Sunday Evening News No 338

2023-08-07 – 2023-08-13

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Wissenschaftskreis Genomik und Gentechnik e.V.

Press Releases -Media / Presse- und Medienberichte

Herzog R.: **„Diskussionen werden einfach idiotisiert“**
Es ist verblüffend: Vor mehr als einem Vierteljahrhundert, am 26. April 1997, hielt der damalige Bundespräsident Roman Herzog seine berühmte „Ruck“-Rede im Berliner Adlon-Hotel. Seine Worte sind heute so aktuell wie damals, wenn er die Lähmung beschreibt, die über dem Land liegt. Wir dokumentieren deswegen heute diese historische Rede. Sie hat einen versöhnlichen Schluss. Von Roman Herzog
https://www.theeuropean.de/roman-herzog/roman-herzog-diskussionen-werden-einfach-idiotisiert/

Worthley D.: **Genetically engineered bacteria can detect cancer cells in a** world-first **experiment**
https://theconversation.com/genetically-engineered-bacteria-can-detect-cancer-cells-in-a-world-first-experiment-211201

Cerier S.: Viewpoint: **Anti-agrobiotech activists claim European farmers who support relaxing the EU's de facto ban on cultivating GMO and gene-edited crops are dupes of Big Ag. Here are the facts**
https://geneticliteracyproject.org/2023/08/10/viewpoint-anti-agrobiotech-activists-claim-european-farmers-who-support-relaxing-the-eus-de-facto-ban-on-cultivating-gmo-and-gene-edited-crops-are-dupes-of-big-ag-here-are-the-facts/

Dionglay C.: **A Short Timeline of EU's Proposal on NGTs**
https://www.isaaa.org/blog/entry/default.asp?BlogDate=8/9/2023

Jorasch P.: **Viewpoint: EU gene-editing regulations requiring traceability and labeling to 'protect co-existence' with organic crops could stop innovation in its tracks**
https://geneticliteracyproject.org/2023/08/07/viewpoint-eu-gene-editing-regulations-requiring-traceability-and-labeling-to-protect-co-existence-with-organic-crops-could-stop-innovation-in-its-tracks/

Brangwyn A.; Zakrzewski J., RD: **Organic vs. Non-Organic Foods: Are they Safer, Better, Tastier?**
https://healthnews.com/nutrition/healthy-eating/organic-vs-non-organic-foods-are-they-safer-better-tastier/

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ▶here: August week 32

Publications – Publikationen

Cooper R.M., Wright J.A., Jia Q. Ng J.Q., Goyne J.M. et al. (2303): **Engineered bacteria detect tumor DNA.** Science 381, Issue 6658, 682-686 | DOI: 10.1126/science.adf3974
Synthetic biology has developed sophisticated cellular biosensors to detect and respond to human disease. However, biosensors have not yet been engineered to detect specific extracellular DNA sequences and mutations. Here, we engineered naturally competent *Acinetobacter baylyi* to detect donor DNA from the genomes of colorectal cancer (CRC) cells, organoids, and tumors. We characterized the functionality of the biosensors in vitro with coculture assays and then validated them in vivo with sensor bacteria delivered to mice harboring colorectal tumors. We observed horizontal gene transfer from the tumor to the sensor bacteria in our mouse model of CRC. This cellular assay for targeted, CRISPR-discriminated horizontal gene transfer (CATCH) enables the biodetection of specific cell-free DNA.
https://www.science.org/doi/10.1126/science.adf3974

Zarate S., Cimadori I., Jones M.S., Roca M.M. Barnhill-Dilling S.K. (2023): **Assessing agricultural gene editing regulation in Latin America. an analysis of how policy windows and policy entrepreneurs shape agricultural gene editing regulatory regimes**. Front. Bioeng. Biotechnol. 11:1209308 | https://doi.org/10.3389/fbioe.2023.1209308
This article explores the new developments and challenges of agricultural Gene Editing (GED) regulation in primarily nine countries of Latin America and the Caribbean (LAC) Region: Argentina, Bolivia, Brazil, Colombia, Guatemala, Honduras, Mexico, Paraguay and Peru. As Gene Editing technology develops, Latin America and the Caribbean regulatory regimes struggle to keep pace. Developers and regulators face challenges such as

consumer perceptions, intellectual property, R&D funding (private and public), training, environmental and social impact, and access to domestic and international markets. Some Latin America and the Caribbean countries (e.g., Argentina) interpret existing legislation to promulgate regulations for biotechnology and Genetically Modified Organisms (GMOs), while others (e.g., Brazil and Honduras) have specific legislation for Genetically Modified Organisms. In both those cases, often a case-by-case approach is chosen to determine whether a Gene Editing organism is subject to Genetically Modified Organisms regulations or not. Other countries such as Peru have opted to ban the technology due to its perceived resemblance to transgenic Genetically Modified Organisms. After presenting the regulatory landscape for agricultural Gene Editing in Latin America and the Caribbean, this article addresses some of the differences and similarities across the region. Some countries have had more foresight and have dedicated resources to increase capacity and develop regulations (e.g., Brazil, Argentina, Colombia, Guatemala, Honduras, Mexico before 2018) while others struggle with bureaucratic limitations and partisanship of policymaking (e.g., Paraguay, Bolivia, Peru, Mexico after 2018). We propose that the differences and similarities between these regulatory regimes have emerged in part as a result of policy entrepreneurs (influential individuals actively involved in policy making) taking advantage of policy windows (opportunities for shaping policy and regulation). The third and remaining sections of this study discuss our main findings. Based on 41 semi structured interviews with regulators, scientists, product developers, NGOs and activists, we arrived at three main findings. First, there seems to be a consensus among most regulators interviewed that having harmonized regimes is a positive step to facilitate product development and deployment, leading to commercialization. Second, reducing bureaucracy (e.g., paper work) and increasing flexibility in regulation go hand in hand to expedite the acquisition of key lab materials required by developers in countries with less robust regimes such as Peru and Bolivia. Finally, developing public and private partnerships, fostering transparency, and increasing the involvement of marginalized groups may increase the legitimacy of Gene Editing regulation.
https://www.frontiersin.org/articles/10.3389/fbioe.2023.1209308/full

Wei W., Grieger K., Cummings C.-L., Loschin N., Kuzma J. (2023): I**dentifying sustainability assessment parameters for genetically engineered agrifoods.** Plants, People, Planet | https://doi.org/10.1002/ppp3.10411

Societal Impact Statement

A diverse portfolio of genetically engineered food crops, as well as animal livestock and fish, are currently being developed and commercialized. To ensure their contributions to long-term sustainability, a broad range of environmental, health, ethical, and societal parameters should be used in their evaluations. This paper proposes a set of parameters to evaluate the sustainability of genetically engineered food and agriculture products and discusses mechanisms to improve their governance and oversight. With such holistic evaluations, genetic engineering applications that are deemed beneficial to sustainable agriculture could be identified in an effort to foster sustainability.

Summary

To achieve international sustainable development goals, food and agricultural production need to rely on sustainable and resilient practices. Traditional breeding as well as the use of new agricultural technologies, including genetic engineering and gene editing, have the potential to help achieve sustainable agrifood production. Although numerous oversight mechanisms exist to guarantee the secure and sustainable advancement and utilization of genetically engineered agrifoods, the majority of these mechanisms heavily depend on a narrow set of parameters to assess risks and safety concerning human health and nontarget organisms. However, a more comprehensive range of parameters should be considered to promote environmental and social sustainability in a more holistic manner. This Opinion article argues that to achieve a more sustainable agrifood production that relies on genetic engineering, governance systems related to new agrifood biotechnologies should incorporate a broader array of environmental, health, ethical, and societal factors to ensure their sustainability in the long-term. To facilitate this process, we propose a set of parameters to help evaluate the sustainability of agrifoods that rely on genetic engineering. We then discuss major challenges and opportunities for formalizing sustainability parameters in US governance policy and decision-making systems. Overall, this work contributes to further developing a more comprehensive assessment framework that aims to minimize potential risks and maximize potential benefits of agrifood biotechnology while also fostering sustainability.
https://nph.onlinelibrary.wiley.com/doi/full/10.1002/ppp3.10411

Furgurson J., Loschin N., Butoto E., Abugu M. et al. (2023): **Seizing the policy moment in crop biotech regulation: an interdisciplinary response to the Executive Order on biotechnology**. Front. Bioeng. Biotechnol. 11:1241537 | https://doi.org/10.3389/fbioe.2023.1241537
https://www.frontiersin.org/articles/10.3389/fbioe.2023.1241537/full

Saripalli, G., Adhikari, L., Amos, C. et al. (2023): **Integration of genetic and genomics resources in einkorn wheat enables precision mapping of important traits.** Commun Biol 6, 835 | https://doi.org/10.1038/s42003-023-05189-z

Einkorn wheat (*Triticum monococcum*) is an ancient grain crop and a close relative of the diploid progenitor (*T. urartu*) of polyploid wheat. It is the only diploid wheat species having both domesticated and wild forms and therefore provides an excellent system to identify domestication genes and genes for traits of interest to utilize in wheat improvement. Here, we leverage genomic advancements for einkorn wheat using an einkorn reference

genome assembly combined with skim-sequencing of a large genetic population of 812 recombinant inbred lines (RILs) developed from a cross between a wild and a domesticated *T. monococcum* accession. We identify 15,919 crossover breakpoints delimited to a median and average interval of 114 Kbp and 219 Kbp, respectively. This high-resolution mapping resource enables us to perform fine-scale mapping of one qualitative (red coleoptile) and one quantitative (spikelet number per spike) trait, resulting in the identification of small physical intervals (400 Kb to 700 Kb) with a limited number of candidate genes. Furthermore, an important domestication locus for brittle rachis is also identified on chromosome 7A. This resource presents an exciting route to perform trait discovery in diploid wheat for agronomically important traits and their further deployment in einkorn as well as tetraploid pasta wheat and hexaploid bread wheat cultivars.
https://www.nature.com/articles/s42003-023-05189-z

Jing, CY., Zhang, FM., Wang, XH. et al. (2023): **Multiple domestications of Asian rice.** Nat. Plants | https://doi.org/10.1038/s41477-023-01476-z
The origin of domesticated Asian rice (*Oryza sativa* L.) has been controversial for more than half a century. The debates have focused on two leading hypotheses: a single domestication event in China or multiple domestication events in geographically separate areas. These two hypotheses differ in their predicted history of genes/alleles selected during domestication. Here we amassed a dataset of 1,578 resequenced genomes, including an expanded sample of wild rice from throughout its geographic range. We identified 993 selected genes that generated phylogenetic trees on which *japonica* and *indica* formed a monophyletic group, suggesting that the domestication alleles of these genes originated only once in either *japonica* or *indica*. Importantly, the domestication alleles of most selected genes (~80%) stemmed from wild rice in China, but the domestication alleles of a substantial minority of selected genes (~20%) originated from wild rice in South and Southeast Asia, demonstrating separate domestication events of Asian rice.
https://www.nature.com/articles/s41477-023-01476-z

Essenberg M., L. McNally K. L., Bayles M.B., Pierce M.L. et al. (2023): **Gene B5 in Cotton Confers High and Broad Resistance to Bacterial Blight and Conditions High Amounts of Sesquiterpenoid Phytoalexins,** Phytopathology | DOI: 10.1094/PHYTO-08-22-0310-FI
Bacterial blight resistance gene B_5 has received little attention since it was first described in 1950. A near-isogenic line (NIL) of *Gossypium hirsutum* cotton, AcB_5, was generated in an otherwise bacterial-blight-susceptible 'Acala 44' background. The introgressed locus B_5 in AcB_5 conferred strong and broad-spectrum resistance to bacterial blight. Segregation patterns of test crosses under Oklahoma field conditions indicated that AcB_5 is likely homozygous for resistance at two loci with partial dominance gene action. In controlled-environment conditions, two of the four copies of B_5 were required for effective resistance. Contrary to expectations of gene-for-gene theory, AcB_5 conferred high resistance toward isogenic strains of *Xanthomonas citri* subsp. *malvacearum* carrying cloned avirulence genes *avrB4*, *avrb7*, *avrBIn*, *avrB101*, and *avrB102*, respectively, and weaker resistance toward the strain carrying cloned *avrb6*. The hypothesis that each *B* gene, in the absence of a polygenic complex, triggers sesquiterpenoid phytoalexin production was tested by measurement of cadalene and lacinilene phytoalexins during resistant responses in five NILs carrying different *B* genes, four other lines carrying multiple resistance genes, as well as susceptible Ac44E. Phytoalexin production was an obvious, but variable, response in all nine resistant lines. AcB_5 accumulated an order of magnitude more of all four phytoalexins than any of the other resistant NILs. Its total levels were comparable to those detected in OK1.2, a highly resistant line that possesses several *B* genes in a polygenic background.
https://apsjournals.apsnet.org/doi/10.1094/PHYTO-08-22-0310-FI

Fawcett, J.A., Takeshima, R., Kikuchi, S. et al. (2023): **Genome sequencing reveals the genetic architecture of heterostyly and domestication history of common buckwheat**. Nat. Plants | https://doi.org/10.1038/s41477-023-01474-1
Common buckwheat, *Fagopyrum esculentum*, is an orphan crop domesticated in southwest China that exhibits heterostylous self-incompatibility. Here we present chromosome-scale assemblies of a self-compatible *F. esculentum* accession and a self-compatible wild relative, *Fagopyrum homotropicum*, together with the resequencing of 104 wild and cultivated *F. esculentum* accessions. Using these genomic data, we report the roles of transposable elements and whole-genome duplications in the evolution of *Fagopyrum*. In addition, we show that (1) the breakdown of heterostyly occurs through the disruption of a hemizygous gene jointly regulating the style length and female compatibility and (2) southeast Tibet was involved in common buckwheat domestication. Moreover, we obtained mutants conferring the waxy phenotype for the first time in buckwheat. These findings demonstrate the utility of our *F. esculentum* assembly as a reference genome and promise to accelerate buckwheat research and breeding.
https://www.nature.com/articles/s41477-023-01474-1

Majeed A., Kui L., Dong Y., Chen J. (2023): **Reference genome facilitates trait development for faba beans.** Trends in Genetics | https://doi.org/10.1016/j.tig.2023.07.003
Reference genomes facilitate trait improvement by aiding in the elucidation of causal genetic elements. Thanks to the recent release of a reference sequence for the faba bean, breeders and geneticists are poised to accelerate precision breeding and genetic improvement of this important crop.
https://www.cell.com/trends/genetics/fulltext/S0168-9525(23)00161-0

Buyel J.F. (2023): **Product safety aspects of plant molecular farming.** Front. Bioeng. Biotechnol. 11:1238917 | https://doi.org/10.3389/fbioe.2023.1238917

Plant molecular farming (PMF) has been promoted since the 1990s as a rapid, cost-effective and (most of all) safe alternative to the cultivation of bacteria or animal cells for the production of biopharmaceutical proteins. Numerous plant species have been investigated for the production of a broad range of protein-based drug candidates. The inherent safety of these products is frequently highlighted as an advantage of PMF because plant viruses do not replicate in humans and vice versa. However, a more nuanced analysis of this principle is required when considering other pathogens because toxic compounds pose a risk even in the absence of replication. Similarly, it is necessary to assess the risks associated with the host system (e.g., the presence of toxic secondary metabolites) and the production approach (e.g., transient expression based on bacterial infiltration substantially increases the endotoxin load). This review considers the most relevant host systems in terms of their toxicity profile, including the presence of secondary metabolites, and the risks arising from the persistence of these substances after downstream processing and product purification. Similarly, we discuss a range of plant pathogens and disease vectors that can influence product safety, for example, due to the release of toxins. The ability of downstream unit operations to remove contaminants and process-related toxic impurities such as endotoxins is also addressed. This overview of plant-based production, focusing on product safety aspects, provides recommendations that will allow stakeholders to choose the most appropriate strategies for process development.
https://www.frontiersin.org/articles/10.3389/fbioe.2023.1238917/full

Yasumoto, S., Muranaka, T. (2023): **Foreign DNA detection in genome-edited potatoes by high-throughput sequencing.** Sci Rep 13, 12246 | https://doi.org/10.1038/s41598-023-38897-x

Genome editing is a powerful breeding technique that introduces mutations into specific gene sequences in genomes. For genome editing in higher plants, nucleotides for artificial nuclease (e.g. TALEN or CRISPR-Cas9) are transiently or stably introduced into the plant cells. After the introduction of mutations by artificial nucleases, it is necessary to select lines that do not contain the foreign nucleotides to overcome GMO regulation; however, there is still no widely legally authorized and approved method for detecting foreign genes in genome-edited crops. Recently, *k*-mer analysis based on next-generation sequencing (NGS) was proposed as a new method for detecting foreign DNA in genome-edited agricultural products. Compared to conventional methods, such as PCR and Southern hybridization, in principle, this method can detect short DNA fragments with high accuracy. However, this method has not yet been applied to genome-edited potatoes. In this study, we evaluated the feasibility of *k*-mer analysis in tetraploid potatoes by computer simulation, and also evaluated whether the *k*-mer method can detect foreign genes with high accuracy by analyzing samples of genome-edited potatoes. We show that when NGS data (at a depth of × 30 the genome size) are used, the *k*-mer method can correctly detect foreign genes in the potato genome even with the insertion of DNA fragments of 20 nt in length. Based on these findings, we expect that *k*-mer analysis will be one of the main methods for detecting foreign genes in genome-edited potatoes.
https://www.nature.com/articles/s41598-023-38897-x

Sünderhauf, D., Klümper, U., Gaze, W.H. et al. (2023): **Interspecific competition can drive plasmid loss from a focal species in a microbial community**. ISME J | https://doi.org/10.1038/s41396-023-01487-w

Plasmids are key disseminators of antimicrobial resistance genes and virulence factors, and it is therefore critical to predict and reduce plasmid spread within microbial communities. The cost of plasmid carriage is a key metric that can be used to predict plasmids' ecological fate, and it is unclear whether plasmid costs are affected by growth partners in a microbial community. We carried out competition experiments and tracked plasmid maintenance using a model system consisting of a synthetic and stable five-species community and a broad host-range plasmid, engineered to carry different payloads. We report that both the cost of plasmid carriage and its long-term maintenance in a focal strain depended on the presence of competitors, and that these interactions were species specific. Addition of growth partners increased the cost of a high-payload plasmid to a focal strain, and accordingly, plasmid loss from the focal species occurred over a shorter time frame. We propose that the destabilising effect of interspecific competition on plasmid maintenance may be leveraged in clinical and natural environments to cure plasmids from focal strains.
https://www.nature.com/articles/s41396-023-01487-w

EFSA

CEP Panel (2023): Scientific Opinion on the safety evaluation of the food enzyme triacylglycerol lipase from the non-genetically modified *Rhizopus arrhizu*s strain AE-TL(B). *EFSA Journal* 2023; 21(8):8099, 17 pp. https://doi.org/10.2903/j.efsa.2023.8099
https://efsa.onlinelibrary.wiley.com/action/showCitFormats?doi=10.2903%2Fj.efsa.2023.8099&mobileUi=0

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. M*ost of *the pdf files can be downloaded directly from the links.*

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