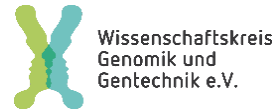


Sunday Evening News No 352

2023-11-13 – 2023-11-19

Compiled and edited by **BGF** Jany



WGG-VBIO - Offener Brief

an den Bundesminister für Ernährung und Landwirtschaft, Cem Özdemir, die Bundesministerin für Umwelt, Naturschutz, nukleare Sicherheit und Verbraucherschutz, Steffi Lemke und die Bundesministerin für Bildung und Forschung, Bettina Stark-Watzinger „**Innovative Technologien als Beitrag zu mehr Nachhaltigkeit: Für eine evidenzbasierte Reform des europäischen Gentechnikrechts**“

Appell an Bundesminister/-innen, sich für evidenzbasiertes europäisches Gentechnikrechts einzusetzen.

Der offene Brief sowie die Anlage der Mitunterzeichner /-innen sind [► hier einsehbar bzw. herunterladbar](#)

Der offene Brief wurde von 463 (+18) Wissenschaftlern /-innen und 8 (+2) Fachgesellschaften mitunterzeichnet und am 09.November 2023 an die Ministerien geschickt.

Sperrfrist: Montag, 20.11.2023, 8:00 Uhr.

Open letter to the Federal Minister of Food and Agriculture, Cem Özdemir, the Federal Minister for the Environment, Nature Conservation, Nuclear Safety and Consumer Protection, Steffi Lemke, and the Federal Minister of Education and Research, Bettina Stark-Watzinger

“**Innovative technologies as a contribution to greater sustainability: For an evidence-based reform of the European GMO legislation**”

Appeal to federal ministers to support evidence-based European genetic engineering law.

The open letter was co-signed by 463 (+18) scientists and 8 (+2) professional societies and sent to the ministries on November 9, 2023.

[► The open letter and the attachment of the co-signatories can be viewed or downloaded here.](#)

Closing date: Monday, 20.11.2023, 8:00 am.

Meetings – Conferences / Tagungen – Konferenzen

Lebensmittelverband: Tagung "Grüner Deal und Vom-Hof-auf-den-Tisch-Strategie: Zwischenbilanz und Ausblick"

13. Dezember 2023 Haus der Land- und Ernährungswirtschaft, Claire-Waldoff-Straße 7
10117 Berlin

Bitte melden Sie sich bis Freitag, 8. Dezember 2023 unter nachfolgendem Link an:

<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

DFG: **Appell an Bundesregierung zur Zustimmung zu EU-Regulierungsvorschlag für neue Züchtungstechniken bei Pflanzen**

https://www.dfg.de/service/presse/pressemitteilungen/2023/pressemitteilung_nr_48/index.html

Rembold M. „**Es ist ein mutiger Schritt der Kommission**“

<https://www.laborjournal.de/editorials/2875.php>

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

<https://phys.org/news/2023-11-evidence-led-gm-crop-uk-tackling.html>

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

Patents and New GMOs: Don't risk the future of our seeds!

<https://www.eurovia.org/wp-content/uploads/2023/11/2023-11-16-NGT-Patents-on-NGT-Statement-EN.pdf>

Global 2000: **Risiko für Zukunft unseres Saatguts: Zivilgesellschaft schlägt Alarm bei EU-Agrarminister:innen**

https://www.ots.at/presseaussendung/OTS_20231117_OTS0011/risiko-fuer-zukunft-unseres-saatguts-zivilgesellschaft-schlaegt-alarm-bei-eu-agrarministerinnen

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 46

Publications – Publikationen

Caccialupi G. (2023): **The Triticeae CBF Gene Cluster—To Frost Resistance and Beyond** Cells, 12 (22), 2606; | <https://doi.org/10.3390/cells12222606>

The pivotal role of CBF/DREB1 transcriptional factors in Triticeae crops involved in the abiotic stress response has been highlighted. The CBFs represent an important hub in the ICE-CBF-COR pathway, which is one of the most relevant mechanisms capable of activating the adaptive response to cold and drought in wheat, barley, and rye. Understanding the intricate mechanisms and regulation of the cluster of CBF genes harbored by the homoeologous chromosome group 5 entails significant potential for the genetic improvement of small grain cereals. Triticeae crops seem to share common mechanisms characterized, however, by some peculiar aspects of the response to stress, highlighting a combined landscape of single-nucleotide variants and copy number variation involving CBF members of subgroup IV. Moreover, while chromosome 5 ploidy appears to confer species-specific levels of resistance, an important involvement of the ICE factor might explain the greater tolerance of rye. By unraveling the genetic basis of abiotic stress tolerance, researchers can develop resilient varieties better equipped to withstand extreme environmental conditions. Hence, advancing our knowledge of CBFs and their interactions represents a promising avenue for improving crop resilience and food security.

<https://www.mdpi.com/2073-4409/12/22/2606>

Movahedi A., Dargiri S.A., Li H., Zhuge, Q., Sun W. (2023): **CRISPR Variants for Gene Editing in Plants: Biosafety Risks and Future Directions**. Int. J. Mol. Sci. 24 (22), 16241; |

<https://doi.org/10.3390/ijms242216241>

The CRISPR genome editing technology is a crucial tool for enabling revolutionary advancements in plant genetic improvement. This review shows the latest developments in CRISPR/Cas9 genome editing system variants, discussing their benefits and limitations for plant improvement. While this technology presents immense opportunities for plant breeding, it also raises serious biosafety concerns that require careful consideration, including potential off-target effects and the unintended transfer of modified genes to other organisms. This paper highlights strategies to mitigate biosafety risks and explores innovative plant gene editing detection methods. Our review investigates the international biosafety guidelines for gene-edited crops, analyzing their broad implications for agricultural and biotechnology research and advancement. We hope to provide illuminating and refined perspectives for industry practitioners and policymakers by evaluating CRISPR genome enhancement in plants.

<https://www.mdpi.com/1422-0067/24/22/16241>

Sukko, N., Kalapanulak, S. & Saithong, T. (2023): **Trehalose metabolism coordinates transcriptional regulatory control and metabolic requirements to trigger the onset of cassava storage root initiation**. Sci Rep 13, 19973 <https://doi.org/10.1038/s41598-023-47095-8>

Cassava storage roots (SR) are an important source of food energy and raw material for a wide range of applications. Understanding SR initiation and the associated regulation is critical to boosting tuber yield in cassava. Decades of transcriptome studies have identified key regulators relevant to SR formation, transcriptional regulation and sugar metabolism. However, there remain uncertainties over the roles of the regulators in modulating the onset of SR development owing to the limitation of the widely applied differential gene expression analysis. Here, we aimed to investigate the regulation underlying the transition from fibrous root (FR) to SR based on Dynamic Network Biomarker (DNB) analysis. Gene expression analysis during cassava root initiation showed the transition period to SR happened in FR during 8 weeks after planting (FR8). Ninety-nine DNB genes associated with SR initiation and development were identified. Interestingly, the role of trehalose metabolism, especially trehalase1 (*TRE1*), in modulating metabolites abundance and coordinating regulatory signaling and carbon substrate availability via the connection of transcriptional regulation and sugar metabolism was highlighted. The results agree with the associated DNB characters of *TRE1* reported in other

transcriptome studies of cassava SR initiation and *Attre1* loss of function in literature. The findings help fill the knowledge gap regarding the regulation underlying cassava SR initiation.
<https://www.nature.com/articles/s41598-023-47095-8>

Polturak, G., Misra, R.C., El-Demerdash, A. et al. (2023): **Discovery of isoflavone phytoalexins in wheat reveals an alternative route to isoflavonoid biosynthesis.** *Nat Commun* 14, 6977 | <https://doi.org/10.1038/s41467-023-42464-3>

Isoflavones are a group of phenolic compounds mostly restricted to plants of the legume family, where they mediate important interactions with plant-associated microbes, including in defense from pathogens and in nodulation. Their well-studied health promoting attributes have made them a prime target for metabolic engineering, both for bioproduction of isoflavones as high-value molecules, and in biofortification of food crops. A key gene in their biosynthesis, isoflavone synthase, was identified in legumes over two decades ago, but little is known about formation of isoflavones outside of this family. Here we identify a specialized wheat-specific isoflavone synthase, TaCYP71F53, which catalyzes a different reaction from the leguminous isoflavone synthases, thus revealing an alternative path to isoflavonoid biosynthesis and providing a non-transgenic route for engineering isoflavone production in wheat. TaCYP71F53 forms part of a biosynthetic gene cluster that produces a naringenin-derived *O*-methylated isoflavone, 5-hydroxy-2',4',7-trimethoxyisoflavone, triticein. Pathogen-induced production and in vitro antimicrobial activity of triticein suggest a defense-related role for this molecule in wheat. Genomic and metabolic analyses of wheat ancestral grasses further show that the triticein gene cluster was introduced into domesticated emmer wheat through natural hybridization ~9000 years ago, and encodes a pathogen-responsive metabolic pathway that is conserved in modern bread wheat varieties.

<https://www.nature.com/articles/s41467-023-42464-3>

Park S., Lee H., Song J., Lim C.J. et al (2023): **Gene editing of authentic *Brassica rapa* flavonol synthase 1 generates dihydroflavonol-accumulating Chinese cabbage.** *Horticulture Research*, uhad239, | <https://doi.org/10.1093/hr/uhad239>

Flavonols are the major class of flavonoids of green Chinese cabbage (*Brassica rapa* subsp. *pekinensis*). The *B. rapa* genome harbors seven flavonol synthase genes (*BrFLSs*), but they have not been functionally characterized. Here, transcriptome analysis showed four *BrFLSs* mainly expressed in Chinese cabbage. Among them, only *BrFLS1* showed major FLS activity and additional flavanone 3 β -hydroxylase (F3H) activity, while *BrFLS2* and *BrFLS3.1* exhibited only marginal F3H activities. We generated *BrFLS1*-knockout (*BrFLS1*-KO) Chinese cabbages using CRISPR/Cas9-mediated genome editing and obtained transgene-free homozygous plants without off-target mutation in the T₁ generation, which were further advanced to the T₂ generation showing normal phenotype. UPLC-ESI-QTOF-MS analysis revealed that flavonol glycosides were dramatically decreased in the T₂ plants, while dihydroflavonol glycosides accumulated concomitantly at corresponding levels. Quantitative PCR analysis revealed that the early steps of phenylpropanoid and flavonoid biosynthetic pathway were up-regulated in the *BrFLS1*-KO plants. In accordance, total phenolic contents were slightly enhanced in the *BrFLS1*-KO plants, which suggests a negative role of flavonols in phenylpropanoid and flavonoid biosynthesis in Chinese cabbage. Phenotypic surveys revealed that the *brfls1* Chinese cabbages showed normal head formation and reproductive phenotypes, but subtle morphological changes in their heads were observed. In addition, their seedlings were susceptible to osmotic stress compared to the controls, suggesting that flavonols play a positive role for osmotic stress tolerance in *B. rapa*. In this study, we showed that CRISPR/Cas9-mediated *BrFLS1*-KO successfully generated a valuable breeding resource of Chinese cabbage with distinctive metabolic traits and that CRISPR/Cas9 can be efficiently applied in functional Chinese cabbage breeding.

<https://academic.oup.com/hr/advance-article/doi/10.1093/hr/uhad239/7420484>

Dwivedi N., Yamamoto S. Zhao Y., Hou G. et al. (2023): **Simultaneous suppression of lignin, tricetin and wall-bound phenolic biosynthesis via the expression of monolignol 4-*O*-methyltransferases in rice.** *Plant Biotechnology Journal* | <https://doi.org/10.1111/pbi.14186>

Grass lignocelluloses feature complex compositions and structures. In addition to the presence of conventional lignin units from monolignols, acylated monolignols and flavonoid tricetin also incorporate into lignin polymer; moreover, hydroxycinnamates, particularly ferulate, cross-link arabinoxylan chains with each other and/or with lignin polymers. These structural complexities make grass lignocellulosics difficult to optimize for effective agro-industrial applications. In the present study, we assess the applications of two engineered monolignol 4-*O*-methyltransferases (MOMTs) in modifying rice lignocellulosic properties. Two MOMTs confer regiospecific *para*-methylation of monolignols but with different catalytic preferences. The expression of MOMTs in rice resulted in differential but drastic suppression of lignin deposition, showing more than 50% decrease in guaiacyl lignin and up to a 90% reduction in syringyl lignin in transgenic lines. Moreover, the levels of arabinoxylan-bound ferulate were reduced by up to 50%, and the levels of tricetin in lignin fraction were also substantially reduced. Concomitantly, up to 11 μ mol/g of the methanol-extractable 4-*O*-methylated ferulic acid and 5–7 μ mol/g 4-*O*-methylated sinapic acid were accumulated in MOMT transgenic lines. Both MOMTs in vitro displayed discernible substrate promiscuity towards a range of phenolics in addition to the dominant substrate monolignols, which partially explains their broad effects on grass phenolic biosynthesis. The cell wall structural and compositional changes resulted in up to 30% increase in saccharification yield of the de-starched rice straw biomass after diluted acid-pretreatment. These results demonstrate an effective strategy to tailor complex grass cell walls to generate improved cellulosic feedstocks for the fermentable sugar-based production of biofuel and bio-chemicals.

<https://onlinelibrary.wiley.com/doi/10.1111/pbi.14186>

Huey, S.L., Konieczynski, E.M., Mehta, N.H. et al. (2023): **A systematic review of the impacts of post-harvest handling on provitamin A, iron and zinc retention in seven biofortified crops.** Nat Food | <https://doi.org/10.1038/s43016-023-00874-y>

Post-harvest handling can affect micronutrient retention in biofortified crops through to the point of consumption. Here we conduct a systematic review identifying 67 articles examining the retention of micronutrients in conventionally bred biofortified maize, orange sweet potato, cassava, pearl millet, rice, beans and wheat. Provitamin A crops maintain high amounts compared with non-biofortified counterparts. Iron and zinc crops have more variability in micronutrient retention dependent on processing method; for maximum iron and zinc content, whole grain product consumption such as whole wheat flour or only slightly milled brown rice is beneficial. We offer preliminary suggestions for households, regulatory bodies and programme implementers to increase consumer awareness on best practices for preparing crops to maximize micronutrient content, while highlighting gaps in the literature. Our online, interactive Micronutrient Retention Dashboard (<https://www.cpnh.cornell.edu/mn-retention-db>) offers an at-a-glance view of the compiled minimum and maximum retention found, organized by processing method. <https://www.nature.com/articles/s43016-023-00874-y#>

Nayeri S., Dehghanian Z., Lajayer B.A., homson A. et al (2023): **CRISPR/Cas9-Mediated genetically edited ornamental and aromatic plants: A promising technology in phytoremediation of heavy metals.** Journal of Cleaner Production 428,139512 | <https://doi.org/10.1016/j.jclepro.2023.139512>

Phytoremediation, as a green, sustainable, and cost-effective plant-based remediation technology has garnered great attention for remediating heavy metals (HMs) from polluted soil and water resources. However, HM type and concentration, phytoremediation method, climatic conditions, type of plant species, potential of biomass production, level of plant sensitivity, and signaling pathways efficiency are all crucial factors affecting plant's phytoremediation performance. Ornamental, medicinal, and aromatic plants with medicinal, pharmaceutical, cosmetics, and decorative uses are promising species for the phytoremediation of HMs from soil and water due to their fast growth and high biomass production. Furthermore, new genetic technologies such as, the clustered regularly interspaced short palindromic repeats – CRISPR associated protein 9 (CRISPR/Cas9) gene/genome editing system, may become a tool that provides sustainable phytoremediation by targeted editing of genes of interest to improve the phytoremediation capacity of the selected ornamental plants (OPs) without raising genetically modified organisms (GMO) concerns. This review summarizes the current state of knowledge associated with protection mechanisms and molecular aspects of plant tolerance to HMs by ornamental, medicinal and aromatic plants. The review also focuses on the use of genetically engineered ornamental and medicinal aromatic plants applying recent advances in CRISPR/Cas9 genome editing to enhance phytoremediation properties. Risk assessments and regulatory approaches associated with environmental protection, livestock, and human health for transgenic plants released into the environment are also discussed. This work elicits interdisciplinary aspects and an understanding of the long-term management of HMs using ornamental, medicinal, and aromatic plants in an innovative way that no prior study has considered.

<https://www.sciencedirect.com/science/article/abs/pii/S0959652623036703>

Harrington S. A. Franceschetti M., Balk J. (2023): **Genetic basis of the historical iron-accumulating *dgl* and *brz* mutants in pea.** The Plant Journal | <https://doi.org/10.1111/tpj.16514>

The *Pisum sativum* (pea) mutants *degenerate leaves (dgl)* and *bronze (brz)* accumulate large amounts of iron in leaves. First described several decades ago, the two mutants have provided important insights into iron homeostasis in plants but the underlying mutations have remained unknown. Using exome sequencing we identified an in-frame deletion associated with *dgl* in a *BRUTUS* homolog. The deletion is absent from wild type and the original parent line. *BRUTUS* belongs to a small family of E3 ubiquitin ligases acting as negative regulators of iron uptake in plants. The *brz* mutation was previously mapped to chromosome 4, and superimposing this region to the pea genome sequence uncovered a mutation in *OPT3*, encoding an oligopeptide transporter with a plant-specific role in metal transport. The causal nature of the mutations was confirmed by additional genetic analyses. Identification of the mutated genes rationalizes many of the previously described phenotypes and provides new insights into shoot-to-root signaling of iron deficiency. Furthermore, the non-lethal mutations in these essential genes suggest new strategies for biofortification of crops with iron.

<https://onlinelibrary.wiley.com/doi/10.1111/tpj.16514>

Tang, H., Lin, S., Deng, J. et al. (2023): **Engineering yeast for the de novo synthesis of jasmonates.** Nat. Synth | <https://doi.org/10.1038/s44160-023-00429-w>

Jasmonates are a class of plant hormones with many agricultural applications and potential medicinal properties. However, the low content of jasmonates in plants and environmental issues with their production make their supply challenging. In the present study, we report the de novo microbial biosynthesis of jasmonic acid and its derivatives, methyl jasmonate and jasmonoyl isoleucine, from glucose using an engineered baker's yeast. The study uses enzymes located in the endoplasmic reticulum and cytosol to generate the intermediates α -linolenic acid and *cis*-12-oxophytodienoic acid. Our final engineered strain, which integrates 15 heterologous genes from diverse plants and fungi and had 3 of its native genes deleted, produces jasmonic acid at titres of 19.0 mg l⁻¹ in flask cultures through in vitro supplementation of α -linolenic acid. In addition to the well-known

natural structures (-)-jasmonic acid and (+)-*epi*-jasmonic acid, the engineered yeast also synthesized the previously unobserved unnatural structures (+)-jasmonic acid and (-)-*epi*-jasmonic acid. These results demonstrate that yeast is a scalable and sustainable platform to produce both naturally occurring jasmonates and those structures not found naturally in plants.

<https://www.nature.com/articles/s44160-023-00429-w>

Capovilla, G., Castro, K.G., Collani, S. et al. (2023): **Chitin degradation by *Synechococcus* WH7803**. Sci Rep 13, 19944 | <https://doi.org/10.1038/s41598-023-47332-0>

Chitin is an abundant, carbon-rich polymer in the marine environment. Chitinase activity has been detected in spent media of *Synechococcus* WH7803 cultures—yet it was unclear which specific enzymes were involved. Here we delivered a CRISPR tool into the cells via electroporation to generate loss-of-function mutants of putative candidates and identified ChiA as the enzyme required for the activity detected in the wild type.

<https://www.nature.com/articles/s41598-023-47332-0>

EFSA

CEP Panel (2023): Safety evaluation of the food enzyme bacillolysin from the non-genetically modified *Bacillus amyloliquefaciens* strain HPN 131. EFSA Journal, 21(11), e8390.

<https://doi.org/10.2903/j.efsa.2023.8390>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8390>

CEP Panel (2023): Safety evaluation of the food enzyme catalase from the non-genetically modified *Aspergillus tubingensis* strain AE-CN. EFSA Journal, 21(11), e8398.

<https://doi.org/10.2903/j.efsa.2023.8398>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8398>

CEP Panel (2023): Safety evaluation of the food enzyme α -l-rhamnosidase from the non-genetically modified *Penicillium adamezii* strain AE-HP. EFSA Journal, 21, 1–13.

<https://doi.org/10.2903/j.efsa.2023.8395>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8395>

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.

Prof. Dr. Klaus-Dieter Jany
Nelkenstrasse 36
D-76351 Linkenheim-Hochstetten
jany@biotech-gm-food.com

Wissenschaftskreis Genomik und Gentechnik
1.Vorsitzender: Prof. Dr. Kl.-D. Jany

jany@wgg-ev.de