

Sunday Evening News No 350

2023-10-30 – 2023-11-05

Compiled and edited by **BGF** Jany



Meetings – Conferences / Tagungen - Konferenzen

Online-Seminar der International Union of Biological Sciences (IUBS) in Zusammenarbeit mit dem VBIO am Donnerstag, den 23. November 2023 von 15.00 – 17.00 Uh

“How will plants adapt to a high CO2 world?”

Prof. Christine H. Foyer, College of Life and Environmental Sciences - University of Birmingham

Bei Interesse registrieren Sie sich bitte für das kostenfreie Online-Seminar:

https://us06web.zoom.us/webinar/register/WN_L3fetlo0TsecgqO3TYgY-g

► **acatech Themenkonferenz: "Food Systems" - Der Weg zu einem nachhaltigen, zukunftsfähigen Ernährungssystem**

80333 München, Karolinenplatz 3 Amerikahaus

31. Januar 2024, 11:00 bis 16:00 Uhr

On **9 November 2023**, we will celebrate **Prof. Marc Van Montagu's 90th birthday**.

To celebrate his dedication and commitment to science and his role in the scientific landscape of Ghent and far beyond, we will organize a **mini-symposium** at **De Oude Vismijn, Ghent**. We will host a few eminent speakers talking about science, its role in society and especially its potential to support a sustainable development of less privileged regions of our planet.

Press Releases -Media / Presse- und Medienberichte

Grünes Netzwerk Evidenzbasierte Politik: **Europas Gentechnikregulierung im Wandel: Was bedeuten eigentlich Wahlfreiheit, Transparenz und Vorsorgeprinzip?**

<https://evidenzbasierte-politik.de/2023/10/30/europas-gentechnikregulierung-im-wandel-was-bedeuten-eigentlich-wahlfreiheit-transparenz-und-vorsorgeprinzip/>

FoodDrink Europe: **Position Paper: New Genomic Techniques**

https://www.fooddrinkeurope.eu/wp-content/uploads/2023/11/231102-FoodDrinkEurope-position-New-Genomic-Techniques_v2.pdf

General Secretariat of the Council: 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 - **European Economic and Social Committee's Opinion**

<https://data.consilium.europa.eu/doc/document/ST-14926-2023-INIT/EN/pdf>

EU Commission proposal for deregulation of new GMOs, the implications for consumers, farmers, and breeders, and why the proposal is scientifically unjustifiable.

Combined presentation by Blanche Magarinos-Rey, Claire Robinson, and Prof Michael Antoniou at the Let's Liberate Diversity! Conference, Dublin 27 October 2023

<https://gmwatch.org/en/20312-eu-commission-proposal-for-deregulation-of-new-gmos>

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

Ledford, H. (2023): **Is CRISPR safe? Genome editing gets its first FDA scrutiny**

Advisers to the US regulatory agency will examine the safety profile of a CRISPR-based treatment for sickle-cell disease.

<https://www.nature.com/articles/d41586-023-03317-7>

Bakhshandeh, S. (2023): **Genome-edited chickens**. Nat Rev Bioeng (2023).

<https://doi.org/10.1038/s44222-023-00136-3>

Yıldırım K., Miladinović D., Sweet J., Akin M., Galović V., Kavas M., Zlatković M. and de Andrade E (2023): **Genome editing for healthy crops: traits, tools and impacts**. *Front. Plant Sci.* 14:1231013. doi: 10.3389/fpls.2023.1231013

Crop cultivars in commercial use have often been selected because they show high levels of resistance to pathogens. However, widespread cultivation of these crops for many years in the environments favorable to a pathogen requires durable forms of resistance to maintain “healthy crops”. Breeding of new varieties tolerant/resistant to biotic stresses by incorporating genetic components related to durable resistance, developing new breeding methods and new active molecules, and improving the Integrated Pest Management strategies have been of great value, but their effectiveness is being challenged by the newly emerging diseases and the rapid change of pathogens due to climatic changes. Genome editing has provided new tools and methods to characterize defense-related genes in crops and improve crop resilience to disease pathogens providing improved food security and future sustainable agricultural systems. In this review, we discuss the principal traits, tools and impacts of utilizing genome editing techniques for achieving of durable resilience and a “healthy plants” concept.

<https://www.frontiersin.org/articles/10.3389/fpls.2023.1231013/full>

Matinvafa, M.A., Makani, S., Parsasharif, N. et al. (2023): **CRISPR-Cas technology secures sustainability through its applications: a review in green biotechnology**. *3 Biotech* 13, 383 (2023). <https://doi.org/10.1007/s13205-023-03786-7>

The CRISPR-Cas system's applications in biotechnology offer a promising avenue for addressing pressing global challenges, such as climate change, environmental pollution, the energy crisis, and the food crisis, thereby advancing sustainability. The ever-growing demand for food due to the projected population of around 9.6 billion by 2050 requires innovation in agriculture. CRISPR-Cas technology emerges as a powerful solution, enhancing crop varieties, optimizing yields, and improving resilience to stressors. It offers multiple gene editing, base editing, and prime editing, surpassing conventional methods. CRISPR-Cas introduces disease and herbicide resistance, high-yielding, drought-tolerant, and water-efficient crops to address rising water utilization and to improve the efficiency of agricultural practices which promise food sustainability and revolutionize agriculture for the benefit of future generations. The application of CRISPR-Cas technology extends beyond agriculture to address environmental challenges. With the adverse impacts of climate change and pollution endangering ecosystems, there is a growing need for sustainable solutions. The technology's potential in carbon capture and reduction through bio-sequestration is a pivotal strategy for combating climate change. Genomic advancements allow for the development of genetically modified organisms, optimizing biofuel and biomaterial production, and contributing to a renewable and sustainable energy future. This study reviews the multifaceted applications of CRISPR-Cas technology in the agricultural and environmental fields and emphasizes its potential to secure a sustainable future.

<https://link.springer.com/article/10.1007/s13205-023-03786-7>

Tsakirpaloglou N., Septiningsih E.M., Michael J. Thomson M. J. (2023): **Guidelines for Performing CRISPR/Cas9 Genome Editing for Gene Validation and Trait Improvement in Crops**. *Plants* 12 (20), 3564; <https://doi.org/10.3390/plants12203564>

With the rapid advances in plant genome editing techniques over the past 10 years, more efficient and powerful crop genome editing applications are now possible. Candidate genes for key traits can be validated using CRISPR/Cas9-based knockouts and through the up- and down-regulation of gene expression. Likewise, new trait improvement approaches can take advantage of targeted editing to improve stress tolerance, disease resistance, and nutritional traits. However, several key steps in the process can prove tricky for researchers who might be new to plant genome editing. Here, we present step-by-step guidelines and best practices for a crop genome editing pipeline that should help to improve the rate of success. Important factors in the process include proper target sequence analysis and single guide RNA (sgRNA) design, sequencing of the target site in the genotypes of interest, performing an in vitro CRISPR/Cas9 ribonucleoprotein (RNP) assay to validate the designed sgRNAs, preparing the transformation constructs, considering a protoplast editing step as further validation, and, finally, stable plant transformation and mutation detection by Sanger and/or next-generation sequencing. With these detailed guidelines, a new user should be able to quickly set up a genome editing pipeline in their crop of interest and start making progress with the different CRISPR/Cas-based editing variants for gene validation and trait improvement purposes.

<https://www.mdpi.com/2223-7747/12/20/3564>

Havlickova L., He Z., Berger M., Wang L. et al. (2023): **Genomics of predictive radiation mutagenesis in oilseed rape: modifying seed oil composition**. *Plant Biotechnology Journal* | <https://doi.org/10.1111/pbi.14220>

Rapeseed is a crop of global importance but there is a need to broaden the genetic diversity available to address breeding objectives. Radiation mutagenesis, supported by genomics, has the potential to supersede genome editing for both gene knockout and copy number increase, but detailed knowledge of the molecular outcomes of radiation treatment is lacking. To address this, we produced a genome re-sequenced panel of 1133 M₂ generation rapeseed plants and analysed large-scale deletions, single nucleotide variants and small insertion–deletion variants affecting gene open reading frames. We show that high radiation doses (2000 Gy) are tolerated, gamma radiation and fast neutron radiation have similar impacts and that segments deleted from the genomes of some plants are inherited as additional copies by their siblings, enabling gene dosage decrease. Of relevance for species with larger genomes, we showed that these large-scale impacts can also be detected

using transcriptome re-sequencing. To test the utility of the approach for predictive alteration of oil fatty acid composition, we produced lines with both decreased and increased copy numbers of *Bna.FAE1* and confirmed the anticipated impacts on erucic acid content. We detected and tested a 21-base deletion expected to abolish function of *Bna.FAD2.A5*, for which we confirmed the predicted reduction in seed oil polyunsaturated fatty acid content. Our improved understanding of the molecular effects of radiation mutagenesis will underpin genomics-led approaches to more efficient introduction of novel genetic variation into the breeding of this crop and provides an exemplar for the predictive improvement of other crops.

<https://onlinelibrary.wiley.com/doi/10.1111/pbi.14220>

Brooks C.J., Atamian H.S., Harmer S.L. (2023): **Multiple light signaling pathways control solar tracking in sunflowers.** *PLoS Biol* 21(10): e3002344 |

<https://doi.org/10.1371/journal.pbio.3002344>

Sunflowers are famous for their ability to track the sun throughout the day and then reorient at night to face east the following morning. This occurs by differential growth patterns, with the east sides of stems growing more during the day and the west sides of stems growing more at night. This process, termed heliotropism, is generally believed to be a specialized form of phototropism; however, the underlying mechanism is unknown. To better understand heliotropism, we compared gene expression patterns in plants undergoing phototropism in a controlled environment and in plants initiating and maintaining heliotropic growth in the field. We found the expected transcriptome signatures of phototropin-mediated phototropism in sunflower stems bending towards monochromatic blue light. Surprisingly, the expression patterns of these phototropism-regulated genes are quite different in heliotropic plants. Most genes rapidly induced during phototropism display only minor differences in expression across solar tracking stems. However, some genes that are both rapidly induced during phototropism and are implicated in growth responses to foliar shade are rapidly induced on the west sides of stems at the onset of heliotropism, suggesting a possible role for red light photoreceptors in solar tracking. To test the involvement of different photoreceptor signaling pathways in heliotropism, we modulated the light environment of plants initiating solar tracking. We found that depletion of either red and far-red light or blue light did not hinder the initiation or maintenance of heliotropism in the field. Together, our results suggest that the transcriptional regulation of heliotropism is distinct from phototropin-mediated phototropism and likely involves inputs from multiple light signaling pathways.

<https://journals.plos.org/plosbiology/article?id=10.1371/journal.pbio.3002344>

Fang, X., Mo, J., Zhou, H. et al. (2023): **Comparative transcriptome analysis of gene responses of salt-tolerant and salt-sensitive rice cultivars to salt stress.** *Sci Rep* 13, 19065 | <https://doi.org/10.1038/s41598-023-46389-1>

Salt stress is one unfavorable factor of global climate change that adversely affects rice plant growth and yield. To identify novel salt-tolerant genes and new varieties of salt-tolerant rice, a better understanding of the molecular regulation mechanism of salt tolerance in rice is needed. In this study we used transcriptome analyses to examine changes in gene expression of salt-tolerant and salt-sensitive rice plants. The salt-tolerant cultivar HH11 and salt-sensitive cultivar IR29 were treated with 200 mM NaCl solution for 0 h, 6 h, 24 h and 48 h at the three leaf stage. Physiological parameters and transcriptome were measured and analyzed after each treatment. Activity of SOD and POD, as well as the MDA and protein content of the two rice cultivars generally increased with increasing time of exposure to NaCl. Meanwhile, the APX activity first increased, then decreased in both cultivars, with maximum values seen at 6 h for IR29 and at 24 h for HH11. The GR and GPX activity of HH11 were stronger than that of IR29 in response to salt stress. The H₂O₂ content first increased at 0–6 h, then decreased at 6–24 h, and then increased again at 24–48 h under salt stress. Compared with IR29, SOD, POD and APX activity of HH11 was more sluggish in response to salt stress, reaching the maximum at 24 h or 48 h. The MDA, H₂O₂ and proline content of HH11 was lower than that of IR29 under salt stress. Relative to untreated HH11 plants (0 h) and those exposed to salt for 6 h, 24 h, and 48 h (H0-H6, H0-H24 and H0-H48), 7462, 6363 and 6636, differentially expressed genes (DEGs), respectively, were identified. For IR29, the respective total DEGs were 7566, 6075 and 6136. GO and KEGG enrichment analysis showed that metabolic pathways related to antioxidative responses and osmotic balance played vital roles in salt stress tolerance. Sucrose and starch metabolism, in addition to flavonoid biosynthesis and glutathione metabolism, showed positive responses to salt stress. Expression of two *SPS* genes (*LOC_Os01g69030* and *LOC_Os08g20660*) and two *GST* genes (*LOC_Os06g12290* and *LOC_Os10g38740*) was up-regulated in both HH11 and IR29, whereas expression of *LOC_Os09g12660*, a glucose-1-phosphate adenylyltransferase gene, and two *SS* genes (*LOC_Os04g17650* and *LOC_Os04g24430*) was up-regulated differential expression in HH11. The results showed that HH11 had more favorable adjustment in antioxidant and osmotic activity than IR29 upon exposure to salt stress, and highlighted candidate genes that could play roles in the function and regulation mechanism of salt tolerance in rice.

<https://www.nature.com/articles/s41598-023-46389-1>

Yow, A.G., Laosuntisuk, K., Young, R. et al. (2023): **Comparative transcriptome analysis reveals candidate genes for cold stress response and early flowering in pineapple.** *Sci Rep* 13, 18890 (2023) | <https://doi.org/10.1038/s41598-023-45722-y>

Pineapple originates from tropical regions in South America and is therefore significantly impacted by cold stress. Periodic cold events in the equatorial regions where pineapple is grown may induce early flowering, also known as precocious flowering, resulting in monetary losses due to small fruit size and the need to make multiple passes for harvesting a single field. Currently, pineapple is one of the most important tropical fruits in the world in terms of consumption, and production losses caused by weather can have major impacts on worldwide exportation potential and economics. To further our understanding of and identify mechanisms for

low-temperature tolerance in pineapple, and to identify the relationship between low-temperature stress and flowering time, we report here a transcriptomic analysis of two pineapple genotypes in response to low-temperature stress. Using meristem tissue collected from precocious flowering-susceptible MD2 and precocious flowering-tolerant Dole-17, we performed pairwise comparisons and weighted gene co-expression network analysis (WGCNA) to identify cold stress, genotype, and floral organ development-specific modules. Dole-17 had a greater increase in expression of genes that confer cold tolerance. The results suggested that low temperature stress in Dole-17 plants induces transcriptional changes to adapt and maintain homeostasis. Comparative transcriptomic analysis revealed differences in cuticular wax biosynthesis, carbohydrate accumulation, and vernalization-related gene expression between genotypes. Cold stress induced changes in ethylene and abscisic acid-mediated pathways differentially between genotypes, suggesting that MD2 may be more susceptible to hormone-mediated early flowering. The differentially expressed genes and module hub genes identified in this study are potential candidates for engineering cold tolerance in pineapple to develop new varieties capable of maintaining normal reproduction cycles under cold stress. In addition, a total of 461 core genes involved in the development of reproductive tissues in pineapple were also identified in this study. This research provides an important genomic resource for understanding molecular networks underlying cold stress response and how cold stress affects flowering time in pineapple.

<https://www.nature.com/articles/s41598-023-45722-y>

Han, B., Zhang, L., Geng, L. et al. (2023): **Greater wax moth control in apiaries can be improved by combining *Bacillus thuringiensis* and entrapments.** *Nat Commun* **14**, 7073 (2023). <https://doi.org/10.1038/s41467-023-42946-4>

The greater wax moth (GWM), *Galleria mellonella* (Lepidoptera: Pyralidae), is a major bee pest that causes significant damage to beehives and results in economic losses. *Bacillus thuringiensis* (Bt) appears as a potential sustainable solution to control this pest. Here, we develop a novel Bt strain (designated BiotGm) that exhibits insecticidal activity against GWM larvae with a LC₅₀ value lower than 2 µg/g, and low toxicity levels to honey bee with a LC₅₀ = 20598.78 µg/mL for larvae and no observed adverse effect concentration = 100 µg/mL for adults. We design an entrapment method consisting of a lure for GWM larvae, BiotGm, and a trapping device that prevents bees from contacting the lure. We find that this method reduces the population of GWM larvae in both laboratory and field trials. Overall, these results provide a promising direction for the application of Bt-based biological control of GWM in beehives, although further optimization remain necessary.

<https://www.nature.com/articles/s41467-023-42946-4>

Asiimwe P., Brown C.R., Ellsworth P.C., Reisig D.D. et al. (2023): **Transgenic cotton expressing Mpp51Aa2 does not adversely impact beneficial non-target hemiptera in the field.** *Crop Protection* **173**, 106384

The modified Mpp51Aa2 (previously Cry51Aa2.834_16) insecticidal [crystal protein](#) derived from [Bacillus thuringiensis](#) (Bt) protects against feeding damage caused by targeted [hemipteran](#) and [thysanopteran](#) pests, and was transformed in cotton to produce the MON 88702 cotton event. As part of an ecological risk assessment, we evaluated the relative impact of MON 88702 on the abundance of predatory Hemiptera, compared to a conventional control. Field trials were established in 2018 at six sites within cotton production regions of the U.S. Specific arthropod populations in MON 88702 and its conventional control (DP393), grown under different insecticide regimes within a randomized complete block design, were assessed at each field site. Arthropod samples were collected 10 times, starting at early squaring and weekly thereafter, over the course of the season at each site, using vertical beat sheets, [sweep nets](#) and visual counts. Across the sites, no significant differences were detected in abundance of predatory Hemiptera (*Orius* spp., *Geocoris* spp., *Nabis* spp., and *Zelus* spp.) between unsprayed MON 88702 and the unsprayed conventional control. In contrast, a broad-spectrum insecticide treatment significantly reduced the abundance of these and other taxa. Consistent with laboratory studies, the lack of differences between unsprayed MON 88702 and the unsprayed control indicates that the cultivation of MON 88702 is unlikely to adversely impact the predatory function associated with these beneficial Hemiptera in the cotton agro ecosystem.

<https://www.sciencedirect.com/science/article/pii/S0261219423002077?via%3Dihub>

Mun S.Y. et al. (2024): ***Pediococcus inopinatus* with a well-developed CRISPR-Cas system dominates in long-term fermented kimchi, Mukeunji,** *Food Microbiology* **117**, 104385 | [DOI: 10.1016/j.fm.2023.104385](https://doi.org/10.1016/j.fm.2023.104385)

Kimchi is produced through a low-temperature fermentation without pre-sterilization, resulting in a heterogeneous microbial community. As fermentation progresses, dominant [lactic acid bacteria](#) (LAB) species emerge and undergo a transition process. In this study, LAB were isolated from *Mukeunji*, a long-term fermented kimchi that is in the final stage of kimchi fermentation process. It was confirmed, through culture-dependent and independent analysis, as well as [metagenome](#) analysis, that *Pediococcus inopinatus* are generally dominant in long-term fermented kimchi. Comparative analysis of the *de novo* assembled whole genome of *P. inopinatus* with other kimchi LAB revealed that this species has a well-developed [clustered regularly interspaced short palindromic repeats](#) (CRISPR) system. The CRISPR system of *P. inopinatus* has an additional copy of the *csa3* gene, a transcription factor for *cas* genes. Indeed, this species not only highly expresses *cas1* and *cas2*, which induce spacer acquisition, but also has many diverse spacers that are actively expressed. These findings indicate that the well-developed CRISPR-Cas system is enabling *P. inopinatus* to dominate in long-fermented kimchi. Overall, this study revealed that LAB with a robust defense system dominate in the final stage of kimchi fermentation and presented a model for the succession mechanism of kimchi LAB.

<https://www.sciencedirect.com/science/article/pii/S0740002023001727?via%3Dihub>

EFSA

BIOHAZ Panel (2023): **Statement on how to interpret the QPS qualification on ‘acquired antimicrobial resistance genes’**. EFSA Journal, 21 (10), 1–13 |

<https://doi.org/10.2903/j.efsa.2023.8323>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8323>

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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