desirable traits. However, these approaches have limitation of being more expensive as well as having complex steps and time-consuming. The CRISPR/Cas genome editing system has been intensively studied for allowing versatile target-specific modifications of crop genome that fruitfully aid in the generation of novel varieties. It is an advanced and promising technology with the potential to meet hunger needs and contribute to food production for the ever-growing human population. This review summarizes the usage of novel CRISPR/Cas genome editing tool for targeted crop improvement in stress resistance, yield, quality and nutritional traits in the desired crop plants.

<https://analyticalsciencejournals.onlinelibrary.wiley.com/doi/epdf/10.1002/biot.202300298>

Kishi-Kaboshi, M., Abe F., Kamiya Y., Kawaura K., Hisano H., Sato K. (2023): **Optimizing genome editing efficiency in wheat: Effects of heat treatments and different promoters for single guide RNA expression.** Plant Biotechnology 40 (3), 237-245 | DOI

<https://doi.org/10.5511/plantbiotechnology.23.0717a>

Genome editing is a promising method for simultaneously mutagenizing homoeologs in the three subgenomes of wheat (*Triticum aestivum* L.). However, the mutation rate via genome editing must be improved in order to analyze gene function and to quickly modify agronomic traits in wheat. Here, we examined the Cas9-induced mutation rates in wheat plants using two promoters for single guide RNA (sgRNA) expression and applying heat treatment during *Agrobacterium tumefaciens*-mediated transformation. Using the *TaU6* promoter instead of the *OsU6* promoter from rice (*Oryza sativa* L.) to drive sgRNA expression greatly improved the Cas9-induced mutation rate. Moreover, a heat treatment of 30°C for 1 day during tissue culture increased the Cas9-induced mutation rate and the variety of mutations obtained compared to tissue culture at the normal temperature (25°C). The same heat treatment did not affect the regeneration rates of transgenic plants but tended to increase the number of transgene integration sites in each transgenic plant. These results lay the foundation for improving the Cas9-induced mutation rate in wheat to enhance research on gene function and crop improvement.

[https://www.jstage.jst.go.jp/article/plantbiotechnology/40/3/40\\_23.0717a/\\_article](https://www.jstage.jst.go.jp/article/plantbiotechnology/40/3/40_23.0717a/_article)

Arndell, T., Chen, J., Sperschneider, J. et al. (2024): **Pooled effector library screening in protoplasts rapidly identifies novel Avr genes.** Nat. Plants | <https://doi.org/10.1038/s41477-024-01641-y>

Crop breeding for durable disease resistance is challenging due to the rapid evolution of pathogen virulence. While progress in resistance (*R*) gene cloning and stacking has accelerated in recent years<sup>1,2,3</sup>, the identification of corresponding avirulence (*Avr*) genes in many pathogens is hampered by the lack of high-throughput screening options. To address this technology gap, we developed a platform for pooled library screening in plant protoplasts to allow rapid identification of interacting *R*–*Avr* pairs. We validated this platform by isolating known and novel *Avr* genes from wheat stem rust (*Puccinia graminis* f. sp. *tritici*) after screening a designed library of putative effectors against individual *R* genes. Rapid *Avr* gene identification provides molecular tools to understand and track pathogen virulence evolution via genotype surveillance, which in turn will lead to optimized *R* gene stacking and deployment strategies. This platform should be broadly applicable to many crop pathogens and could potentially be adapted for screening genes involved in other protoplast-selectable traits.

<https://www.nature.com/articles/s41477-024-01641-y>

Czembor J.H., Czembor E., Krystek M., Pukacki J. (2023): **AgroGenome: Interactive Genomic-Based Web Server Developed Based on Data Collected for Accessions Stored in Polish Genebank.** Agriculture 13 (1), 193; <https://doi.org/10.3390/agriculture13010193>

New intensive farming systems have resulted in a narrowing of the genetic diversity used in breeding programs. Breeders are looking for new sources of variation of specific traits to make genetic progress in adaptation to changing environmental conditions. Genomics-based plant germplasm research seeks to apply the techniques of genomics to germplasm characterization. Using these new methods and obtained data, plant breeders can increase the rate of genetic gains in specific breeding programs. Due to the complexity of heterogeneous sources of information, it is necessary to collect large quantities of referenced data. Molecular platforms are becoming increasingly important for the development of strategic germplasm resources for more effective molecular breeding of new cultivars. Following this trend in plant breeding, the AgroGenome portal for precise breeding programs was developed based on data collected for accessions stored in the Polish Genebank. It combines passport data of genotypes, phenotypic characteristics and interactive GWAS analysis visualization on the Manhattan plots based on GWAS results and on JBrowse interface. The AgroGenome portal can be utilized by breeders or researchers to explore diversity among investigated genomes. It is especially important to identify markers for tracking specific traits and identify QTL. The AgroGenome portal facilitates the exploitation and use of plant genetic resources stored in the Polish Genebank.

<https://www.mdpi.com/2077-0472/13/1/193>

dos Santos-Donado, P.R., Donado-Pestana, C.M., Rondán-Sanabria, G.G. et al. (2024): **Two-dimensional gel and shotgun proteomics approaches for the comparative evaluation of genetically modified maize.** Food Measure | <https://doi.org/10.1007/s11694-024-02397-x>

In the safety risk assessment of genetically modified (GM) crops, it is imperative to evaluate potential unintended effects derived from genetic manipulation. Here, we analyzed the differential proteomic signatures and compositional equivalence of two GM insect- and herbicide-resistant maize cultivars (named here as GM1 and GM2), extensively cultivated and commercialized in Brazil, and their respective conventional counterparts (CON1 and CON2). Complementary 2-DE-based and bottom-up shotgun proteomic analysis were used. All cultivars presented similar chemical compositions between the GMs and CONs, with values expected for *Zea mays* species. A total of 22 and 21 differentially expressed proteins (DEPs) were identified in the 2-DE proteomic analysis for the GM1 vs. CON1 and GM2 vs. CON2 comparisons, respectively. In same order, 11 and 16 DEPs were identified in the bottom-up shotgun proteomic. DEPs were related to various biological processes including metabolism, energy, storage, defense, and cell stress. Vicilin-like embryo storage protein, tubulin, ADP-glucose pyrophosphorylase endosperm large subunit, globulin-1, and cytosolic 3-phosphoglycerate kinase, were consistently identified using both proteomic approaches. Of particular interest, vicilin-like embryo, identified as a natural allergen in maize, was down-regulated in the GM1 event compared to CON1. Our findings provide insights into potential unintended effects revealed through proteomic methodologies, utilizing both gel-based and gel-free techniques to identify alterations in protein abundance influenced by transgenic modification.

<https://link.springer.com/article/10.1007/s11694-024-02397-x>

Zhu X., Zhang J., Pan R., Zhang K., Dai H. (2024): **CRISPR/Cas12a-mediated entropy-driven electrochemical biosensor for detection of genetically modified maize Mon810**. *Analytica Chimica Acta* 1296, 342290 | <https://doi.org/10.1016/j.aca.2024.342290>

Genetically modified crops (GMOs) have led to significant, if not revolutionary, agricultural advances. The development of GMOs requires necessary regulations, which depend on the detection of GMOs. A sensitive and specific biosensor for the detection of transgenic crops is crucial to improve the detection efficiency of GMOs. Here, we developed a CRISPR/Cas12a-mediated entropy-driven electrochemiluminescence (ECL) biosensor for the sensitive and specific detection of MON810, the world's most widely used transgenic insect-resistant maize. We designed two crRNAs to activate CRISPR/Cas12a, allowing it to cut non-specific single strands, and we modified the DNA tetrahedron (DT) on the surface of the gold electrode to diminish non-specific adsorption. The entropy-driven chain displacement reaction with the target DNA takes place for amplification. After optimization, the biosensor has satisfactory accuracy and selectivity, with a linear range of ECL of 1–106 fM and a limit of detection (LOD) of 3.3 fM by the 3 $\sigma$  method. The biosensor does not require polymerase chain reaction (PCR) amplification or complex sample processing, which dramatically improves transgenic crop detection efficiency. This new biosensor achieves rapid, sensitive, and highly specific detection of transgenic crops, and has great potential for large-scale field detection of transgenic crops.

<https://www.sciencedirect.com/science/article/abs/pii/S0003267024000916?via%3Dihub>

Madsen C.K., Brearley C.A., Harholt J., Brinch-Pedersen H. (2024): **Optimized barley phytase gene expression by focused FIND-IT screening for mutations in cis-acting regulatory elements**

*Front. Plant Sci., Sec. Plant Breeding* 15 - 2024 | <https://doi.org/10.3389/fpls.2024.1372049>

**Introduction:** Induced modification of plant gene expression is of both fundamental and applied importance. Cis-acting regulatory elements (CREs) are major determinants of the spatiotemporal strength of gene expression. Yet, there are few examples where induced genetic variation in predetermined CREs has been exploited to improve or investigate crop plants.

**Methods:** The digital PCR based FIND-IT technology was applied to discover barley mutants with CRE variants in the promoter of the nutritional important barley grain phytase (*PAPhy\_a*) gene.

**Results and discussion:** Mutants with higher or lower gene expression and ultimately higher or lower mature grain phytase activity (MGPA), respectively, were discovered. Field trials and inositol phosphate profiling during germination showed that *PAPhy\_a* does not influence agronomic performance under the trial conditions but it does shorten the lag time of phosphate mobilization during germination. Higher endogenous MGPA is an improvement of grain quality for feed use as it improves the phosphate bioavailability for monogastric animals. Moreover, as the targeted CRE motifs of the *PAPhy\_a* promoter are shared with a range of seed expressed genes like key cereal and legume storage genes, the current results demonstrates a concept for modulating individual gene expression levels of a range of seed genes.

<https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2024.1372049/full>

This article is part of the Research Topic Mutational Breeding: From Induced Mutations to Site-Directed Mutagenesis [View all 4 articles](#)

## EFSA

In January/February 2024, EFSA published the [► results of the safety assessments of 16 food enzymes](#). Five food enzymes originate from GMMOs. Two food enzymes (transglutaminase, leucyl-aminopeptidase) were classified as "unsafe" because the safety margin between the exposure level and the NOAEL is too small.

In January/February 2024, EFSA received [► 14 new applications for the safety assessment](#) of food enzymes. 11 of these enzymes derive from GMMOs.

In den Monaten Januar/Februar 2024 hat die EFSA die [▶ Ergebnisse der Sicherheitsbewertungen von 16 Lebensmittelenzymen veröffentlicht](#). Fünf Lebensmittelenzyme stammen aus GMMO. Zwei Lebensmittelenzyme ( Transglutaminase, Leucyl-Aminopeptidase) wurden als "unsicher" eingestuft, da der Sicherheitsabstand zwischen der Expositions menge und dem NOAEL zu klein ist.

In den Monaten Januar/Februar 2024 sind [▶ 14 neue Anträge zur Sicherheitswertung](#) von Lebensmittelenzymen bei der EFSA eingegangen. 11 davon beziehen sich auf Enzyme aus GMMO.

EFSA CEP Panel (2024): Safety evaluation of the food enzyme bacillolysin from the non-genetically modified *Bacillus amyloliquefaciens* strain DP-Cyb74. *EFSA Journal*, 22(2), e8612.  
<https://doi.org/10.2903/j.efsa.2024.8612>  
<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2024.8612>

EFSA CEP Panel (2024): Safety evaluation of the food enzyme thermolysin from the non-genetically modified *Anoxybacillus caldiproteolyticus* strain AE-TP. *EFSA Journal*, 22(2), e8634.  
<https://doi.org/10.2903/j.efsa.2024.8634>  
<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2024.8634>

EFSA CEP Panel (2024): Safety evaluation of the food enzyme mucorpepsin from the non-genetically modified *Rhizomucor miehei* strain M19-21. *EFSA Journal*, 22(2), e8633.  
<https://doi.org/10.2903/j.efsa.2024.8633>  
<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2024.8633>

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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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