

Sunday Evening News No 342

2023-09-04. – 2023-09-10

Compiled and edited by **BGF** Jany



Meetings - Veranstaltungen

Konferenz zur besseren Nutzung von Forschungsdaten erstmals in Karlsruhe

Veranstaltungsort: Audimax auf dem Campus Süd des KIT, Gebäude 30.95, Straße am Forum 1, 76131 Karlsruhe. Dienstag, 12. September 2023

<https://idw-online.de/de/news819809>

VBIO: **Biodiversität und Klimaveränderung und deren Wechselwirkung** am 26. September um 17:00 Uhr. Weitere Informationen und den link zur Anmeldung finden Sie hier:

<https://www.vbio.de/aktuelles/details/vbio-vortragsreihe-zum-thema-biodiversitaet-und-klimaveraenderung-und-deren-wechselwirkung>

Press Releases -Media / Presse- und Medienberichte

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

<https://www.fei-bonn.de/presse/pressemitteilungen/pm-20230908-belitz-medaille-jany>

VBIO-WGG: Vorschlag der EU-Kommission zu Neuen Genomischen Techniken berücksichtigt Empfehlungen und Interessen der Wissenschaft

<https://idw-online.de/de/news820281>

und [▶ hier das Statement](#):

Der WGG hat seine Meinung gesagt:

https://ec.europa.eu/info/law/better-regulation/have-your-say/initiatives/13119-Legislation-for-plants-produced-by-certain-new-genomic-techniques/F3436041_de

Nachgang zur Festveranstaltung zur 250. ZKBS-Sitzung

https://www.zkbs-online.de/ZKBS/SharedDocs/00_Fachmeldungen/2023/2023_09_05_Fa_ZKBS_250.html

Willingmann: Sollten Chancen genomischer Verfahren nutzen

<https://www.faz.net/agenturmeldungen/dpa/willingmann-sollten-chancen-genomischer-verfahren-nutzen-19161492.html>

Landtag Sachsen-Anhalt: Mit Gentechnik zur Ernährungssicherheit

<https://www.landtag.sachsen-anhalt.de/ad-biotechnologie>

Neubert K : Neue Gentechnik: „Grüne sollen Widerstände abbauen“

<https://www.euractiv.de/section/landwirtschaft-und-ernahrung/news/neue-gentechnik-gruene-sollen-widerstaende-abbauen/>

Pelekanaki M.: Griechischer Agrarminister unterstützt neue Gentechnik

<https://www.euractiv.de/section/europa-kompakt/news/griechischer-agrarminister-unterstuetzt-neue-gentechnik/>

EU ministers discuss how to apply new technologies for a more sustainable agriculture

<https://spanish-presidency.consilium.europa.eu/en/news/informal-ministerial-meeting-agriculture-cordoba-5-september/>

Dahm J.: Agrifood Brief: Özdemissing in action

<https://www.euractiv.com/section/agriculture-food/news/agrifood-brief-ozdemissing-in-action/>

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

Hansen C. W. and Wingender A.M. (2023): **National and Global Impacts of Genetically Modified Crops**. *American Economic Review: Insights*, 5 (2): 224-40. DOI: 10.1257/aeri.20220144

We estimate the impact of genetically modified (GM) crops on countrywide yields, harvested area, and trade using a triple-differences rollout design that exploits variation in the availability of GM seeds across crops, countries, and time. We find positive impacts on yields, especially in poor countries. Our estimates imply that without GM crops, the world would have needed 3.4 percent additional cropland to keep global agricultural output at its 2019 level. We also find that bans on GM cultivation have limited the global gain from GM adoption to one-third of its potential. Poor countries would benefit most from lifting such bans. <https://www.aeaweb.org/articles?id=10.1257/aeri.20220144>

Weisenfeld U., Hauerwaas A., Elshiewy O., Halder P., Wessler J., Cingiz K., Broer J. (2023): **Beyond plastic – Consumers prefer food packaging derived from genetically modified plants**. *Research Policy* 52, 104883 | <https://doi.org/10.1016/j.respol.2023.104883>

The technology of genetically modified organisms (GMO) and especially genetically modified plants (GMP) applied in agriculture is a key element in a bioeconomy-based sustainability transition. However, consumers in many European countries allegedly disapprove of 'green biotechnology'. Drawing on innovation adoption and risk perception literature, we explore the acceptance of GMP-based food packaging. Fossil-fuel-based production and plastic waste have become a major concern in many societies, and GMP-based technologies might offer solutions. Taking fully degradable material based on GMP as an example to replace conventional plastic in many applications, we present new insights into the GMP debate using a choice-based conjoint analysis in four European countries. Our results show that GMP-based packaging material is preferred to conventional plastic packaging in all countries. We present implications for research policies. <https://www.sciencedirect.com/science/article/pii/S0048733323001671?via%3Dihub>

Fristoe, T.S., Bleilevens, J., Kinlock, N.L. et al. (2023): **Evolutionary imbalance, climate and human history jointly shape the global biogeography of alien plants**. *Nat Ecol Evol* <https://doi.org/10.1038/s41559-023-02172-z>

Human activities are causing global biotic redistribution, translocating species and providing them with opportunities to establish populations beyond their native ranges. Species originating from certain global regions, however, are disproportionately represented among naturalized aliens. The evolutionary imbalance hypothesis posits that differences in absolute fitness among biogeographic divisions determine outcomes when biotas mix. Here, we compile data from native and alien distributions for nearly the entire global seed plant flora and find that biogeographic conditions predicted to drive evolutionary imbalance act alongside climate and anthropogenic factors to shape flows of successful aliens among regional biotas. Successful aliens tend to originate from large, biodiverse regions that support abundant populations and where species evolve against a diverse backdrop of competitors and enemies. We also reveal that these same native distribution characteristics are shared among the plants that humans select for cultivation and economic use. In addition to influencing species' innate potentials as invaders, we therefore suggest that evolutionary imbalance shapes plants' relationships with humans, impacting which species are translocated beyond their native distributions. <https://www.nature.com/articles/s41559-023-02172-z>

Pandolfini T., Mezzetti B. and Folta K. (2023): **Editorial: Advances in genetic engineering strategies for fruit crop breeding, volume II**. *Front. Plant Sci.* 14:1264914. doi: 10.3389/fpls.2023.1264914 <https://www.frontiersin.org/articles/10.3389/fpls.2023.1264914/full>

Sundaram L.S., Ajioka J.W., Molloy J.C. (2023): **Synthetic biology regulation in Europe: containment, release and beyond**. *Synthetic Biology*, 8 (1), ysad009 | <https://doi.org/10.1093/synbio/ysad009>

While synthetic biology is hoped to hold promise and potential to address pressing global challenges, the issue of regulation is an under-appreciated challenge. Particularly in Europe, the regulatory frameworks involved are rooted in historical concepts based on containment and release. Through a series of case studies including a field-use biosensor intended to detect arsenic in well water in Nepal and Bangladesh, and insects engineered for sterility, we explore the implications that this regulatory and conceptual divide has had on the deployment of synthetic biology projects in different national contexts. We then consider some of the broader impacts that regulation can have on the development of synthetic biology as a field, not only in Europe but also globally, with a particular emphasis on low- and middle-income countries. We propose that future regulatory adaptability would be increased by moving away from a containment and release dichotomy and toward a more comprehensive assessment that accounts for the possibility of varying degrees of 'contained release' <https://academic.oup.com/synbio/article/8/1/ysad009/7133777?login=true>

Flaherty, D., Hoefnagel I., Hogervorst P.A.M., Klaassen P. (2023): **Transitioning to a Circular Economy Safely and Sustainably: A Qualitative Exploration of System Barriers and Drivers for Industrial Biotechnology in the EU.** Available at SSRN: <https://ssrn.com/abstract=4534460> or <http://dx.doi.org/10.2139/ssrn.4534460>

Innovations in industrial biotechnology promise great potential for contributing to the biological cycle of the circular economy. However, the environmental impacts of industrial biotechnology and sustainability benefits differ greatly depending on the type of biomass, the microorganism being used, and the biobased material being made. To prevent ill effects like land use changes, or the unintended environmental release of potentially harmful microorganisms, it is important to consider the values of safety (for human health and the environment), and wider environmental and planetary sustainability when designing industrial biotechnology applications for the circular economy. Transitions such as the one from a linear to a circular economy are shaped in the dynamics between political, societal, economic, and technological developments. Thus, for industrial biotechnological innovations to enter a circular economy transition, developments in knowledge, regulations, finance, economy, behavior, and culture are necessary. Stakeholders working with industrial biotechnology innovation, policies, and within the industrial biotechnology field are therefore important actors to consider when exploring the potential of industrial biotechnology in the circular economy transition. The main goal of this work is to explore those actors' perceptions of the barriers and drivers of legislation, culture, and the market for industrial biotechnology to provide context into whether, and if so, how industrial biotechnology might eventually reduce our dependency on fossil-based raw materials and further enable the circular economy. Results indicate that tensions occur between the goals of safety and sustainability in practice, policy, legislation, and culture. Within the European Union certain market, policy, and societal actors have historically been reluctant to support the use of genetically modified microorganisms for industrial biotechnology. This hinders early research and development and appears to be preventing optimally sustainable industrial biotechnology applications from entering the market, which hinders the realization of sustainability goals. But the tide might be changing, as market and societal actors are learning how to navigate the tensions between safety and sustainability, they more openly underscore the sustainability benefits of using genetically modified microorganisms over safety concerns. However, for industrial biotechnology to contribute to a timely circular economy transition, European policy and legislation must accelerate the development of integrated policies to address safety, sustainability, and circularity needs.

https://papers.ssrn.com/sol3/papers.cfm?abstract_id=4534460

Chaudhary N., Salgotra R.K., Chauhan B.S. (2023): **Genetic Enhancement of Cereals Using Genomic Resources for Nutritional Food Security.** *Genes* 2023, 14(9), 1770 |

<https://doi.org/10.3390/genes14091770>

Advances in genomics resources have facilitated the evolution of cereal crops with enhanced yield, improved nutritional values, and heightened resistance to various biotic and abiotic stresses. Genomic approaches present a promising avenue for the development of high-yielding varieties, thereby ensuring food and nutritional security. Significant improvements have been made within the omics domain, specifically in genomics, transcriptomics, and proteomics. The advent of Next-Generation Sequencing (NGS) techniques has yielded an immense volume of data, accompanied by substantial progress in bioinformatic tools for proficient analysis. The synergy between genomics and computational tools has been acknowledged as pivotal for unravelling the intricate mechanisms governing genome-wide gene regulation. Within this review, the essential genomic resources are delineated, and their harmonization in the enhancement of cereal crop varieties is expounded upon, with a paramount focus on fulfilling the nutritional requisites of humankind. Furthermore, an encompassing compendium of the available genomic resources for cereal crops is presented, accompanied by an elucidation of their judicious utilization in the advancement of crop attributes.

<https://www.mdpi.com/2073-4425/14/9/1770>

Ramu, P., Srivastava, R.K., Sanyal, A. et al. (2023): **Improved pearl millet genomes representing the global heterotic pool offer a framework for molecular breeding applications.** *Commun Biol* 6, 902 <https://doi.org/10.1038/s42003-023-05258-3>

High-quality reference genome assemblies, representative of global heterotic patterns, offer an ideal platform to accurately characterize and utilize genetic variation in the primary gene pool of hybrid crops. Here we report three platinum grade *de-novo*, near gap-free, chromosome-level reference genome assemblies from the active breeding germplasm in pearl millet with a high degree of contiguity, completeness, and accuracy. An improved Tift genome (Tift23D₂B₁-P1-P5) assembly has a contig N50 ~ 7,000-fold (126 Mb) compared to the previous version and better alignment in centromeric regions. Comparative genome analyses of these three lines clearly demonstrate a high level of collinearity and multiple structural variations, including inversions greater than 1 Mb. Differential genes in improved Tift genome are enriched for serine O-acetyltransferase and glycerol-3-phosphate metabolic process which play an important role in improving the nutritional quality of seed protein and disease resistance in plants, respectively. Multiple marker-trait associations are identified for a range of agronomic traits, including grain yield through genome-wide association study. Improved genome assemblies and marker resources developed in this study provide a comprehensive framework/platform for future applications such as marker-assisted selection of mono/oligogenic traits as well as whole-genome prediction and haplotype-based breeding of complex traits.

<https://www.nature.com/articles/s42003-023-05258-3>

Zhang, Z., Huang, J., Yao, Y. et al. (2023): **Environmental impacts of cotton and opportunities for improvement.** Nat Rev Earth Environ | <https://doi.org/10.1038/s43017-023-00476-z>

Cotton — supplying approximately a quarter of global textile fibres — has various environmental impacts, including water use, toxicity, eutrophication and greenhouse gas emissions. In this Review, we identify these impacts across multiple life cycle stages. Environmental impacts at the cultivation stage depend on levels of irrigation, pesticide and fertilizer applications. At the textile manufacturing stage, impacts depend on energy infrastructure and manufacturing technologies. At the use phase, impacts depend on consumer habits related to buying, washing, drying and ironing. Depending on the impact category and country, cotton cultivation, manufacturing or use can dominate such impacts. For example, the use phase dominates greenhouse gas emissions in countries with carbon-intensive energy grids. Use of alternative fibres has the potential to reduce these environmental impacts, particularly jute and flax, which have much lower water demands. Opportunities for farmers, manufacturers and consumers to improve the environmental sustainability of cotton textiles include, among others, improving water-use efficiency in agriculture, innovative recycling and laundering less frequently. Future cotton sustainability assessments are needed to fill data gaps related to developing and emerging countries, the number of uses of a cotton garment and further environmental impacts such as salinization, as well as socio-economic impacts.

<https://www.nature.com/articles/s43017-023-00476-z>

Vercellino R.B., Hernández F., Presotto A. (2023): **The role of intraspecific crop–weed hybridization in the evolution of weediness and invasiveness: Cultivated and weedy radish (*Raphanus sativus*) as a case study.** Am J Bot. 2023; e16217 |

<https://doi.org/10.1002/ajb2.16217>

Premise: The phenotype of hybrids between a crop and its wild or weed counterpart is usually intermediate and maladapted compared to that of their parents; however, hybridization has sometimes been associated with increased fitness, potentially leading to enhanced weediness and invasiveness. Since the ecological context and maternal genetic effects may affect hybrid fitness, they could influence the evolutionary outcomes of hybridization. Here, we evaluated the performance of first-generation crop–weed hybrids of *Raphanus sativus* and their parents in two contrasting ecological conditions.

Methods: Using experimental hybridization and outdoor common garden experiments, we assessed differences in time to flowering, survival to maturity, plant biomass, and reproductive components between bidirectional crop–weed hybrids and their parents in agrestal (wheat cultivation, fertilization, weeding) and ruderal (human-disturbed, uncultivated area) conditions over 2 years. Results: Crop, weeds, and bidirectional hybrids overlapped at least partially during the flowering period, indicating a high probability of gene flow. Hybrids survived to maturity at rates at least as successful as their parents and had higher plant biomass and fecundity, which resulted in higher fitness compared to their parents in both environments, without any differences associated with the direction of the hybridization.

Conclusions: Intraspecific crop–weed hybridization, regardless of the cross direction, has the potential to promote weediness in weedy *R. sativus* in agrestal and ruderal environments, increasing the chances for introgression of crop alleles into weed populations. This is the first report of intraspecific crop–weed hybridization in *R. sativus*.

<https://bsapubs.onlinelibrary.wiley.com/doi/10.1002/ajb2.16217>

Gu, Z., Gong, J., Zhu, Z. et al. (2023): **Structure and function of rice hybrid genomes reveal genetic basis and optimal performance of heterosis.** Nat Genet |

<https://doi.org/10.1038/s41588-023-01495-8>

Exploitation of crop heterosis is crucial for increasing global agriculture production. However, the quantitative genomic analysis of heterosis was lacking, and there is currently no effective prediction tool to optimize cross-combinations. Here 2,839 rice hybrid cultivars and 9,839 segregation individuals were resequenced and phenotyped. Our findings demonstrated that *indica–indica* hybrid-improving breeding was a process that broadened genetic resources, pyramided breeding-favorable alleles through combinatorial selection and collaboratively improved both parents by eliminating the inferior alleles at negative dominant loci.

Furthermore, we revealed that widespread genetic complementarity contributed to *indica–japonica* intersubspecific heterosis in yield traits, with dominance effect loci making a greater contribution to phenotypic variance than overdominance effect loci. On the basis of the comprehensive dataset, a genomic model applicable to diverse rice varieties was developed and optimized to predict the performance of hybrid combinations. Our data offer a valuable resource for advancing the understanding and facilitating the utilization of heterosis in rice.

<https://www.nature.com/articles/s41588-023-01495-8>

Ascurra T., Zhang Y.C., Toghiani L., Hua A. et al. (2023): **Functional diversification of a wild potato immune receptor at its center of origin.** Science 381(6660), 891–897 |

<https://doi.org/10.1126/science.adg5261>.

Plant cell surface pattern recognition receptors (PRRs) and intracellular immune receptors cooperate to provide immunity to microbial infection. Both receptor families have coevolved at an accelerated rate, but the evolution and diversification of PRRs is poorly understood. We have isolated potato surface receptor Pep-13 receptor unit (PERU) that senses Pep-13, a conserved immunogenic peptide pattern from plant pathogenic *Phytophthora* species. PERU, a leucine-rich repeat receptor kinase, is a bona fide PRR that binds Pep-13 and enhances immunity to *Phytophthora infestans* infection. Diversification in ligand binding specificities of PERU can be

traced to sympatric wild tuber-bearing *Solanum* populations in the Central Andes. Our study reveals the evolution of cell surface immune receptor alleles in wild potato populations that recognize ligand variants not recognized by others.

<https://www.science.org/doi/10.1126/science.adg5261>

Gruber K. and Melton L.: (2023): CRISPR upgrades insect proteins for feed

A new generation of companies is pursuing insect larvae as a protein source for animal feed, fertilizer, biofuels and even as ingredients for burgers and shakes. The insects promise to deliver cheaper and more sustainable alternatives to soy and fishmeal, with the added benefit that larvae can be raised on organic waste.

<https://www.nature.com/articles/s41587-023-01902-9>

Trexler, M., Bányai, L., Kerekes, K. et al. (2023): Evolution of termination codons of proteins and the TAG-TGA paradox. Sci Rep 13, 14294 | <https://doi.org/10.1038/s41598-023-41410-z>

In most eukaryotes and prokaryotes TGA is used at a significantly higher frequency than TAG as termination codon of protein-coding genes. Although this phenomenon has been recognized several years ago, there is no generally accepted explanation for the TAG-TGA paradox. Our analyses of human mutation data revealed that out of the eighteen sense codons that can give rise to a nonsense codon by single base substitution, the CGA codon is exceptional: it gives rise to the TGA stop codon at an order of magnitude higher rate than the other codons. Here we propose that the TAG-TGA paradox is due to methylation and hypermutability of CpG dinucleotides. In harmony with this explanation, we show that the coding genomes of organisms with strong CpG methylation have a significant bias for TGA whereas those from organisms that lack CpG methylation use TGA and TAG termination codons with similar probability.

<https://www.nature.com/articles/s41598-023-41410-z>

Liu Y. Chunyan Xu C.; Zhou H. et al, (2023). The crystal structures of Sau3AI with and without bound DNA suggest a self-activation-based DNA cleavage mechanism, Structure | DOI: 10.1016/j.str.2023.08.005

The type II restriction endonuclease Sau3AI cleaves the sequence 5'-GATC-3' in double-strand DNA producing two sticky ends. Sau3AI cuts both DNA strands regardless of methylation status. Here, we report the crystal structures of the active site mutant Sau3AI-E64A and the C-terminal domain Sau3AI-C with a bound GATC substrate. Interestingly, the catalytic site of the N-terminal domain (Sau3AI-N) is spatially blocked by the C-terminal domain, suggesting a potential self-inhibition of the enzyme. Interruption of Sau3AI-C binding to substrate DNA disrupts Sau3AI function, suggesting a functional linkage between the N- and C-terminal domains. We propose that Sau3AI-C behaves as an allosteric effector binding one GATC substrate, which triggers a conformational change to open the N-terminal catalytic site, resulting in the subsequent GATC recognition by Sau3AI-N and cleavage of the second GATC site. Our data indicate that Sau3AI and UbaLAI might represent a new subclass of type IIE restriction enzymes.

[https://www.cell.com/structure/fulltext/S0969-2126\(23\)00283-](https://www.cell.com/structure/fulltext/S0969-2126(23)00283-6)

[6? returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0969212623002836%3Fshowall%3Dtrue](https://www.cell.com/structure/fulltext/S0969-2126(23)00283-6?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0969212623002836%3Fshowall%3Dtrue)

Genotoxicity concerns for base and prime editors in hematopoietic stem cells. Nat Biotechnol (2023). <https://doi.org/10.1038/s41587-023-01916-3>

Although base and prime editors can be highly efficient in human hematopoietic stem cells, we find they can cause adverse cellular responses, including reduced engraftment and the generation of DNA double-strand breaks and genotoxic byproducts, albeit at a lower frequency than Cas9. We also find that base editors increase the genome-wide mutagenic load.

<https://www.nature.com/articles/s41587-023-01916-3>

Yuan, J., Ma L., Wang Y., Xu X. et al. (2023): A recently evolved BAHD acetyltransferase, responsible for bitter soyasaponin A production, is indispensable for soybean seed germination. JIPB | <https://doi.org/10.1111/jipb.13553>

Soyasaponins are major small molecules that accumulate in soybean (*Glycine max*) seeds. Among them, type-A soyasaponins, fully acetylated at the terminal sugar of their C22 sugar chain, are responsible for the bitter taste of soybean-derived foods. However, the molecular basis for the acetylation of type-A soyasaponins remains unclear. Here, we identify and characterize *GmSSAcT1*, encoding a BADH-type soyasaponin acetyltransferase that catalyzes three or four consecutive acetylations on type-A soyasaponins *in vitro* and *in planta*. Phylogenetic analysis and biochemical assays suggest that *GmSSAcT1* likely evolved from acyltransferases present in leguminous plants involved in isoflavonoid acylation. Loss-of-function mutants of *GmSSAcT1* exhibited impaired seed germination, which attribute to the excessive accumulation of null-acetylated type-A soyasaponins. We conclude that *GmSSAcT1* not only functions as a detoxification gene for high accumulation of type-A soyasaponins in soybean seeds but is also a promising target for breeding new soybean varieties with lower bitter soyasaponin content.

<https://onlinelibrary.wiley.com/doi/10.1111/jipb.13553>

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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