

Sunday Evening News No 343

2023-09-11. – 2023-09-17

Compiled and edited by **BGF** Jany



Press Releases -Media / Presse- und Medienberichte

EuropaBio: European Commission proposal on New Genomic Techniques – a first step towards modernizing the EU GMO framework

<https://www.europabio.org/european-commission-proposal-on-new-genomic-techniques-a-first-step-towards-modernizing-the-eu-gmo-framework/>

[https://www.europabio.org/wp-content/uploads/2023/09/EuropaBio-policy-asks Commission-proposal-NGTs_September-2023.pdf](https://www.europabio.org/wp-content/uploads/2023/09/EuropaBio-policy-asks_Commission-proposal-NGTs_September-2023.pdf)

OPTA Europe calls on EU legislators to stand firmly on the side of agroecology, which excludes gene editing

<https://www.bioecoactual.com/en/2023/09/14/opta-europe-calls-on-eu-legislators-to-stand-firmly-on-the-side-of-agroecology-which-excludes-gene-editing/>

https://opta-eu.org/wp-content/uploads/2023/09/OPTA_Europe_comments-NGTs_010923.pdf

Testbiotech: Technology assessment is a must!

<https://www.testbiotech.org/en/impact-assessment>

Testbiotech warns about the far-reaching deregulation of New GE plants

<https://www.testbiotech.org/en/news/testbiotech-warns-about-far-reaching-deregulation-new-ge-plants>

https://www.testbiotech.org/sites/default/files/Testbiotech_Background_NGT_Regulation_final.pdf

Jötten F.: Gentechnik vs. Bio?: „Ich würde gerne aus der Polarisierung heraus“

<https://www.tagesspiegel.de/wissen/gentechnik-vs-bio-ich-wuerde-gerne-aus-der-polarisierung-heraus-10454503.html>

FEI: Engagiert für die Gemeinschaftsforschung: Prof. Dr. Klaus-Dieter Jany erhält Belitz-Medaille des FEI

<https://idw-online.de/de/news?print=1&id=820399>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): September week 36

Publications – Publikationen

Vanderschuren, H., Chatukuta, P., Weigel, D. et al. (2023): **A new chance for genome editing in Europe**. Nat Biotechnol | <https://doi.org/10.1038/s41587-023-01969-4>

Mahmood M.A and Shahid Mansoor S. (2023): **Einkorn genomics reveals ancient roots of domesticated wheat**. Cell Genomics 3 (9), 100406 | <https://doi.org/10.1016/j.xgen.2023.100406>

Wheat is an important staple food crop that underwent complex genome duplications. During domestication, genetic changes occurred, improving modern wheat, but understanding its phylogenetic history has been lacking. Mahmood and Mansoor discuss a recent publication demonstrating the evolutionary history of domesticated wheat (*Triticum monococcum*), providing opportunities for advancements in cereal improvement [https://www.cell.com/cell-genomics/pdf/S2666-979X\(23\)00220-3.pdf](https://www.cell.com/cell-genomics/pdf/S2666-979X(23)00220-3.pdf)

Antoniou M.N., Robinson C., Castro I., Hilbeck A. (2023): **Agricultural GMOs and their associated pesticides: misinformation, science, and evidence**. Environmental Sciences Europe 35:76 | <https://doi.org/10.1186/s12302-023-00787-4>

Misinformation has always existed, but it became a major preoccupation during the COVID-19 pandemic due to its ability to affect public health choices, decisions, and policy. In their article, “Misinformation in the media: Global coverage of GMOs 2019–2021” (GM Crops & Food, 17 Nov 2022), Mark Lynas et al. characterise critics of agricultural genetically modified organisms (GMOs) and their associated pesticides as purveyors of “misinformation”. They draw an equivalence between critics of agricultural GMOs and people who make false claims about climate change, COVID-19, and vaccines. We examined their main claims on these GMOs—for example, that there is a scientific consensus that they are safe for health and the environment—in the light of the scientific evidence and public discussion on this topic. We found that their claims are biased and misleading and ignore or omit crucial evidence. We conclude that based on the evidence provided, Lynas et al. article can

itself be classed as misinformation and could therefore mislead the general public as well as the scientific community.

<https://enveurope.springeropen.com/articles/10.1186/s12302-023-00787-4>

Mega, R., Kim, J.S., Tanaka, H. et al. (2023): **Metabolic and transcriptomic profiling during wheat seed development under progressive drought conditions**. *Sci Rep* 13, 15001 | <https://doi.org/10.1038/s41598-023-42093-2>

Globally, bread wheat (*Triticum aestivum*) is one of the most important staple foods; when exposed to drought, wheat yields decline. Although much research has been performed to generate higher yield wheat cultivars, there have been few studies on improving end-product quality under drought stress, even though wheat is processed into flour to produce so many foods, such as bread, noodles, pancakes, cakes, and cookies. Recently, wheat cultivation has been affected by severe drought caused by global climate change. In previous studies, seed shrinkage was observed in wheat exposed to continuous drought stress during seed development. In this study, we investigated how progressive drought stress affected seed development by metabolomic and transcriptomic analyses. Metabolite profiling revealed the drought-sensitive line reduced accumulation of proline and sugar compared with the water-saving, drought-tolerant transgenic line overexpressing the abscisic acid receptor TaPYL4 under drought conditions in spikelets with developing seeds. Meanwhile, the expressions of genes involved in translation, starch biosynthesis, and proline and arginine biosynthesis was downregulated in the drought-sensitive line. These findings suggest that seed shrinkage, exemplifying a deficiency in endosperm, arose from the hindered biosynthesis of crucial components including seed storage proteins, starch, amino acids, and sugars, ultimately leading to their inadequate accumulation within spikelets. Water-saving drought tolerant traits of wheat would aid in supporting seed formation under drought conditions. <https://www.nature.com/articles/s41598-023-42093-2>

Singh, A., Pandey, H., Pandey, S. et al. (2023): **Drought stress in maize: stress perception to molecular response and strategies for its improvement**. *Funct Integr Genomics* 23, 296 | <https://doi.org/10.1007/s10142-023-01226-6>

Given the future demand for food crops, increasing crop productivity in drought-prone rainfed areas has become essential. Drought-tolerant varieties are warranted to solve this problem in major crops, with drought tolerance as a high-priority trait for future research. Maize is one such crop affected by drought stress, which limits production, resulting in substantial economic losses. It became a more serious issue due to global climate change. The most drought sensitive among all stages of maize is the reproductive stages and the most important for overall maize production. The exact molecular basis of reproductive drought sensitivity remains unclear due to genes' complex regulation of drought stress. Understanding the molecular biology and signaling of the unexplored area of reproductive drought tolerance will provide an opportunity to develop climate-smart drought-tolerant next-generation maize cultivars. In recent decades, significant progress has been made in maize to understand the drought tolerance mechanism. However, improving maize drought tolerance through breeding is ineffective due to the complex nature and multigenic control of drought traits. With the help of advanced breeding techniques, molecular genetics, and a precision genome editing approach like CRISPR-Cas, candidate genes for drought-tolerant maize can be identified and targeted. This review summarizes the effects of drought stress on each growth stage of maize, potential genes, and transcription factors that determine drought tolerance. In addition, we discussed drought stress sensing, its molecular mechanisms, different approaches to developing drought-resistant maize varieties, and how molecular breeding and genome editing will help with the current unpredictable climate change.

<https://link.springer.com/article/10.1007/s10142-023-01226-6>

Azim, M.A., Mahmud, K., Islam, N. et al. (2023): **History and Current Status of Sugarcane Breeding, Germplasm Development and Molecular Approaches in Bangladesh**. *Sugar Tech* | <https://doi.org/10.1007/s12355-023-01315-7>

Bangladesh is one of the sugarcane-producing countries in the South Asian region. The present sugar production accounts for approximately 4.5%, and jaggery production accounts for 20.5% of overall consumption. In the 2020–2021 cropping season, the country produced 7.37 million tons of sugarcane in a harvest area of 0.17 million hectares. The average sugarcane yield is around 70 t/ha, with a sugar yield of 5.49 t/ha. Due to the competition for cereals and other short-duration crops, the area under cane cultivation is decreasing substantially, resulting in the reduction in total sugarcane production. In recent decades, Bangladesh has made great strides in producing new sugarcane varieties through controlled crossbreeding, with the majority of current commercial varieties coming from regional breeding programs. The main goals of the sugarcane breeding program in Bangladesh are high productivity with high sugar content, early maturity, good ratooning ability, resilience, and resistance to the biotic and abiotic challenges of sugarcane. Improved sugarcane varieties have significantly increased sugar recovery from 12.43 to 13.89% and production from 83 t/ha in 1963 to 106 t/ha in 2022–2023. Micropropagation aimed at improving sugarcane varieties has enabled rapid propagation and accelerated acceptance of new varieties. This article provides a brief overview of the development of sugarcane in Bangladesh over time, as well as a discussion of current research difficulties and methodological methods, such as introgression-based, biotechnological, and molecular genetic breeding techniques.

<https://link.springer.com/article/10.1007/s12355-023-01315-7>

Liu, F., Zhao, J., Sun, H. et al. (2023): **Genomes of cultivated and wild *Capsicum* species provide insights into pepper domestication and population differentiation.** Nat Commun 14, 5487 | <https://doi.org/10.1038/s41467-023-41251-4>

Pepper (*Capsicum* spp.) is one of the earliest cultivated crops and includes five domesticated species, *C. annuum* var. *annuum*, *C. chinense*, *C. frutescens*, *C. baccatum* var. *pendulum* and *C. pubescens*. Here, we report a pepper graph pan-genome and a genome variation map of 500 accessions from the five domesticated *Capsicum* species and close wild relatives. We identify highly differentiated genomic regions among the domesticated peppers that underlie their natural variations in flowering time, characteristic flavors, and unique resistances to biotic and abiotic stresses. Domestication sweeps detected in *C. annuum* var. *annuum* and *C. baccatum* var. *pendulum* are mostly different, and the common domestication traits, including fruit size, shape and pungency, are achieved mainly through the selection of distinct genomic regions between these two cultivated species. Introgressions from *C. baccatum* into *C. chinense* and *C. frutescens* are detected, including those providing genetic sources for various biotic and abiotic stress tolerances.
<https://www.nature.com/articles/s41467-023-41251-4>

Kaufman S., Boxshall A. (2023): **Eleven enablers of science thought leadership to facilitate knowledge exchange in environmental regulation.** Environmental Science & Policy 147, 336-348 | <https://doi.org/10.1016/j.envsci.2023.06.018>

Evidence informed environmental policy and decision-making remains aspirational. Knowledge exchange literature indicates necessary supportive elements and activities but acknowledges a gap in understanding of interpersonal and relational aspects. Inquiry is particularly lacking into the roles and potential of internal expert advice, especially in the micro-level instrumental decisions regulators make daily. We identify these characteristics as 'science thought leadership' (STL) and explore their role in experiences of successful decision support in environmental regulation. Forty-four cases in Victoria, Australia, and Florida, USA, were identified and analysed via appreciative inquiry methods. The cases prioritized in this process highlight environmental regulatory decisions, administrative in nature yet part of the policy cycle, as important sites of STL. STL is a set of characteristics and capabilities underpinning effective knowledge exchange, leading to better evidence-informed decisions. It is a series of 11 inter-related personal, professional and organisational enablers pivotal in cases when problem definition is contested, and legitimacy must be demonstrated. Integration, expertise and decisiveness in uncertainty is present when organisations and management value science and experts, and are externally accountable to justify decisions. Based on the findings, we present a conceptual model of STL and a checklist for its presence to assist both government and universities to recognize, work with and support STLs as crucial facilitators of evidence informed decision making.
<https://www.sciencedirect.com/science/article/pii/S1462901123001764>

Su, M., Li, F., Wang, Y. et al. (2023): **Molecular basis and engineering of miniature Cas12f with C-rich PAM specificity.** Nat Chem Biol | <https://doi.org/10.1038/s41589-023-01420-4>
CRISPR–Cas12f nucleases are currently one of the smallest genome editors, exhibiting advantages for efficient delivery via cargo-size-limited adeno-associated virus delivery vehicles. Most characterized Cas12f nucleases recognize similar T-rich protospacer adjacent motifs (PAMs) for DNA targeting, substantially restricting their targeting scope. Here we report the cryogenic electron microscopy structure and engineering of a miniature *Clostridium novyi* Cas12f1 nuclease (CnCas12f1, 497 amino acids) with rare C-rich PAM specificity. Structural characterizations revealed detailed PAM recognition, asymmetric homodimer formation and single guide RNA (sgRNA) association mechanisms. sgRNA engineering transformed CRISPR–CnCas12f1, which initially was incapable of genome targeting in bacteria, into an effective genome editor in human cells. Our results facilitate further understanding of CRISPR–Cas12f1 working mechanism and expand the mini-CRISPR toolbox.
<https://www.nature.com/articles/s41589-023-01420-4>

Zeng, H., Yuan, Q., Peng, F. et al. (2023): **A split and inducible adenine base editor for precise in vivo base editing.** Nat Commun 14, 5573 | <https://doi.org/10.1038/s41467-023-41331-5>

DNA base editors use deaminases fused to a programmable DNA-binding protein for targeted nucleotide conversion. However, the most widely used TadA deaminases lack post-translational control in living cells. Here, we present a split adenine base editor (sABE) that utilizes chemically induced dimerization (CID) to control the catalytic activity of the deoxyadenosine deaminase TadA-8e. sABE shows high on-target editing activity comparable to the original ABE with TadA-8e (ABE8e) upon rapamycin induction while maintaining low background activity without induction. Importantly, sABE exhibits a narrower activity window on DNA and higher precision than ABE8e, with an improved single-to-double ratio of adenine editing and reduced genomic and transcriptomic off-target effects. sABE can achieve gene knockout through multiplex splice donor disruption in human cells. Furthermore, when delivered via dual adeno-associated virus vectors, sABE can efficiently convert a single A•T base pair to a G•C base pair on the *PCSK9* gene in mouse liver, demonstrating in vivo CID-controlled DNA base editing. Thus, sABE enables precise control of base editing, which will have broad implications for basic research and in vivo therapeutic applications.
<https://www.nature.com/articles/s41467-023-41331-5>

Tomita, A., Sasanuma, H., Owa, T. et al. (2023): **Inducing multiple nicks promotes interhomolog homologous recombination to correct heterozygous mutations in somatic cells.** Nat Commun 14, 5607 | <https://doi.org/10.1038/s41467-023-41048-5>

CRISPR/Cas9-mediated gene editing has great potential utility for treating genetic diseases. However, its therapeutic applications are limited by unintended genomic alterations arising from DNA double-strand breaks and random integration of exogenous DNA. In this study, we propose NICER, a method for correcting heterozygous mutations that employs multiple nicks (MNs) induced by Cas9 nickase and a homologous chromosome as an endogenous repair template. Although a single nick near the mutation site rarely leads to successful gene correction, additional nicks on homologous chromosomes strongly enhance gene correction efficiency via interhomolog homologous recombination (IH-HR). This process partially depends on BRCA1 and BRCA2, suggesting the existence of several distinct pathways for MN-induced IH-HR. According to a genomic analysis, NICER rarely induces unintended genomic alterations. Furthermore, NICER restores the expression of disease-causing genes in cells derived from genetic diseases with compound heterozygous mutations. Overall, NICER provides a precise strategy for gene correction.

<https://www.nature.com/articles/s41467-023-41048-5>

Jang J.H. (2023): **Loss of function of pollen-expressed phospholipase OsMATL2 triggers haploid induction in japonica rice**, *Plant Physiology* (2023). DOI: [10.1093/plphys/kiad422](https://doi.org/10.1093/plphys/kiad422)

Hossain, M.J., Bakhsh, A., Joyia, F.A. et al. (2023): **Engineering of insecticidal hybrid gene into potato chloroplast genome exhibits promising control of Colorado potato beetle, *Leptinotarsa decemlineata* (Coleoptera: Chrysomelidae)**. *Transgenic Res* |

<https://doi.org/10.1007/s11248-023-00366-6>

The potato chloroplast was transformed with codon optimized synthetic hybrid cry gene (*SN19*) to mitigate crop losses by Colorado potato beetle (CPB). The bombarded explants (leaves and internode) were cultured on MS medium supplemented with BAP (2.0 mg/l), NAA (0.2 mg/l), TDZ (2.0 mg/l) and GA3 (0.1 mg/l); spectinomycin 50 mg/l was used as a selection agent in the medium. Leaf explants of cultivar Kuroda induced highest percentage (92%) of callus where cultivar Santeae produced the highest percentage (85.7%) of transplastomic shoots. Sante and Challenger showed 9.6% shoot regeneration efficiency followed by cultivar Simply Red (8.8%). PCR amplification yielded 16 positive transplastomic plantlets out of 21 spectinomycin resistant ones. Target gene integration was confirmed by PCR and Southern blot, whereas RT-qPCR was used to assess the expression level of transgene. The localization of visual marker gene *gfp* was tracked by laser scanning confocal microscopy which confirmed its expression in chloroplasts of leaf cells. The transplastomic plants ensured high mortality to both larvae and adult CPB. Foliage consumption and weight gain of CPB fed on transplastomic leaves were lower compared to the control plants. Successful implementation of current research findings can lead to a viable solution to CPB mediated potato losses globally.

<https://link.springer.com/article/10.1007/s11248-023-00366-6>

Ratcliffe, N.A., Furtado Pacheco, J.P., Dyson, P. et al. (2023): **Overview of paratransgenesis as a strategy to control pathogen transmission by insect vectors**. *Parasites Vectors* 15, 112 (2022). <https://doi.org/10.1186/s13071-021-05132-3>

This article presents an overview of paratransgenesis as a strategy to control pathogen transmission by insect vectors. It first briefly summarises some of the disease-causing pathogens vectored by insects and emphasises the need for innovative control methods to counter the threat of resistance by both the vector insect to pesticides and the pathogens to therapeutic drugs. Subsequently, the state of art of paratransgenesis is described, which is a particularly ingenious method currently under development in many important vector insects that could provide an additional powerful tool for use in integrated pest control programmes. The requirements and recent advances of the paratransgenesis technique are detailed and an overview is given of the microorganisms selected for genetic modification, the effector molecules to be expressed and the environmental spread of the transgenic bacteria into wild insect populations. The results of experimental models of paratransgenesis developed with triatomines, mosquitoes, sandflies and tsetse flies are analysed. Finally, the regulatory and safety rules to be satisfied for the successful environmental release of the genetically engineered organisms produced in paratransgenesis are considered.

<https://parasitesandvectors.biomedcentral.com/articles/10.1186/s13071-021-05132-3>

Bost J., Recalde A., Waßmer B., Wagner A., Siebers B., Albers S.-V. (2023): **Application of the endogenous CRISPR-Cas type I-D system for genetic engineering in the thermoacidophilic archaeon *Sulfolobus acidocaldarius*** *Front. Microbiol. Sec. Biology of Archaea* Volume 14 - 2023 | doi: [10.3389/fmicb.2023.1254891](https://doi.org/10.3389/fmicb.2023.1254891)

CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) -Cas systems are widely distributed among bacteria and archaea. In this study, we demonstrate the successful utilization of the type I-D CRISPR-Cas system for genetic engineering in the thermoacidophilic archaeon *Sulfolobus acidocaldarius*. Given its extreme growth conditions characterized by a temperature of 75 °C and pH 3, an uracil auxotrophic selection system was previously established, providing a basis for our investigations. We developed a novel plasmid specifically designed for genome editing, which incorporates a mini CRISPR array that can be induced using xylose, resulting in targeted DNA cleavage. Additionally, we integrated a gene encoding the β -galactosidase of *Saccharolobus solfataricus* into the plasmid, enabling blue-white screening and facilitating the mutant screening process. Through the introduction of donor DNA containing genomic modifications into the plasmid, we successfully generated deletion mutants and point mutations in the genome of *S. acidocaldarius*. Exploiting the PAM (Protospacer Adjacent Motif) dependence of type I systems, we experimentally confirmed the functionality of three different PAMs (CCA, GTA, and TCA) through a self-targeting assessment assay and the gene deletion of

upsE. Our findings elucidate the application of the endogenous Type I-D CRISPR-Cas system for genetic engineering in *S. acidocaldarius*, thus expanding its genetic toolbox.

<https://www.frontiersin.org/articles/10.3389/fmicb.2023.1254891/abstract>

Li T, Menegatti S, Crook N. (2023): **Breakdown of polyethylene terephthalate microplastics under saltwater conditions using engineered *Vibrio natriegens***. *AIChE Journal*. e182228 | doi:[10.1002/aic.18228](https://doi.org/10.1002/aic.18228)

Poly(ethylene terephthalate) (PET) is a highly recyclable plastic that has been extensively used and manufactured. Like other plastics, PET resists natural degradation, thus accumulating in the environment. Several recycling strategies have been applied to PET, but these tend to result in downcycled products that eventually end up in landfills. This accumulation of landfilled PET waste contributes to the formation of microplastics, which pose a serious threat to marine life and ecosystems, and potentially to human health. To address this issue, our project leveraged synthetic biology to develop a whole-cell biocatalyst capable of depolymerizing PET in seawater environments by using the fast-growing, nonpathogenic, moderate halophile *Vibrio natriegens*. By leveraging a two-enzyme system—comprising a chimera of *IsPETase* and *IsMHETase* from *Ideonella sakaiensis*—displayed on *V. natriegens*, we constructed whole-cell catalysts that depolymerize PET and convert it into its monomers in salt-containing media and at a temperature of 30°C.

<https://aiche.onlinelibrary.wiley.com/doi/10.1002/aic.18228><https://aiche.onlinelibrary.wiley.com/doi/10.1002/aic.18228>

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