

# Sunday Evening News No 368

2024-03-11 – 2024-03-17

Compiled and edited by **BGF** Jany



## Meetings – Conferences / Veranstaltungen - Konferenzen

Zur Erinnerung

**DFG: Die Zukunft der Ernährung: Welche Rolle spielen gentechnisch veränderte Pflanzen?**

Talkreihe „Enter Science“ thematisiert „grüne Gentechnik“ / Expert\*innen und Publikum diskutieren am 20. März in der Bundeskunsthalle

<https://www.dfg.de/de/service/presse/pressemitteilungen/2024/pressemitteilung-nr-07>

**Forum Institut: 11th International Conference: IP Protection for Plant Innovation 2024**

<https://www.forum-institut.de/seminar/24061130-ip-protection-for-plant-innovation-2024>

## Press Releases -Media / Presse- und Medienberichte

**Piller W.: Gentechnik im Pflanzenbau: Gottesgabe oder Teufelswerk?**

<https://www.wochenblatt-dlv.de/feld-stall/pflanzenbau/gentechnik-pflanzenbau-gottesgabe-teufelswerk-576120>

**Spencer D. & Jana Gäbert J.: Pflanzenzüchtung vor dem Aktenberg - Neuregulierung von NGTs in der EU: Bitte lesen Sie das Kleingedruckte!**

DE: <https://progressive-agrarwende.org/pflanzenzuechtung-vor-dem-aktenberg/>

EN: <https://oekoprogramm.org/en/plant-breeding-in-the-eu-at-a-regulatory-impasse/>

**GM Watch: European Commission turns its back on science to back new GMO deregulation**

<https://gmwatch.org/en/106-news/latest-news/20392>

**Kilger U.: The EU Commission strikes again – New patent ban?**

<https://european-biotechnology.com/up-to-date/backgrounds-stories/story/the-eu-commission-strikes-again-new-patent-ban.html>

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 11-2024

## Publications – Publikationen

**Bohle F., Schneider R., Mundorf J., Zühl L., Simon S., Engelhard M. (2024): Where does the EU path on new genomic techniques lead us?** Front. Genome Ed. 6: 1377117 | doi: 10.3389/fgeed

Recently, the European Commission (EC) published a regulatory proposal on plants generated with new genomic techniques (NGTs) (5 July 2023). According to this proposal, NGT plant applications are categorized into category 1 NGT (NGT1) and category 2 NGT (NGT2) based on their molecular characteristics, which diverges from the current legislation centered around Directive 2001/18/EC. To demonstrate where the path of the proposal leads to in practice, we applied the proposed criteria for categorization to a list of NGT plant applications currently in the commercialization pipeline. Combining literature research and a descriptive statistical approach, we can show that 94% of the plant applications affected by the EC proposal, would be classified as NGT1 and thus would receive market approval without risk assessment, monitoring, and sufficient labeling provisions. The remaining 6% of applications would be classified as NGT2 plants, for which, in deviation from the current regulation, an adapted risk assessment is proposed. Screening of the intended traits in the pipeline highlights that certain NGT1 plants can pose similar environmental risks (e.g., invasiveness) to other genetically modified organisms (GMOs), as defined in Directive 2001/18/EC. For example, NGT1 applications based on RNA interference technology can exhibit insecticidal effects with potential side effects on non-target organisms (i.e., other insects). Our quantitative and case-specific elaboration of how the current EC regulatory proposal would affect the environment, health, and consumer protection will be informative for decision-makers and politicians.

<https://www.frontiersin.org/articles/10.3389/fgeed.2024.1377117/full>

**Purnhagen, K.P. and Molitorisová A. (2024): Citizen Jury on New Genomic Techniques - Final Report ( 2024)** February 2024, Available at SSRN: <https://ssrn.com/abstract=4719681>

Kim D., Kock M.A., Lamping M., Batista R.H.D., Hilty R.M., Slowinski P., Steinhardt M. (2024): **New Genomic Techniques and Intellectual Property Law: Challenges and Solutions for the Plant Breeding Sector** – Position Statement of the Max Planck Institute for Innovation and Competition: Munich, 8 January 2024 *GRUR International*, ikae017, <https://doi.org/10.1093/grurint/ikae017>

On 5 July 2023, the European Commission proposed a regulation aiming to ease the requirements for the marketing authorisation of plants obtained through certain new genomic techniques (NGTs) within the European Union (EU). While NGTs are expected to become more attractive to breeders and farmers, the complexity of the intellectual property (IP) landscape surrounding these techniques and resulting products may negatively impact technology diffusion and innovation. Given numerous concerns related to IP protection for NGTs and NGT-derived plants, this Position Statement from the Max Planck Institute for Innovation and Competition presents a set of policy recommendations for facilitating access to and utilisation of IP-protected NGTs and NGT-derived products in the breeding sector.

<https://academic.oup.com/grurint/advance-article/doi/10.1093/grurint/ikae017/7627934?searchresult=1&login=false>

Goodman R.E. (2024): **Twenty-eight years of GM Food and feed without harm: why not accept them?** *GM Crops & Food*, 15 :1, 40-50, DOI: [10.1080/21645698.2024.2305944](https://doi.org/10.1080/21645698.2024.2305944)

Since the first genetically engineered or modified crops or organisms (GMO) were approved for commercial production in 1995, no new GMO has been proven to be a hazard or cause harm to human consumers. These modifications have improved crop efficiency, reduced losses to insect pests, reduced losses to viral and microbial plant pathogens and improved drought tolerance. A few have focused on nutritional improvements producing beta carotene in Golden Rice. Regulators in the United States and countries signing the CODEX Alimentarius and Cartagena Biosafety agreements have evaluated human and animal food safety considering potential risks of allergenicity, toxicity, nutritional and anti-nutritional risks. They consider risks for non-target organisms and the environment. There are no cases where post-market surveillance has uncovered harm to consumers or the environment including potential transfer of DNA from the GMO to non-target organisms. In fact, many GMOs have helped improve production, yield and reduced risks from chemical insecticides or fungicides. Yet there are generic calls to label foods containing any genetic modification as a GMO and refusing to allow GM events to be labeled as organic. Many African countries have accepted the Cartagena Protocol as a tool to keep GM events out of their countries while facing food insecurity. The rationale for those restrictions are not rational. Other issues related to genetic diversity, seed production and environmental safety must be addressed. What can be done to increase acceptance of safe and nutritious foods as the population increases, land for cultivation is reduced and energy costs soar?

<https://doi.org/10.1080/21645698.2024.2305944>

Hackfort, S. (2024): **Democratization through precision technologies? Unveiling power, participation, and property rights in the agricultural bioeconomy.** *Front. Polit. Sci., Sec. Politics of Technology Volume 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://doi.org/10.3389/fpos.2024.1363044>

Sarma, S., Thomas, S.C. & Kamat, R. (2024): **It takes two to tango with CRISPR: a history and overview of augmenting the technology for genetic engineering.** *Proc.Indian Natl. Sci. Acad.* | <https://doi.org/10.1007/s43538-024-00251-8>

The revolutionary CRISPR genome editing system has undoubtedly reshaped the landscape of molecular biology and biotechnology. While CRISPR offers unprecedented precision and versatility, its intrinsic efficiency has been a subject of ongoing exploration and refinement. Recent years have witnessed a growing focus on harnessing the power of CRISPR in synergy with complementary techniques such as nanoparticles, liposomes, genetic engineering methods viz. Cre-loxP, FRT, RNA interference, AAVS1 etc. to substantially enhance gene editing capabilities. The current study aims to shed light on the innovative approaches and strategies that have emerged to bolster CRISPR's efficiency through synergistic partnerships with other molecular tools. We describe

the advantages, and potential challenges associated with these collaborative approaches. Additionally, we highlight recent breakthroughs and promising applications that have arisen from the amalgamation of CRISPR with these techniques. The augmentation of CRISPR through these synergistic partnerships not only addresses efficiency concerns but also opens new horizons for the precise manipulation of the genome, fostering exciting prospects in basic research and therapeutic interventions.

<https://link.springer.com/article/10.1007/s43538-024-00251-8>

Satasiya, P., Patel, S., Patel, R. et al. (2024): **Meta-analysis of identified genomic regions and candidate genes underlying salinity tolerance in rice (*Oryza sativa* L.)**. Sci Rep 14, 5730

<https://doi.org/10.1038/s41598-024-54764-9>

Rice output has grown globally, yet abiotic factors are still a key cause for worry. Salinity stress seems to have the more impact on crop production out of all abiotic stresses. Currently one of the most significant challenges in paddy breeding for salinity tolerance with the help of QTLs, is to determine the QTLs having the best chance of improving salinity tolerance with the least amount of background noise from the tolerant parent. Minimizing the size of the QTL confidence interval (CI) is essential in order to primarily include the genes responsible for salinity stress tolerance. By considering that, a genome-wide meta-QTL analysis on 768 QTLs from 35 rice populations published from 2001 to 2022 was conducted to identify consensus regions and the candidate genes underlying those regions responsible for the salinity tolerance, as it reduces the confidence interval (CI) to many folds from the initial QTL studies. In the present investigation, a total of 65 MQTLs were extracted with an average CI reduced from 17.35 to 1.66 cM including the smallest of 0.01 cM. Identification of the MQTLs for individual traits and then classifying the target traits into correlated morphological, physiological and biochemical aspects, resulted in more efficient interpretation of the salinity tolerance, identifying the candidate genes and to understand the salinity tolerance mechanism as a whole. The results of this study have a huge potential to improve the rice genotypes for salinity tolerance with the help of MAS and MABC.

<https://www.nature.com/articles/s41598-024-54764-9>

Das, H.K., Kaushik, M. & Mandal, P.K. (2024): **Inadequate lysine content of wheat endosperm proteins-possibility of correcting it by CRISPR-Cas system of genome editing**. J. Plant Biochem. Biotechnol. |

<https://doi.org/10.1007/s13562-024-00881-5>

Proteins in endosperms of mature wheat seeds contain ~ 2.5% lysine. Proteins in endosperms of immature wheat seeds after 8 days of anthesis, interestingly contain ~ 8% lysine. Wheat endosperm proteins collected 15 days after anthesis, when treated with proteases isolated from endosperms 20 days after anthesis, released 10.2% lysine and 5.6% leucine. In contrast, the same proteins, when treated with proteases isolated from endosperms 8 days after anthesis, released 7.0% lysine and 12.0% leucine. The protease C, that could cleave polylysine, but could not cleave polyaspartic acid and polyglutamic acid, appeared only at 16 days after anthesis and continued to be present till 28 days after anthesis. Soybean trypsin inhibitor inhibited the activity of protease C completely. Transcriptome analysis of developing wheat seeds has revealed the presence of three major transcripts containing trypsin-like domains. The amounts of these three transcripts increased from 2 weeks after anthesis to 4 weeks after anthesis and decreased thereafter. If a wheat variety could be created which is devoid of protease C or the above mentioned trypsin like proteases, the lysine content of endosperm proteins of that variety would possibly be higher. This could today be achieved by using the CRISPR-Cas systems of genome editing.

<https://link.springer.com/article/10.1007/s13562-024-00881-5>

Rengasamy, B., Manna, M., Thajuddin, N.B. et al. (2024): **Breeding rice for yield improvement through CRISPR/Cas9 genome editing method: current technologies and examples**. Physiol Mol Biol Plants |

<https://doi.org/10.1007/s12298-024-01423-y>

The impending climate change is threatening the rice productivity of the Asian subcontinent as instances of crop failures due to adverse abiotic and biotic stress factors are becoming common occurrences. CRISPR-Cas9 mediated genome editing offers a potential solution for improving rice yield as well as its stress adaptation. This technology allows modification of plant's genetic elements and is not dependent on foreign DNA/gene insertion for incorporating a particular trait. In this review, we have discussed various CRISPR-Cas9 mediated genome editing tools for gene knockout, gene knock-in, simultaneously disrupting multiple genes by multiplexing, base editing and prime editing the genes. The review here also presents how these genome editing technologies have been employed to improve rice productivity by directly targeting the yield related genes or by indirectly manipulating various abiotic and biotic stress responsive genes. Lately, many countries treat genome-edited crops as non-GMOs because of the absence of foreign DNA in the final product. Thus, genome edited rice plants with improved yield attributes and stress resilience are expected to be accepted by the public and solve food crisis of a major portion of the globe.

<https://link.springer.com/article/10.1007/s12298-024-01423-y>

Lu G., Liu P., Wu Q., Zhang S. et al. (2024): **Sugarcane breeding: a fantastic past and promising future driven by technology and methods**. Front. Plant Sci., Sec. Plant Breeding 15 |

<https://doi.org/10.3389/fpls.2024.1375934>

Sugarcane is the most important sugar and energy crop in the world. During sugarcane breeding, technology is the requirement and methods are the means. As we know, seed is the cornerstone of the development of the sugarcane industry. Over the past century, with the advancement of technology and the expansion of methods, sugarcane breeding has continued to improve, and sugarcane production has realized a leaping

growth, providing a large amount of essential sugar and clean energy for the long-term mankind development, especially in the face of the future threats of world population explosion, reduction of available arable land, and various biotic and abiotic stresses. Moreover, due to narrow genetic foundation, serious varietal degradation, lack of breakthrough varieties, as well as long breeding cycle and low probability of gene polymerization, it is particularly important to realize the leapfrog development of sugarcane breeding by seizing the opportunity for the emerging Breeding 4.0, and making full use of modern biotechnology including but not limited to whole genome selection, transgene, gene editing, and synthetic biology, combined with information technology such as remote sensing and deep learning. In view of this, we focus on sugarcane breeding from the perspective of technology and methods, reviewing the main history, pointing out the current status and challenges, and providing a reasonable outlook on the prospects of smart breeding.  
<https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2024.1375934/full>

Durand, K., An, H. & Nam, K. (2024): Invasive fall armyworms are corn strain. *Sci Rep* 14, 5696 (2024). <https://doi.org/10.1038/s41598-024-56301-0>

The fall armyworm (*Spodoptera frugiperda*) is one of the major pest insects in diverse crop plants, including maize, rice, and cotton. While the fall armyworm is native to North and South America, its invasion was first reported in West Africa in 2016. Since then, this species has rapidly spread across Sub-Saharan Africa, Asia, and Oceania, as well as Egypt and Cyprus. The fall armyworm is composed of two sympatric strains, the corn and rice strains, designated to their preferred host plants, in native areas. It remains surprisingly unclear whether invasive fall armyworms belong to the corn strain, rice strain, or hybrids of the two, despite a large number of population genetics studies. In this study, we performed population genomics analyses using globally collected 116 samples to identify the strains of invasive fall armyworms. We observed that invasive fall armyworms are genomically most similar to the corn strain. The reconstructed phylogenetic tree supports the hypothesis that invasive fall armyworms originated from the corn strain. All genomic loci of invasive populations exhibit higher genetic similarity to the corn strains compared to the rice strains. Furthermore, we found no evidence of gene flow from rice strains to invasive populations at any genomic locus. These results demonstrate that invasive fall armyworms belong to the corn strain. These results suggest that invasive fall armyworms likely have very limited potential to infest rice. Therefore, the management plan should primarily focus on crops preferred by the corn strain.

<https://www.nature.com/articles/s41598-024-56301-0>

Sperschneider, J., Yildirim, G., Rizzi, Y.S. et al. (2023): **Arbuscular mycorrhizal fungi heterokaryons have two nuclear populations with distinct roles in host–plant interactions.**

*Nat Microbiol* 8, 2142–2153 | <https://doi.org/10.1038/s41564-023-01495-8>

Arbuscular mycorrhizal fungi (AMF) are prominent root symbionts that can carry thousands of nuclei deriving from two parental strains in a large syncytium. These co-existing genomes can also vary in abundance with changing environmental conditions. Here we assemble the nuclear genomes of all four publicly available AMF heterokaryons using PacBio high-fidelity and Hi-C sequencing. We find that the two co-existing genomes of these strains are phylogenetically related but differ in structure, content and epigenetics. We confirm that AMF heterokaryon genomes vary in relative abundance across conditions and show this can lead to nucleus-specific differences in expression during interactions with plants. Population analyses also reveal signatures of genetic exchange indicative of past events of sexual reproduction in these strains. This work uncovers the origin and contribution of two nuclear genomes in AMF heterokaryons and opens avenues for the improvement and environmental application of these strains.

<https://www.nature.com/articles/s41564-023-01495-8>

Habig M., Grasse A.V., Müller J, +2 , and Cremer S. (2024): **Frequent horizontal chromosome transfer between asexual fungal insect pathogens.** *PNAS* | DOI: [10.1073/pnas.2316284121](https://doi.org/10.1073/pnas.2316284121)

Entire chromosomes are typically only transmitted vertically from one generation to the next. The horizontal transfer of such chromosomes has long been considered improbable, yet gained recent support in several pathogenic fungi where it may affect the fitness or host specificity. To date, it is unknown how these transfers occur, how common they are, and whether they can occur between different species. In this study, we show multiple independent instances of horizontal transfers of the same accessory chromosome between two distinct strains of the asexual entomopathogenic fungus *Metarhizium robertsii* during experimental co-infection of its insect host, the Argentine ant. Notably, only the one chromosome—but no other—was transferred from the donor to the recipient strain. The recipient strain, now harboring the accessory chromosome, exhibited a competitive advantage under certain host conditions. By phylogenetic analysis, we further demonstrate that the same accessory chromosome was horizontally transferred in a natural environment between *M. robertsii* and another congeneric insect pathogen, *Metarhizium guizhouense*. Hence, horizontal chromosome transfer is not limited to the observed frequent events within species during experimental infections but also occurs naturally across species. The accessory chromosome that was transferred contains genes that may be involved in its preferential horizontal transfer or support its establishment. These genes encode putative histones and histone-modifying enzymes, as well as putative virulence factors. Our study reveals that both intra- and interspecies horizontal transfer of entire chromosomes is more frequent than previously assumed, likely representing a not uncommon mechanism for gene exchange.

<https://www.pnas.org/doi/10.1073/pnas.2316284121>

Nguyen D.T., Mitchell D.A., van der Donk W. A. (2024): **Genome Mining for New Enzyme Chemistry.** *ACS Catal.* 2024, 14, XXX, 4536–4553 | <https://doi.org/10.1021/acscatal.3c06322>

A revolution in the field of biocatalysis has enabled scalable access to compounds of high societal values using enzymes. The construction of biocatalytic routes relies on the reservoir of available enzymatic transformations. A review of uncharacterized proteins predicted from genomic sequencing projects shows that a treasure trove of enzyme chemistry awaits to be uncovered. This Review highlights enzymatic transformations discovered through various genome mining methods and showcases their potential future applications in biocatalysis.  
<https://pubs.acs.org/doi/10.1021/acscatal.3c06322>

Silva F.F., Rabelo N.G., Reis K.C., Cassiano C.S.S. et al. (2024): **Foreshadowing an exponential market: A brief story, applications, and perspectives of CRISPR/Cas system for the production of (hemi-)cellulases in filamentous fungi.** Fungal Biology Reviews 49, 100366 | <https://doi.org/10.1016/j.fbr.2024.100366>

The demand to develop protein production systems that are both economically and scientifically viable is reflected in the global scenario, where filamentous fungi, due to their interesting characteristics such as the high capacity to secrete proteins into the culture medium, growth in relatively simple substrates and robust post-translational machinery, among others, are presented as promising alternatives for the creation and establishment of these systems. Currently, these organisms produce a wide range of proteins, such as glycosidases, lipases, and proteases, for example. Scientific and technological development has increasingly allowed the evolution of molecular biology techniques that facilitate the genetic modification of organisms, thus, stimulating the establishment of new protein production systems. Amongst these techniques, it is possible to highlight the CRISPR/Cas system, a relatively simple, low-cost, and high-efficient tool for genetic modifications. Filamentous fungi, organisms widely used for protein production, have been used in a relatively low number of studies related to the production of (hemi-)cellulases using the CRISPR/Cas system as a genomic editing tool. (Hemi-)cellulases, enzymes that catalyze the breakdown of saccharides, are a class of enzymes that are highly researched and applied in several biotechnological areas in order to obtain a wide range of value-added bioproducts, such as bioethanol, for example. In this context, this review aims to illustrate the scenario of the application of the CRISPR/Cas technique for the production of (hemi-)cellulases, highlighting the main studies to date and the perspectives of a market that tends to grow exponentially in the coming years.  
<https://www.sciencedirect.com/science/article/abs/pii/S1749461324000113>

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Wie immer wird für Hinweise und der Zusendung von Publikationen und sonstigen Informationen gedankt. pdf-Dateien können meist direkt aus den links heruntergeladen werden.

*As always, I thank you all for hints and for publications. Most of the pdf files can be downloaded directly from the links.*

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