

Sunday Evening News No 369

2024-03-18 – 2024-03-24

Compiled and edited by **BGF** Jany



Wissenschaftskreis
Genomik und
Gentechnik e.V.

Meetings – Conferences / Veranstaltungen - Konferenzen

GASBmeetsPAW: Gentechnik Knackpunkt #3: Patente

Am 10. April geht es endlich weiter mit der dritten Staffel von #GASBmeetsPAW

Anmeldung: https://us02web.zoom.us/webinar/register/WN_YKQHT_jCRBiNQBUaDbtrw#/registration

Grüne Gentechnik im Blickpunkt von Naturwissenschaft, Ethik und Politik" – Kaiserschild Lectures

Zeit: 7. Mai 2024, 13.00-17.00 Uhr

Ort: Aula am Campus der Universität Wien Spitalgasse 2, Hof 1.11, 1090 Wien

https://www.postgraduatecenter.at/aktuelles/veranstaltungen/details/news/gruene-gentechnik-im-blickpunkt-von-naturwissenschaft-ethik-und-politik-kaiserschild-lectures/?tx_news_pi1%5Bcontroller%5D=News&tx_news_pi1%5Baction%5D=detail&cHash=11e4d625f3a3c319d027acd0355eb6e5

Press Releases -Media / Presse- und Medienberichte

Vaughan A: Revealed: the first gene-edited crops to be farmed in UK

<https://www.thetimes.co.uk/article/revealed-the-first-gene-edited-crops-to-be-farmed-in-uk-5gjc2s6jg> (behind paywall) see GM Watch

GM-Watch: GM gene-edited crop trials will be planted on English farms

<https://mailchi.mp/gmwatch.org/daily-digest-vqz6v8ryry?e=ca15334802>

ECVC celebrates a first victory against GMO/NGT deregulation

<https://www.eurovia.org/press-releases/ecvc-celebrates-a-first-victory-against-gmo-ngt-deregulation/>

Meshaka D.: Patents pose a real threat to two plant breeders

<https://infogm.org/en/patents-pose-a-real-threat-to-two-plant-breeders/>

EU agriculture MEPs vote to exempt 'old varieties' from seed marketing rules

https://www.euractiv.com/section/agriculture-food/news/eu-agriculture-meps-vote-to-exempt-old-varieties-from-seed-marketing-rules/?_ga=2.266585738.58816231.1710949910-1594607389.1710949910

Gidding L.V. Biotech Matters: Innovation in Agricultural Biotechnology

<https://itif.org/publications/2024/03/19/biotech-matters-innovation-in-agricultural-biotechnology/>
and more.

Overcoming Obstacles to Gene-Edited Solutions to Climate Challenges

<https://itif.org/publications/2024/02/23/overcoming-obstacles-to-gene-edited-solutions-to-climate-challenges/>

Innovations Like These Will Help Solve the Climate Crisis: Introduction to "Synthetic Biology and Greenhouse Gases"

<https://itif.org/publications/2024/02/23/innovations-like-these-will-help-solve-the-climate-crisis/>

Was es zur neuen Pflanzenzüchtung zu wissen lohnt

CrisprCas ist als Begriff vielen bekannt, vor allem aus einigen Diskussionen. Dabei geht es vor

<https://www.gemuese-online.de/aktuelles/nachrichten/was-es-zur-neuen-pflanzenzuechtung-zu-wissen-lohnt,QUIEPTc4Nzk3MjUmTUIEPTe4ODU3MQ.html>

EU-Entscheidung zu neuen Pflanzenzüchtungsmethoden: Hintergründe und Stellungnahmen

<https://www.gemuese-online.de/aktuelles/nachrichten/hintergruende-und-stellungnahmen,QUIEPTc4Nzk3MjQmTUIEPTe4ODU3MQ.html>

VLOG: 15 Jahre „Ohne GenTechnik“-Siegel: Rekordumsatz zum Jubiläum

<https://www.ohnegentechnik.org/artikel/15-jahre-ohne-gentechnik-siegel-rekordumsatz-zum-jubilaeum>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): March Week 12-2024

Publications – Publikationen

Qaim M. (2009): **The Economics of Genetically Modified Crops** . Annual Review of Resource Economics 1, 665-694 | <https://doi.org/10.1146/annurev.resource.050708.144203>
Genetically modified (GM) crops have been used commercially for more than 10 years. Available impact studies of insect-resistant and herbicide-tolerant crops show that these technologies are beneficial to farmers and consumers, producing large aggregate welfare gains as well as positive effects for the environment and human health. The advantages of future applications could even be much bigger. Given a conducive institutional framework, GM crops can contribute significantly to global food security and poverty reduction. Nonetheless, widespread public reservations have led to a complex system of regulations. Overregulation has become a real threat for the further development and use of GM crops. The costs in terms of foregone benefits may be large, especially for developing countries. Economics research has an important role to play in designing efficient regulatory mechanisms and agricultural innovation systems.
<https://www.annualreviews.org/content/journals/10.1146/annurev.resource.050708.144203>

Rallapalli K.L.,and Komor A.C. (2023): **The Design and Application of DNA-Editing Enzymes as Base Editors**. Annual Review of Biochemistry 92:43-79 | <https://doi.org/10.1146/annurev-biochem-052521-013938>
DNA-editing enzymes perform chemical reactions on DNA nucleobases. These reactions can change the genetic identity of the modified base or modulate gene expression. Interest in DNA-editing enzymes has burgeoned in recent years due to the advent of clustered regularly interspaced short palindromic repeat-associated (CRISPR-Cas) systems, which can be used to direct their DNA-editing activity to specific genomic loci of interest. In this review, we showcase DNA-editing enzymes that have been repurposed or redesigned and developed into programmable base editors. These include deaminases, glycosylases, methyltransferases, and demethylases. We highlight the astounding degree to which these enzymes have been redesigned, evolved, and refined and present these collective engineering efforts as a paragon for future efforts to repurpose and engineer other families of enzymes. Collectively, base editors derived from these DNA-editing enzymes facilitate programmable point mutation introduction and gene expression modulation by targeted chemical modification of nucleobases.
<https://www.annualreviews.org/content/journals/10.1146/annurev-biochem-052521-013938>

Moreno-Castro C., Krzewińska A., Dzimińska M. (2024): **How Citizens View Science Communication**. Pathways to Knowledge | <https://doi.org/10.4324/9781003400943>
Science communication aims at the successful sharing and explanation of science-related topics to a wider audience. In order to enhance communication between science and society, a better understanding of citizens' habits and perceptions is needed. Therefore, it is vital to understand how citizens acquire knowledge about science-related issues, how this knowledge affects their beliefs, opinions and perceptions, and what sources of information they choose to learn about science – and how they assess their reliability. This book addresses these questions, based on the analyses of public consultations data from Italy, Poland, Portugal, Slovakia and Spain, concerned with the science communication of issues including climate change, vaccines, complementary and alternative medicine (CAM) and genetically modified organisms (GMOs). Sharing experiences of how to engage citizens in public consultation, it provides insights into the mobilisation of interest in science and offers recommendations on how to improve science communication.
<https://www.taylorfrancis.com/books/oa-edit/10.4324/9781003400943/citizens-view-science-communication-carolina-moreno-castro-aneta-krzewi%C5%84ska-ma%C5%82gorzata-dzimi%C5%84ska>

Delicado A., Moreno- Castro C., Brondi S., Wiktorowicz J., Diener L.: **5 Perceptions of science information on climate change and GMOs** | DOI: 10.4324/9781003400943-6

Hackfort S. (2024): **Democratization through precision technologies? Unveiling power, participation, and property rights in the agricultural bioeconomy**. Front. Polit. Sci.6 - 2024 | <https://doi.org/10.3389/fpos.2024.1363044>
This piece addresses the political dimension of sustainability in the agricultural bioeconomy by focusing on power, participation, and property rights around key technologies. Bioeconomy policies aim to establish economic systems based on renewable resources such as plants and microorganisms to reduce dependence on fossil resources. To achieve this, they rely on economic growth and increased biomass production through high-tech innovations. This direction has sparked important critique of the environmental and social sustainability of such projects. However, little attention has been paid in the bioeconomy literature to the political dimension surrounding key precision technologies such as data-driven precision agriculture (PA) or precision breeding technologies using new genomic techniques (NGT). The political dimension includes questions of power, participation, and property rights regarding these technologies and the distribution of the benefits and burdens they generate. This lack of attention is particularly pertinent given the recurring and promising claims that precision technologies not only enhance environmental sustainability, but also contribute to the democratization of food and biomass production. This contribution addresses this claim in asking whether we

can really speak of a democratization of the agricultural bioeconomy through these precision technologies. Drawing on (own) empirical research and historical evidence, it concludes that current patterns are neither driving nor indicative of a democratization. On the contrary, corporate control, unequal access, distribution, and property rights over data and patents point to few gains for small firms and breeders, but to a reproduction of farmers' dependencies, and less transparency for consumers.

<https://www.frontiersin.org/articles/10.3389/fpos.2024.1363044/full>

Atia, M., Jiang, W., Sedeek, K. et al. (2024): **Crop bioengineering via gene editing: reshaping the future of agriculture.** *Plant Cell Rep* **43**, 98 <https://doi.org/10.1007/s00299-024-03183-1>

Genome-editing technologies have revolutionized research in plant biology, with major implications for agriculture and worldwide food security, particularly in the face of challenges such as climate change and increasing human populations. Among these technologies, clustered regularly interspaced short palindromic repeats [CRISPR]–CRISPR-associated protein [Cas] systems are now widely used for editing crop plant genomes. In this review, we provide an overview of CRISPR–Cas technology and its most significant applications for improving crop sustainability. We also review current and potential technological advances that will aid in the future breeding of crops to enhance food security worldwide. Finally, we discuss the obstacles and challenges that must be overcome to realize the maximum potential of genome-editing technologies for future crop and food production.

<https://link.springer.com/article/10.1007/s00299-024-03183-1>

Mathew I.E., Rhein H.S, Yang J, Gradogna A. et al. (2024): **Sequential removal of cation/H⁺ exchangers reveals their additive role in elemental distribution, calcium depletion and anoxia tolerance.** *Plant , Cell, Environment* **747** (2), Pages 557-57 |

<https://doi.org/10.1111/pce.14756>

Multiple *Arabidopsis* H⁺/Cation exchangers (CAXs) participate in high-capacity transport into the vacuole. Previous studies have analysed single and double mutants that marginally reduced transport; however, assessing phenotypes caused by transport loss has proven enigmatic. Here, we generated quadruple mutants (*cax1-4*: qKO) that exhibited growth inhibition, an 85% reduction in tonoplast-localised H⁺/Ca transport, and enhanced tolerance to anoxic conditions compared to CAX1 mutants. Leveraging inductively coupled plasma mass spectrometry (ICP-MS) and synchrotron X-ray fluorescence (SXRF), we demonstrate CAX transporters work together to regulate leaf elemental content: ICP-MS analysis showed that the elemental concentrations in leaves strongly correlated with the number of CAX mutations; SXRF imaging showed changes in element partitioning not present in single CAX mutants and qKO had a 40% reduction in calcium (Ca) abundance.

<https://onlinelibrary.wiley.com/doi/epdf/10.1111/pce.14756>

He, X., Wang, D., Jiang, Y. et al. (2024): **Heritable microbiome variation is correlated with source environment in locally adapted maize varieties.** *Nat. Plants* |

<https://doi.org/10.1038/s41477-024-01654-7>

Beneficial interactions with microorganisms are pivotal for crop performance and resilience. However, it remains unclear how heritable the microbiome is with respect to the host plant genotype and to what extent host genetic mechanisms can modulate plant–microbiota interactions in the face of environmental stresses. Here we surveyed 3,168 root and rhizosphere microbiome samples from 129 accessions of locally adapted *Zea*, sourced from diverse habitats and grown under control and different stress conditions. We quantified stress treatment and host genotype effects on the microbiome. Plant genotype and source environment were predictive of microbiome abundance. Genome-wide association analysis identified host genetic variants linked to both rhizosphere microbiome abundance and source environment. We identified transposon insertions in a candidate gene linked to both the abundance of a keystone bacterium *Massilia* in our controlled experiments and total soil nitrogen in the source environment. Isolation and controlled inoculation of *Massilia* alone can contribute to root development, whole-plant biomass production and adaptation to low nitrogen availability. We conclude that locally adapted maize varieties exert patterns of genetic control on their root and rhizosphere microbiomes that follow variation in their home environments, consistent with a role in tolerance to prevailing stress

<https://www.nature.com/articles/s41477-024-01654-7>

Zhou J. Kathiresan N., Yu Z., Rivera L.F. et al. (2024): **A high-performance computational workflow to accelerate GATK SNP detection across a 25-genome dataset,** *BMC Biology* | DOI: [10.1186/s12915-024-01820-5](https://doi.org/10.1186/s12915-024-01820-5)

Background: Single-nucleotide polymorphisms (SNPs) are the most widely used form of molecular genetic variation studies. As reference genomes and resequencing data sets expand exponentially, tools must be in place to call SNPs at a similar pace. The genome analysis toolkit (GATK) is one of the most widely used SNP calling software tools publicly available, but unfortunately, high-performance computing versions of this tool have yet to become widely available and affordable.

Results: Here we report an open-source high-performance computing genome variant calling workflow (HPC-GVCW) for GATK that can run on multiple computing platforms from supercomputers to desktop machines. We benchmarked HPC-GVCW on multiple crop species for performance and accuracy with comparable results with previously published reports (using GATK alone). Finally, we used HPC-GVCW in production mode to call SNPs on a “subpopulation aware” 16-genome rice reference panel with ~ 3000 resequenced rice accessions. The entire process took ~ 16 weeks and resulted in the identification of an average of 27.3 M SNPs/genome and the

discovery of ~ 2.3 million novel SNPs that were not present in the flagship reference genome for rice (i.e., IRGSP RefSeq).

Conclusions: This study developed an open-source pipeline (HPC-GVCW) to run GATK on HPC platforms, which significantly improved the speed at which SNPs can be called. The workflow is widely applicable as demonstrated successfully for four major crop species with genomes ranging in size from 400 Mb to 2.4 Gb. Using HPC-GVCW in production mode to call SNPs on a 25 multi-crop-reference genome data set produced over 1.1 billion SNPs that were publicly released for functional and breeding studies. For rice, many novel SNPs were identified and were found to reside within genes and open chromatin regions that are predicted to have functional consequences. Combined, our results demonstrate the usefulness of combining a high-performance SNP calling architecture solution with a subpopulation-aware reference genome panel for rapid SNP discovery and public deployment.

<https://bmcbiol.biomedcentral.com/articles/10.1186/s12915-024-01820-5>

Prasad, K., Gadeela, H., Bommineni, P.R. et al. (2024) | **CRISPR/Cas9-mediated mutagenesis of phytoene desaturase in pigeonpea and groundnut.** *Funct Integr Genomics* 24, 57

<https://doi.org/10.1007/s10142-024-01336-9>

The CRISPR/Cas9 technology, renowned for its ability to induce precise genetic alterations in various crop species, has encountered challenges in its application to grain legume crops such as pigeonpea and groundnut. Despite attempts at gene editing in groundnut, the low rates of transformation and editing have impeded its widespread adoption in producing genetically modified plants. This study seeks to establish an effective CRISPR/Cas9 system in pigeonpea and groundnut through *Agrobacterium*-mediated transformation, with a focus on targeting the *phytoene desaturase* (*PDS*) gene. The *PDS* gene is pivotal in carotenoid biosynthesis, and its disruption leads to albino phenotypes and dwarfism. Two constructs (one each for pigeonpea and groundnut) were developed for the *PDS* gene, and transformation was carried out using different explants (leaf petiolar tissue for pigeonpea and cotyledonary nodes for groundnut). By adjusting the composition of the growth media and refining *Agrobacterium* infection techniques, transformation efficiencies of 15.2% in pigeonpea and 20% in groundnut were achieved. Mutation in *PDS* resulted in albino phenotype, with editing efficiencies ranging from 4 to 6%. Sequence analysis uncovered a nucleotide deletion (A) in pigeonpea and an A insertion in groundnut, leading to a premature stop codon and, thereby, an albino phenotype. This research offers a significant foundation for the swift assessment and enhancement of CRISPR/Cas9-based genome editing technologies in legume crops.

<https://link.springer.com/article/10.1007/s10142-024-01336-9>

Zhou, S., Luo, G., Yang, Q. et al. (2024) | **A chromosome-level genome assembly of yellow stem borer (*Scirpophaga incertulas*).** *Sci Data* 11, 279 | <https://doi.org/10.1038/s41597-024-03108-3>

The yellow stem borer *Scirpophaga incertulas* is the dominant pest of rice in tropical Asia. However, the lack of genomic resources makes it difficult to understand their invasiveness and ecological adaptation. A high-quality chromosome-level genome of *S. incertulas*, a monophagous rice pest, was assembled by combining Illumina short reads, PacBio HiFi long sequencing, and Hi-C scaffolding technology. The final genome size was 695.65 Mb, with a scaffold N50 of 28.02 Mb, and 93.50% of the assembled sequences were anchored to 22 chromosomes. BUSCO analysis demonstrated that this genome assembly had a high level of completeness, with 97.65% gene coverage. A total of 14,850 protein-coding genes and 366.98 Mb of transposable elements were identified. In addition, comparative genomic analyses indicated that chemosensory processes and detoxification capacity may play critical roles in the specialized host preference of *S. incertulas*. In summary, the chromosome-level genome assembly of *S. incertulas* provides a valuable genetic resource for understanding the biological characteristics of its invasiveness and developing an efficient management strategy.

<https://www.nature.com/articles/s41597-024-03108-3>

Ahsanuzzaman, Husain H., Zilberman D. (2024): **Complementarity of field studies and RCTs: evidence from Bt eggplant in Bangladesh.** *European Review of Agricultural Economics*, jbae003, | <https://doi.org/10.1093/erae/jbae003>

Randomised control trials (RCTs) and field studies are two empirical approaches. We conducted a field study analysing the adoption of Bt eggplant in Bangladesh and compared the results of previous RCTs. We find that Bt eggplant raises yields, lowers total cost and pesticide costs and generates a price premium compared to non-Bt eggplant, increasing profits by 23 per cent. We also identify factors contributing to adopting Bt eggplant, including better access to credit, farm sizes and expected profitability. Our low-cost field study confirms the impact assessment results of RCTs and provides insight into factors affecting adoption.

<https://academic.oup.com/erae/advance-article-abstract/doi/10.1093/erae/jbae003/7631898?redirectedFrom=fulltext&login=false>

Nakai S., Roberts A.F., Simmons A.R., Hiratsuka K., Miano D.W. and Vesprini F. (2024): **Introduction and scientific justification of data transportability for confined field testing for the ERA of GM plants.** *Front. Bioeng. Biotechnol.* 12:1359388. | doi: 10.3389/fbioe.2024.1359388

The concept of Data Transportability (DT) of Confined Field Testing (CFT) to support the Environmental Risk Assessment (ERA) of Genetically Modified (GM) plants was first introduced in the literature by Garcia-Alonso et al., in 2014. Since then, DT has been discussed in many countries and regions as a concept to prevent

duplication of regulatory studies without compromising quality of the ERA. However, despite its usefulness and scientific justification, DT is not well adopted at this time and many regulatory agencies around the world require additional in-country CFT be conducted before approving GM plants. Based on the current circumstances, the authors organized a parallel session entitled “*Introduction and Scientific Justification of DT for CFT for the ERA of GM plants*” at 16th ISBR (the International Society for Biosafety Research). This session mainly consisted of the following three parts. The first two speakers, Andrew Roberts and Abigail Simmons provided an overview of DT and examples of conditions for the transportability of field data/conclusions advocated in the peer-reviewed scientific journals. Next, the current status of DT adoption in some countries/regions such as Japan and Africa, and a theoretical case study for Argentina were introduced by Kazuyuki Hiratsuka, Douglas Miano, and Facundo Vesprini, respectively. Lastly, a risk hypothesis-based approach for DT which was developed in advance by the five speakers of this parallel session, was introduced. During the discussion, there was a common understanding that transition to the risk hypothesis-based approach for DT was scientifically appropriate, considering the accumulated evidences that several countries have conducted confirmatory local CFT for more than 20 years but they have not detected any differences related to the ERA assessment endpoints in GM crops. The risk hypothesis-based approach for DT introduced here is expected to play an important role in discussions on the implementation of DT in various parts of the world in the future. <https://www.frontiersin.org/articles/10.3389/fbioe.2024.1359388/full>

Fan J., Zhang Y., Li W., Li Z. et al. (2024): **Multidimensional Optimization of *Saccharomyces cerevisiae* for Carotenoid Overproduction**. BioDesign Research 6, 0026 | DOI: [10.34133/bdr.0026](https://doi.org/10.34133/bdr.0026)

Microbial synthesis of carotenoids is a highly desirable alternative to plant extraction and chemical synthesis. In this study, we investigated multidimensional strategies to improve the carotenoid synthesis in the industrial workhorse of *Saccharomyces cerevisiae*. First, we rewired the yeast central metabolism by optimizing non-oxidative glycolysis pathway for an improved acetyl-CoA supply. Second, we restricted the consumption of farnesyl pyrophosphate (FPP) by the down-regulation of squalene synthase using the PEST degron. Third, we further explored the human lipid binding/transfer protein saposin B (hSapB)-mediated metabolic sink for an enhanced storage of lipophilic carotenoids. Last, the copper-induced GAL expression system was engineered to function in the yeast–peptone–dextrose medium for an increased biomass accumulation. By combining the abovementioned strategies, the final engineered yeast produced 166.79 ± 10.43 mg/l β -carotene in shake flasks, which was nearly 5-fold improvement of the parental carotenoid-producing strain. Together, we envision that multidimensional strategies reported here might be applicable to other hosts for the future industrial development of carotenoid synthesis from renewable feedstocks. <https://spj.science.org/doi/10.34133/bdr.0026>

EFSA

GMO Panel (2024): Assessment of genetically modified maize DP202216 for food and feed uses, under Regulation (EC) No 1829/2003 (application EFSA-GMO-NL-2019-159). EFSA Journal, 22(3), e8655. <https://doi.org/10.2903/j.efsa.2024.8655> <https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2024.8655>

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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