

Sunday Evening News No 367

2024-03-04 – 2024-03-10

Compiled and edited by **BGF** Jany



Meetings – Conferences / Veranstaltungen - Konferenzen

Zur Erinnerung: Grüne Gentechnik

Mit einem neuen Gesetz will die EU die Blockade gegenüber gentechnischen Verfahren durchbrechen. Experten diskutieren über den Nutzen und die Risiken neuer Züchtungen aus dem Genlabor am 4. April im Schloss Herrenhausen.

04.04.2024 ab 19:00 bis 21:00 Uhr Hannover

<https://www.hannover.de/Veranstaltungskalender/Wissenschaft-Wirtschaft/Gr%C3%BCne-Gentechnik>

<https://www.volkswagenstiftung.de/de>

Press Releases -Media / Presse- und Medienberichte

kfi: EFI empfiehlt Dual-Use & KI-Forschung zu stärken

<https://www.forschung-und-lehre.de/politik/efi-empfoehlt-dual-use-ki-forschung-zu-staerken-6280>

DubockA.C.: Investigative paper published in the Medical Research Archives journal

<https://www.goldenrice.org/>

Crymann T.: Frankreich soll Risikobericht zu NGTs unterschlagen haben

<https://background.tagesspiegel.de/agrar-ernaehrung/frankreich-soll-risikobericht-zu-ngts-unterschlagen-haben>

Informationsdienst Gentechnik: Neue Gentechnik: Französische Behörde warnt vor Risiken

<https://www.keine-gentechnik.de/nachricht/34923?cHash=5e5f1270f41460fd6c1fc990fb74d1ea>

GM Watch: Risks of new GMOs: French food safety agency ANSES recommends case-by-case assessment

<https://www.gmwatch.org/en/106-news/latest-news/20391-risks-of-new-gmos-french-food-safety-agency-anses-recommends-case-by-case-assessment>

Paudal: ANSES recommends a “case by case” assessment

<https://www.paudal.com/2024/03/08/anses-recommends-a-case-by-case-assessment/>

arc2020: EU Food Safety Agency to Give New Opinion on New Genomic Techniques/New GMOs

<https://www.arc2020.eu/eu-food-safety-agency-to-give-new-opinion-on-new-genomic-techniques-new-gmos/>

Lovelles H.: New Genomic Techniques: EU proposal both promising and controversial

<https://www.lexology.com/library/detail.aspx?g=b0c77bab-7941-4067-a61c-bf3284ab5fa2>

Meshaka D.: Excluding GMOs/NGTs from patentability would be an illusion

<https://infogm.org/en/excluding-gmos-ngts-from-patentability-would-be-an-illusion/>

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 10-2024

Publications – Publikationen

EFI – Expertenkommission Forschung und Innovation (2024): Gutachten zu Forschung, Innovation und technologischer Leistungsfähigkeit Deutschlands 2024, Berlin: EFI.

https://www.e-fi.de/fileadmin/Assets/Gutachten/2024/EFI_Gutachten_2024_24124.pdf

Born C.: (2024): Neue Regeln für geneditierte Pflanzen in Europa?

Der Verordnungsvorschlag der EU-Kommission zu neuen genomischen Verfahren in der Pflanzenzüchtung

https://www.jura.uni-freiburg.de/de/institute/ioeffr2/downloads/online-papers/fip-1-2024_born_regulierung-geneditierter-pflanzen

Winter, G. (2024): **The European Union's deregulation of plants obtained from new genomic techniques: a critique and an alternative option.** *Environ Sci Eur* 36, 47 (2024). <https://doi.org/10.1186/s12302-024-00867-z>

The EU is about to relax its oversight of genetically modified organisms, focusing on plants and products that are obtained through certain new genomic techniques. The aim is to promote new genomic techniques as an innovative technology and employing it as a means to transform agriculture to sustainability. The present contribution describes and evaluates the planned reform. It discusses whether standards of legal certainty and legitimacy are met, how environmental side-effects are taken into account, how sustainability goals are integrated, what socio-economic effects are to be expected, and whether higher rank law is respected. As several shortcomings are found an alternative approach is submitted that combines a certain easing of administrative oversight with better integration of sustainability goals. Auspices for organic and conventional GMO-free agriculture are also sketched out.

<https://enveurope.springeropen.com/articles/10.1186/s12302-024-00867-z>

Monaco A., Kotz J., Al Masri M., Allmeta A., Purnhagen K.P. & König L.M., (2024): **Consumers' perception of novel foods and the impact of heuristics and biases: A systematic review.** *Appetite* | doi: <https://doi.org/10.1016/j.appet.2024.107285>.

According to the definition adopted in the European Union, novel foods are foods that were not consumed to a significant degree within the Union before 15 of May 1997. This includes cultivated meat and insects. Novel foods are meant to play a critical role in the transition towards sustainable food systems. However, their success depends on whether and to what extent they will be incorporated into the diets at the population level. This review investigates consumers' perception of novel food products by narratively synthesising results on the influence of heuristics and biases triggered by emotions, personality traits, and socio-cultural factors. Empirical studies conducted in Western countries and published in English after 1997 were eligible, which led to 182 studies being included. Notably, most included studies focused on insects and cultivated meat. Disgust and fear are shown to be the main emotions driving rejection of novel foods, together with food neophobia and specific cultural norms common across countries included in the scope of the review. Familiarity with novel foods and curiosity both led to higher acceptance. Despite being investigated directly in a minority of studies, heuristics and related biases mostly fell under the "affect", the "natural-is-better", and the "trust" heuristics. The review also discusses to what extent consumers' perception reflects in the regulatory framework applicable to novel foods in the European Union, how it influences the regulation of insects and cultivated meat and which lessons can be drawn for the future of the regulatory framework.

<https://osf.io/preprints/osf/5js72>

Menary J, Fuller SS (2024): **New genomic techniques, old divides: Stakeholder attitudes towards new biotechnology regulation in the EU and UK.** *PLoS ONE* 19(3): e0287276.

<https://doi.org/10.1371/journal.pone.0287276>

The European Union and United Kingdom are in the process of establishing new regulation regarding the use of new genomic techniques in crop and animal breeding. As part of this process, consultations have been launched to understand the views of stakeholders towards the use of new genomic techniques in plant and animal breeding. The responsible research and innovation framework emphasises the importance of dialogue between technology developers and stakeholders, including the public, but what are the opinions of stakeholders towards the regulation of NGTs in Europe and do they view these consultations as opportunities to engage with technology governance? We conducted semi-structured interviews with experts from a range of agri-food stakeholder groups in the European Union and United Kingdom to understand current attitudes towards new biotechnology regulation, how they viewed the process of consultation in both places and what influence they felt they had in shaping regulations. We found that the discussion is similar in both EU and UK, with predictable and fixed opinions determined by attitudes towards the perceived risks associated with direct mutagenesis. Both UK and EU consultations were considered to have the same weaknesses and stakeholders discussed a desire for more dialogic forms of engagement. We highlight several options for new forms of involvement in biotechnology regulation by exploring relevant responsible research and innovation literature.

<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0287276>

Hwarari, D., Radani, Y., Ke, Y. *et al.* **CRISPR/Cas genome editing in plants: mechanisms, applications, and overcoming bottlenecks.** *Funct Integr Genomics* 24, 50 (2024).

<https://doi.org/10.1007/s10142-024-01314-1>

The CRISPR/Cas systems have emerged as transformative tools for precisely manipulating plant genomes and enhancement. It has provided unparalleled applications from modifying the plant genomes to resistant enhancement. This review manuscript summarises the mechanism, application, and current challenges in the CRISPR/Cas genome editing technology. It addresses the molecular mechanisms of different Cas genes, elucidating their applications in various plants through crop improvement, disease resistance, and trait improvement. The advent of the CRISPR/Cas systems has enabled researchers to precisely modify plant genomes through gene knockouts, knock-ins, and gene expression modulation. Despite these successes, the CRISPR/Cas technology faces challenges, including off-target effects, Cas toxicity, and efficiency. In this manuscript, we also discuss these challenges and outline ongoing strategies employed to overcome these challenges, including the development of novel CRISPR/Cas variants with improved specificity and specific

delivery methods for different plant species. The manuscript will conclude by addressing the future perspectives of the CRISPR/Cas technology in plants. Although this review manuscript is not conclusive, it aims to provide immense insights into the current state and future potential of CRISPR/Cas in sustainable and secure plant production.

<https://link.springer.com/article/10.1007/s10142-024-01314-1>

Fuglie K.O., Echeverria R.G. (2024): **The economic impact of CGIAR-related crop technologies on agricultural productivity in developing countries, 1961–2020.** World Development 176, 106523 | <https://doi.org/10.1016/j.worlddev.2023.106523>

The international agricultural research centers that comprise the CGIAR got their start in the 1960s. They soon made major contributions to crop improvement in developing countries, particular in rice and wheat in Asia. Today, farmers can acquire new technologies from many sources, and evidence of whether the CGIAR continues to play an important role in crop improvement has become dated. This paper brings together an expanded set of evidence on the diffusion and productivity impact of CGIAR crop research through 2020, and breaks out these impacts by crop, region, and over time. By 2016–2020, CGIAR-related crop technologies had been adopted on at least 221 million hectares across Asia, Africa and Latin America, generating [economic welfare](#) gains of \$47 billion annually. In the 2010s, technology adoption and welfare impacts were increasing by about \$600 million annually, almost as much as in the 1990s. In the early days of the “Green Revolution,” these welfare impacts were largely confined to rice and wheat in Asia, but in recent decades have grown to include a larger range of crops and geographies, notably cassava and maize in Sub-Saharan Africa. Although improved crop varieties have been the main technology through which CGIAR crop centers have achieved these impacts, CGIAR-related integrated pest management and natural resource management technologies have also made significant contributions to crop productivity. In addition to raising farm income, productivity gains in staple crops have lowered food prices, thereby benefitting the whole population. This is a key reason why agricultural productivity growth, and food crop productivity growth in particular, has had greater impacts on poverty reduction in low-income countries than comparable productivity growth in other sectors.

<https://www.sciencedirect.com/science/article/pii/S0305750X23003418#s0045>

Ciren D., Zebell S., Lippman Z.B. (2024): **Extreme restructuring of *cis*-regulatory regions controlling a deeply conserved plant stem cell regulator.** PLoS Genet 20(3): e1011174. <https://doi.org/10.1371/journal.pgen.1011174>

A striking paradox is that genes with conserved protein sequence, function and expression pattern over deep time often exhibit extremely divergent *cis*-regulatory sequences. It remains unclear how such drastic *cis*-regulatory evolution across species allows preservation of gene function, and to what extent these differences influence how *cis*-regulatory variation arising within species impacts phenotypic change. Here, we investigated these questions using a plant stem cell regulator conserved in expression pattern and function over ~125 million years. Using *in-vivo* genome editing in two distantly related models, *Arabidopsis thaliana* (Arabidopsis) and *Solanum lycopersicum* (tomato), we generated over 70 deletion alleles in the upstream and downstream regions of the stem cell repressor gene *CLAVATA3* (*CLV3*) and compared their individual and combined effects on a shared phenotype, the number of carpels that make fruits. We found that sequences upstream of tomato *CLV3* are highly sensitive to even small perturbations compared to its downstream region. In contrast, Arabidopsis *CLV3* function is tolerant to severe disruptions both upstream and downstream of the coding sequence. Combining upstream and downstream deletions also revealed a different regulatory outcome. Whereas phenotypic enhancement from adding downstream mutations was predominantly weak and additive in tomato, mutating both regions of Arabidopsis *CLV3* caused substantial and synergistic effects, demonstrating distinct distribution and redundancy of functional *cis*-regulatory sequences. Our results demonstrate remarkable malleability in *cis*-regulatory structural organization of a deeply conserved plant stem cell regulator and suggest that major reconfiguration of *cis*-regulatory sequence space is a common yet cryptic evolutionary force altering genotype-to-phenotype relationships from regulatory variation in conserved genes. Finally, our findings underscore the need for lineage-specific dissection of the spatial architecture of *cis*-regulation to effectively engineer trait variation from conserved productivity genes in crops.

<https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1011174>

Mathur S., Singh D., Rajan R. (2024): **Chapter Ten - Recent advances in plant translational genomics for crop improvement.** Advances in Protein Chemistry and Structural Biology 139, 335-382 | <https://doi.org/10.1016/bs.apcsb.2023.11.009>

The growing population, climate change, and limited agricultural resources put enormous pressure on agricultural systems. A plateau in crop yields is occurring and extreme weather events and urbanization threaten the livelihood of farmers. It is imperative that immediate attention is paid to addressing the increasing food demand, ensuring resilience against emerging threats, and meeting the demand for more nutritious, safer food. Under uncertain conditions, it is essential to expand genetic diversity and discover novel crop varieties or variations to develop higher and more stable yields. Genomics plays a significant role in developing abundant and nutrient-dense food crops. An alternative to traditional breeding approach, translational genomics is able to improve breeding programs in a more efficient and precise manner by translating genomic concepts into practical tools. Crop breeding based on genomics offers potential solutions to overcome the limitations of conventional breeding methods, including improved crop varieties that provide more nutritional value and are protected from biotic and abiotic stresses. Genetic markers, such as SNPs and ESTs, contribute to the discovery of QTLs controlling agronomic traits and stress tolerance. In order to meet the growing demand for food, there is a need to incorporate QTLs into breeding programs using marker-assisted selection/breeding and transgenic

technologies. This chapter primarily focuses on the recent advances that are made in translational genomics for crop improvement and various omics techniques including transcriptomics, metagenomics, pangenomics, single cell omics etc. Numerous genome editing techniques including CRISPR Cas technology and their applications in crop improvement had been discussed.

<https://www.sciencedirect.com/science/article/abs/pii/S1876162323000986>

Raza, A., Chen, H., Zhang, C. et al. (2024): **Designing future peanut: the power of genomics-assisted breeding.** Theor Appl Genet 137, 66 | <https://doi.org/10.1007/s00122-024-04575-3>
Cultivated peanut (*Arachis hypogaea* L.), a legume crop greatly valued for its nourishing food, cooking oil, and fodder, is extensively grown worldwide. Despite decades of classical breeding efforts, the actual on-farm yield of peanut remains below its potential productivity due to the complicated interplay of genotype, environment, and management factors, as well as their intricate interactions. Integrating modern genomics tools into crop breeding is necessary to fast-track breeding efficiency and rapid progress. When combined with speed breeding methods, this integration can substantially accelerate the breeding process, leading to faster access of improved varieties to farmers. Availability of high-quality reference genomes for wild diploid progenitors and cultivated peanuts has accelerated the process of gene/quantitative locus discovery, developing markers and genotyping assays as well as a few molecular breeding products with improved resistance and oil quality. The use of new breeding tools, e.g., genomic selection, haplotype-based breeding, speed breeding, high-throughput phenotyping, and genome editing, is probable to boost genetic gains in peanut. Moreover, renewed attention to efficient selection and exploitation of targeted genetic resources is also needed to design high-quality and high-yielding peanut cultivars with main adaptation attributes. In this context, the combination of genomics-assisted breeding (GAB), genome editing, and speed breeding hold great potential in designing future improved peanut cultivars to meet market and food supply demands.
<https://link.springer.com/article/10.1007/s00122-024-04575-3>

Kumari, N., Kumar, A., Sharma, S. et al. (2024): **CRISPR/Cas system for the traits enhancement in potato (*Solanum tuberosum* L.): present status and future prospectives.** J. Plant Biochem. Biotechnol. | <https://doi.org/10.1007/s13562-024-00878-0>
The increasing global population projected to reach 9.7 billion by 2050 from the current 7.7 billion, which is going to significantly impact food availability. Therefore, current global agricultural production needs to be increased to feed the unconstrained growing population. The changing climatic condition due to anthropogenic activities also makes the conditions more challenging to meet the required crop productivity in the future. Potato is third most consumed staple food. The current cultivation and demand of potato is particularly more in developing countries with high levels of poverty, hunger, and malnutrition because it is cheap source of nutrition and easily available. Potato is severely infected by a number of diseases, insect pests, and abiotic environmental conditions. Amidst the backdrop of climate change, the situation is deteriorating. Projections indicate that the average potato productivity in India's primary potato-growing states, responsible for approximately 90% of the nation's total potato output, is expected to decline by 2.0% in the 2050s and a more substantial 6.4% in the 2080s. Therefore to develop tolerance in plants to cope with changing environmental condition is need of hour to feed the overgrowing population. In this review, we discussed the application of CRISPR to enhance the crop productivity and develop biotic and abiotic stress-tolerant in potato to face the current changing climatic conditions is also discussed. The review also sheds light on the future prospects of CRISPR/Cas technology for potato breeding, including potential challenges and opportunities.
<https://link.springer.com/article/10.1007/s13562-024-00878-0>

Dmitrijeva, M., Tackmann, J., Matias Rodrigues, J.F. et al. (2024): **A global survey of prokaryotic genomes reveals the eco-evolutionary pressures driving horizontal gene transfer.** Nat Ecol Evol | <https://doi.org/10.1038/s41559-024-02357-0>
Horizontal gene transfer, the exchange of genetic material through means other than reproduction, is a fundamental force in prokaryotic genome evolution. Genomic persistence of horizontally transferred genes has been shown to be influenced by both ecological and evolutionary factors. However, there is limited availability of ecological information about species other than the habitats from which they were isolated, which has prevented a deeper exploration of ecological contributions to horizontal gene transfer. Here we focus on transfers detected through comparison of individual gene trees to the species tree, assessing the distribution of gene-exchanging prokaryotes across over a million environmental sequencing samples. By analysing detected horizontal gene transfer events, we show distinct functional profiles for recent versus old events. Although most genes transferred are part of the accessory genome, genes transferred earlier in evolution tend to be more ubiquitous within present-day species. We find that co-occurring, interacting and high-abundance species tend to exchange more genes. Finally, we show that host-associated specialist species are most likely to exchange genes with other host-associated specialist species, whereas species found across different habitats have similar gene exchange rates irrespective of their preferred habitat. Our study covers an unprecedented scale of integrated horizontal gene transfer and environmental information, highlighting broad eco-evolutionary trends.
<https://www.nature.com/articles/s41559-024-02357-0>

Lim, J., Park, C., Kim, M. et al. (2024): **Advances in single-cell omics and multiomics for high-resolution molecular profiling.** Exp Mol Med | <https://doi.org/10.1038/s12276-024-01186-2>
Single-cell omics technologies have revolutionized molecular profiling by providing high-resolution insights into cellular heterogeneity and complexity. Traditional bulk omics approaches average signals from heterogeneous

cell populations, thereby obscuring important cellular nuances. Single-cell omics studies enable the analysis of individual cells and reveal diverse cell types, dynamic cellular states, and rare cell populations. These techniques offer unprecedented resolution and sensitivity, enabling researchers to unravel the molecular landscape of individual cells. Furthermore, the integration of multimodal omics data within a single cell provides a comprehensive and holistic view of cellular processes. By combining multiple omics dimensions, multimodal omics approaches can facilitate the elucidation of complex cellular interactions, regulatory networks, and molecular mechanisms. This integrative approach enhances our understanding of cellular systems, from development to disease. This review provides an overview of the recent advances in single-cell and multimodal omics for high-resolution molecular profiling. We discuss the principles and methodologies for representatives of each omics method, highlighting the strengths and limitations of the different techniques. In addition, we present case studies demonstrating the applications of single-cell and multimodal omics in various fields, including developmental biology, neurobiology, cancer research, immunology, and precision medicine.
<https://www.nature.com/articles/s12276-024-01186-2>

Fogarty E.C., Schechter M.S., Lolans K., Sheahan M.L. et al. (2024): **A cryptic plasmid is among the most numerous genetic elements in the human gut.** *Cell* 187, 1206–1222 | <https://doi.org/10.1016/j.cell.2024.01.039>

Plasmids are extrachromosomal genetic elements that often encode fitness-enhancing features. However, many bacteria carry “cryptic” plasmids that do not confer clear beneficial functions. We identified one such cryptic plasmid, pBI143, which is ubiquitous across industrialized gut microbiomes and is 14 times as numerous as crAssphage, currently established as the most abundant extrachromosomal genetic element in the human gut. The majority of mutations in pBI143 accumulate in specific positions across thousands of metagenomes, indicating strong purifying selection. pBI143 is monoclonal in most individuals, likely due to the priority effect of the version first acquired, often from one’s mother. pBI143 can transfer between Bacteroidales, and although it does not appear to impact bacterial host fitness in vivo, it can transiently acquire additional genetic content. We identified important practical applications of pBI143, including its use in identifying human fecal contamination and its potential as an alternative approach to track human colonic inflammatory states.
[https://www.cell.com/cell/fulltext/S0092-8674\(24\)00107-7?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867424001077%3Fshowall%3Dtrue](https://www.cell.com/cell/fulltext/S0092-8674(24)00107-7?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867424001077%3Fshowall%3Dtrue)

EFSA:

CEP Panel (2024): Safety evaluation of the food enzyme mucorpepsin from the non-genetically modified *Rhizomucor miehei* strain LP-N836. *EFSA Journal*, 22(3), e8631.
<https://doi.org/10.2903/j.efsa.2024.8631>
<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2024.8631>

EFSA CEP Panel (2024): Safety evaluation of the food enzyme α -galactosidase from the genetically modified *Saccharomyces cerevisiae* strain CBS 615.94. *EFSA Journal*, 22(3), e8606.
<https://doi.org/10.2903/j.efsa.2024.8606>
<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2024.8606>

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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