Sunday Evening News No 351

2023-11-06 – 2023-11-12

Compiled and edited by ***BGF*** Jany

Wissenschaftskreis Genomik und Gentechnik e.V.

Meetings – Conferences / Tagungen - Konferenzen

Leopoldina: **Die Wissenschaft unter Beschuss. Zum Umgang mit Fälschung und Leugnung**
Mittwoch, 22. November 2023, 17:00 bis 19:45
Leopoldina-Vortragssaal, Jägerberg 1, 06108 Halle (Saale) und Online
Anmeldung: https://www.leopoldina.org/form/anmeldung-die-wissenschaft-unter-beschuss/

Press Releases -Media / Presse- und Medienberichte

VLOG-Newsletter 05/2023
https://www.ohnegentechnik.org/vlog-newsletter-november-2023

Aurelia Stiftung: **Handelskonzerne bei Neuer Gentechnik gespalten: ALDI und REWE für Risikoprüfung und Kennzeichnung,** LIDL und EDEKA dagegen
https://www.presseportal.de/pm/134345/5644013

Simon M.: **Neue Gentechniken: EVP will Vorschlag abschwächen und stößt auf Widerstand**
https://www.euractiv.de/section/landwirtschaft-und-ernahrung/news/neue-gentechniken-evp-will-vorschlag-abschwaechen-und-stoesst-auf-widerstand/

IEDE News: **Brussels clears the way for Crispr-cas admission**
https://iede.news/en/european-parliament/ep-environmental-committee-clears-the-way-for-accelerated-admission-of-crispr-cas/

EPSO statement on the European Commission's legal proposal for a Regulation of the European Parliament and of the Council on plants obtained by certain new genomic techniques and their food and feed ….
https://epsoweb.org/epso/epso-statement-on-the-european-commissions-legal-proposal-for-a-regulation-of-the-european-parliament-and-of-the-council-on-plants-obtained-by-certain-new-genomic-techniques-and-their-food-an/2023/11/06/

FDA: **Science and History of GMOs and Other Food Modification Processes**
https://www.fda.gov/food/agricultural-biotechnology/science-and-history-gmos-and-other-food-modification-processes

Incorvaia D.: **These 8 GMOs tell a brief history of genetic modification**
The first genetically modified organism was introduced 50 years ago
https://www.sciencenews.org/article/8-gmo-history-genetic-modification

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ▶here: November week 45

Publications – Publikationen

Lacy K. and McFadden J. (2023): **Consumer acceptance of genetically engineered potatoes: The role of information and agreement.** *Journal of the Agricultural and Applied Economics Association*. 1–19. https://doi.org/10.1002/jaa2.80
Many foods cooked at high temperatures produce acrylamide, a probable carcinogen, and neurotoxin. We evaluate how consumers' purchase intentions for potato products and subjective knowledge about conventional foods, genetically engineered (G.E.) foods, and acrylamide respond to information treatments. Information and prior purchases positively influence intentions to purchase potatoes but negatively influence purchase intentions for potato chips and French fries. Value-of-information calculations suggest industry-focused and private-company perspectives are worth $0.01-$0.02/person per month. Our results have practical implications for food system actors seeking to better understand the broader determinants of consumer acceptance behaviors as they relate to G.E. foods that reduce health concerns.
https://onlinelibrary.wiley.com/doi/full/10.1002/jaa2.80

Niazi, S.K. (2023): **Gene Editing: The Regulatory Perspective**. Encyclopedia 3, 1345–1357. https://doi.org/10.3390/encyclopedia3040096
Gene or genome editing, often known as GE, is a technique utilized to modify, eliminate, or substitute a mutated gene at the DNA level. It serves as a valuable tool in the field of genetic manipulation. Gene therapy (GT) is a therapeutic approach that aims to correct mutations by delivering a functional gene copy into the body. In contrast, the mutated gene remains in the genome. It is considered a form of medical intervention. No approval has been granted for any product manufactured by GE, in contrast to the approval of 22 medications produced by GT. These GT products are priced at millions of US dollars each dose. The Food and Drug Administration (FDA) has recently implemented a guideline about gene editing, which aims to facilitate the expedited creation of genetically engineered (GE) goods. However, the FDA must provide further elucidation and necessary revisions to enhance the rationality of this guideline.
https://www.mdpi.com/2673-8392/3/4/96

Cardi T., Murovec J., Bakhsh A., Boniecka J. et al. (2023): **CRISPR/Cas-mediated plant genome editing: outstanding challenges a decade after implementation.** Trends Plant Sci 28 (10):1144-1165 | DOI: 10.1016/j.tplants.2023.05.012
The discovery of the CRISPR/Cas genome-editing system has revolutionized our understanding of the plant genome. CRISPR/Cas has been used for over a decade to modify plant genomes for the study of specific genes and biosynthetic pathways as well as to speed up breeding in many plant species, including both model and non-model crops. Although the CRISPR/Cas system is very efficient for genome editing, many bottlenecks and challenges slow down further improvement and applications. In this review we discuss the challenges that can occur during tissue culture, transformation, regeneration, and mutant detection. We also review the opportunities provided by new CRISPR platforms and specific applications related to gene regulation, abiotic and biotic stress response improvement, and de novo domestication of plants.
https://www.cell.com/action/showPdf?pii=S1360-1385%2823%2900164-4

Aravind, B., Molla, K., Mangrauthia, S.K. et al. (2023): **Strategies to improve genome editing efficiency in crop plants.** J. Plant Biochem. Biotechnol. | https://doi.org/10.1007/s13562-023-00860-2
Genome editing technology comprises site-directed mutagenesis of genomes, involving alterations of few bases to precise replacement of a fragment or an entire gene sequence. Among multiple types of genome editing technologies developed, CRISPR-Cas9 and its latest variants have been revolutionizing the field of genetic engineering and plant biotechnology. Despite several advantages the CRISPR-Cas9 technology offers, it often suffers from low efficiency in creating desirable mutants in several crop plant species. In this review, we discuss various emerging strategies to improve genome editing efficiency in crop plants. The strategies include increased expression of genome editing components using high efficiency viral vectors, employment of inhibitors of chromatin modifiers, and using plant DNA viruses as donor DNA carriers. Additionally, we also discuss strategies to obtain transgene-free genome edited crops.
https://link.springer.com/article/10.1007/s13562-023-00860-2

Pathi, K.M.; Sprink, T. (2023): From Petri Dish to Field: **Plant Tissue Culture and Genetic Engineering of Oats for Improved Agricultural Outcomes**. Plants 12, 378 | https://doi.org/10.3390/plants12213782
Oats (Avena sativa) hold immense economic and nutritional value as a versatile crop. They have long been recognized as an exceptional choice for human consumption and animal feed. Oats' unique components, including proteins, starches, and β-glucans, have led to its widespread use in various food products such as bread, noodles, flakes, and milk. The popularity of oat milk as a vegan alternative to dairy milk has soared due to the increasing number of vegetarians/vegans and growing environmental awareness. Oat milk offers a sustainable option with reduced greenhouse gas emissions during its production, rendering it an appropriate choice for individuals who are lactose-intolerant or have dairy allergies. To ensure improved adaptability and enhanced nutrition, the development of new oat varieties is crucial, considering factors like cultivation, climate, and growing conditions. Plant cell culture plays a crucial role in both traditional and contemporary breeding methods. In classical breeding, plant cell culture facilitates the rapid production of double haploid plants, which can be employed to accelerate the breeding process. In modern breeding methods, it enables genetic manipulation and precise genome editing at the cellular level. This review delves into the importance of oats and their diverse applications, highlighting the advantages of plant cell culture in both classical and modern breeding methods. Specifically, it provides an overview of plant tissue culture, encompassing genetic transformation, haploid technology, protoplast technology, and genome editing.
https://www.mdpi.com/2223-7747/12/21/3782

Chowdhury, R.H., Eti, F.S., Ahmed, R. et al. (2023): **Drought-responsive genes in tomato: meta-analysis of gene expression using machine learning.** Sci Rep 13, 19374 | https://doi.org/10.1038/s41598-023-45942-2
Plants have diverse molecular mechanisms to protect themselves from biotic and abiotic stressors and adapt to changing environments. To uncover the genetic potential of plants, it is crucial to understand how they adapt to adverse conditions by analyzing their genomic data. We analyzed RNA-Seq data from different tomato genotypes, tissue types, and drought durations. We used a time series scale to identify early and late drought-

responsive gene modules and applied a machine learning method to identify the best responsive genes to drought. We demonstrated six candidate genes of tomato viz. Fasciclin-like arabinogalactan protein 2 (*FLA2*), Amino acid transporter family protein (*ASCT*), Arginine decarboxylase 1 (*ADC1*), Protein NRT1/PTR family 7.3 (*NPF7.3*), BAG family molecular chaperone regulator 5 (*BAG5*) and Dicer-like 2b (*DCL2b*) were responsive to drought. We constructed gene association networks to identify their potential interactors and found them drought-responsive. The identified candidate genes can help to explore the adaptation of tomato plants to drought. Furthermore, these candidate genes can have far-reaching implications for molecular breeding and genome editing in tomatoes, providing insights into the molecular mechanisms that underlie drought adaptation. This research underscores the importance of the genetic basis of plant adaptation, particularly in changing climates and growing populations.
https://www.nature.com/articles/s41598-023-45942-2

Ding, L.; Chen, G.; Chen, X.; Wang, X.; Lu, Y.; Liang, Z.; Xu, J.; Peng, C. (2023**): Analysis of the Unintended Effects of the Bacillus thuringiensis Insecticidal Protein in Genetically Modified Rice Using Untargeted Transcriptomics.** Processes 11, 3202 | https://doi.org/10.3390/pr11113202
The safety and unintended effects of genetically modified (GM) crops have been the focus of public attention. Transcriptome analysis is a powerful tool to assess the potential impact of genetic modification on plant genomes. In this study, three transgenic (KMD, KF6, and TT51-1) and three non-transgenic (XS11, MH86, and MH63) rice varieties were assessed at the genomic and protein levels. The results of polymerase chain reaction (PCR) and Cry1Ab/1Ac speed test strips showed that the Bt gene was successfully expressed in transgenic rice. The results of RNA-seq analysis to analyze the unintended effects of transgenic Bt rice showed fewer differentially expressed genes (DEGs) between the transgenic and non-transgenic rice varieties than among the different varieties. Meanwhile, the results of principal component analysis and cluster analysis found no significant genetic variation between the transgenic and non-transgenic rice varieties, except for the presence of Bt in transgenic rice. There were only two co-upregulated DEGs and no co-downregulated DEGs among three comparison groups. Although there were various DEGs among the groups, the two co-upregulated DEGs were not related to any significantly enriched gene ontology (GO) term or Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway, indicating that the differences among the subgroups were more likely caused by complex environmental or genetic factors, rather than unintended effects due to Bt expression. This study provides useful information to further explore the unexpected effects and safety of GM rice.
https://www.mdpi.com/2227-9717/11/11/3202

Huang Q., Lariviere P.J., Powell J.W., Moran N.A. (2023): **Engineered gut symbiont inhibits microsporidian parasite and improves honey bee survival**. PNAS 120 (25) e2220922120 https://doi.org/10.1073/pnas.2220922120
Honey bees (*Apis mellifera*) are critical agricultural pollinators as well as model organisms for research on development, behavior, memory, and learning. The parasite *Nosema ceranae*, a common cause of honey bee colony collapse, has developed resistance to small-molecule therapeutics. An alternative long-term strategy to combat *Nosema* infection is therefore urgently needed, with synthetic biology offering a potential solution. Honey bees harbor specialized bacterial gut symbionts that are transmitted within hives. Previously, these have been engineered to inhibit ectoparasitic mites by expressing double-stranded RNA (dsRNA) targeting essential mite genes, via activation of the mite RNA interference (RNAi) pathway. In this study, we engineered a honey bee gut symbiont to express dsRNA targeting essential genes of *N. ceranae* via the parasite's own RNAi machinery. The engineered symbiont sharply reduced *Nosema* proliferation and improved bee survival following the parasite challenge. This protection was observed in both newly emerged and older forager bees. Furthermore, engineered symbionts were transmitted among cohoused bees, suggesting that introducing engineered symbionts to hives could result in colony-level protection.
https://www.pnas.org/doi/10.1073/pnas.2220922120

Ntui V.O., Tripathi J.N., Kariuki S., Tripathi L. (2023): **Cassava molecular genetics and genomics for enhanced resistance to diseases and pests:** Molecular Plant Pathology | https://doi.org/10.1111/mpp.13402
Cassava (*Manihot esculenta*) is one of the most important sources of dietary calories in the tropics, playing a central role in food and economic security for smallholder farmers. Cassava production is highly constrained by several pests and diseases, mostly cassava mosaic disease (CMD) and cassava brown streak disease (CBSD). These diseases cause significant yield losses, affecting food security and the livelihoods of smallholder farmers. Developing resistant varieties is a good way of increasing cassava productivity. Although some levels of resistance have been developed for some of these diseases, there is observed breakdown in resistance for some diseases, such as CMD. A frequent re-evaluation of existing disease resistance traits is required to make sure they are still able to withstand the pressure associated with pest and pathogen evolution. Modern breeding approaches such as genomic-assisted selection in addition to biotechnology techniques like classical genetic engineering or genome editing can accelerate the development of pest- and disease-resistant cassava varieties. This article summarizes current developments and discusses the potential of using molecular genetics and genomics to produce cassava varieties resistant to diseases and pests.
https://bsppjournals.onlinelibrary.wiley.com/doi/10.1111/mpp.13402

Gutierrez A.P., Kenmore P.E. and Ponti L. (2023): **Hybrid Bt cotton is failing in India: cautions for Africa.** Environ Sci Eur 35, 93 | https://doi.org/10.1186/s12302-023-00804-6

This paper reviews the ongoing failure of hybrid transgenic Bt (*Bacillus thuringiensis*) cotton unique to India. The underlying cause for this failure is the high cost of hybrid seed that imposes a suboptimal long-season low plant density system that limits yield potential and has associated elevated levels of late-season pests. Indian hybrid Bt cotton production is further complicated by the development of resistance to Bt toxins in the key pest, the native pink bollworm (*Pectinophora gossypiella* Saunders, PBW), resulting in increased insecticide use that induces ecological disruption and outbreaks of highly destructive secondary pests. Rainfed cotton production uncertainty is further exacerbated by the variable monsoon rains. While hybrid cotton produces fertile seed, the resulting plant phenotypes are highly variable preventing farmers from replanting saved seed, forcing them to buy seed yearly (i.e., market capture), and effectively protecting industry Intellectual Property Rights (IPRs). The lessons gained from the ongoing market failure of hybrid Bt cotton in India are of utmost importance to its proposed introduction to Africa where, similar to India, cotton is grown mainly in poor rainfed smallholder family farms, and hence similar private–corporate conflicts of interest will occur. Holistic field agroecological studies and weather-driven mechanistic analyses are suggested to help foresee ecological and economic challenges in cotton production in Africa.
High-density short-season (HD-SS) non-hybrid non-genetically modified irrigated and rainfed cottons are viable alternatives for India that can potentially produce double the yields of the current low-density hybrid system.
https://enveurope.springeropen.com/articles/10.1186/s12302-023-00804-6

Taghon G J. and Strychalski E.A. (2023): **Rise of synthetic yeast: Charting courses to new applications.** Cell Genomics | DOI:https://doi.org/10.1016/j.xgen.2023.100438
Microbes have long provided us with important capabilities, and the genome engineering of microbes has greatly empowered research and applications in biotechnology. This is especially true with the emergence of synthetic biology and recent advances in genome engineering to control microbial behavior. A fully synthetic, rationally designed genome promises opportunities for unprecedented control of cellular function. As a eukaryotic workhorse for research and industrial use, yeast is an organism at the forefront of synthetic biology; the tools and engineered cellular platform being delivered by the Sc2.0 consortium are enabling a new era of bespoke biology. This issue highlights recent advances delivered by this consortium, but hurdles remain to maximize the impact of engineered eukaryotic cells more broadly.
https://www.cell.com/cell-genomics/fulltext/S2666-979X(23)00273-2

Schindler, D.; Walker, R.S.K.; Jiang, S.; Brooks, A.N. et al: (2023): **Design, construction, and functional characterization of a tRNA neochromosome in yeast.** Cell | https://doi.org/10.1016/j.cell.2023.10.015
Here, we report the design, construction, and characterization of a tRNA neochromosome, a designer chromosome that functions as an additional, *de novo* counterpart to the native complement of *Saccharomyces cerevisiae*. Intending to address one of the central design principles of the Sc2.0 project, the ∼190-kb tRNA neochromosome houses all 275 relocated nuclear tRNA genes. To maximize stability, the design incorporates orthogonal genetic elements from non-*S. cerevisiae* yeast species. Furthermore, the presence of 283 *rox* recombination sites enables an orthogonal tRNA SCRaMbLE system. Following construction in yeast, we obtained evidence of a potent selective force, manifesting as a spontaneous doubling in cell ploidy. Furthermore, tRNA sequencing, transcriptomics, proteomics, nucleosome mapping, replication profiling, FISH, and Hi-C were undertaken to investigate questions of tRNA neochromosome behavior and function. Its construction demonstrates the remarkable tractability of the yeast model and opens up opportunities to directly test hypotheses surrounding these essential non-coding RNAs.
https://www.cell.com/cell/fulltext/S0092-8674(23)01130-3?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867423011303%3Fshowall%3Dtrue

Zhao Y., Coelho C, Hughes A.L. et al. (2023): **Debugging and consolidating multiple synthetic chromosomes reveals combinatorial genetic interactions.** Celll | https://doi.org/10.1016/j.cell.2023.09.025
The Sc2.0 project is building a eukaryotic synthetic genome from scratch. A major milestone has been achieved with all individual Sc2.0 chromosomes assembled. Here, we describe the consolidation of multiple synthetic chromosomes using advanced endoreduplication intercrossing with tRNA expression cassettes to generate a strain with 6.5 synthetic chromosomes. The 3D chromosome organization and transcript isoform profiles were evaluated using Hi-C and long-read direct RNA sequencing. We developed CRISPR Directed Biallelic *URA3*-assisted Genome Scan, or "CRISPR D-BUGS," to map phenotypic variants caused by specific designer modifications, known as "bugs." We first fine-mapped a bug in synthetic chromosome II (*synII*) and then discovered a combinatorial interaction associated with *synIII* and *synX*, revealing an unexpected genetic interaction that links transcriptional regulation, inositol metabolism, and $tRNA_{Ser}^{CGA}$ abundance. Finally, to expedite consolidation, we employed chromosome substitution to incorporate the largest chromosome (*synIV*), thereby consolidating >50% of the Sc2.0 genome in one strain.
https://www.cell.com/cell/fulltext/S0092-8674(23)01079-6

Kerr D.R., Concepcion J.C.T., Riechers D.E. (2023): **Inheritance of resistance to S-metolachlor in a waterhemp (Amaranthus tuberculatus) population from central Illinois**, Weed Science | DOI: 10.1017/wsc.2023.63
Waterhemp [Amaranthus tuberculatus (Moq.) Sauer] is a dioecious weed that has evolved resistance to very-long-chain fatty acid (VLCFA) elongase-inhibiting herbicides via rapid metabolism. Although detoxification

enzyme activities are associated with S-metolachlor resistance in two multiple herbicide-resistant (MHR) A. tuberculatus populations from Illinois, the genetic basis of resistance is unknown. Therefore, our goal was to investigate inheritance of S-metolachlor resistance in the Stanford, Illinois Resistant (SIR) population. Specifically, our research objectives were to: i) generate a uniformly resistant, full-sib near inbred line (DK3-2) via three generations of recurrent selection for resistance using preemergence S-metolachlor, ii) develop A. tuberculatus populations segregating for S-metolachlor resistance via reciprocal single plant (one male × one female) full-sib mating of DK3-2 and a VLCFA inhibiting herbicide-sensitive population, SEN, iii) quantify S-metolachlor resistance levels in parental lines and their F1 progenies via greenhouse dose-response analysis, and iv) evaluate inheritance of S-metolachlor resistance in F2 progenies. Dose-response analysis using 6 to 8 S-metolachlor concentrations (0.015–15.0 µM; varying per population) generated lethal dose (LD) estimates of 50% (LD50) and 90% (LD90) for SIR, SEN, DK3-2 and F1 progenies. Lethal dose estimates indicated DK3-2 has a higher magnitude of S-metolachlor resistance than the SIR population, demonstrating single crosses significantly increased S-metolachlor resistance in DK3-2. Levels of S-metolachlor resistance in F1 populations were intermediate compared to DK3-2 and SEN. Segregation of S-metolachlor resistance in F2 families from the paternal-derived lines fit a single-gene model (R:S = 3:1), indicating a single, dominant gene confers S-metolachlor resistance in SIR. However, F2 segregation results from the maternal-derived lines fit a duplicate recessive epistasis model (R:S = 9:7), indicating a second recessive gene may also modify S-metolachlor resistance in SIR. Results and germplasm derived from this research can assist in identifying the gene(s) conferring resistance to S-metolachlor in A. tuberculatus.
https://www.cambridge.org/core/journals/weed-science/article/abs/inheritance-of-resistance-to-smetolachlor-in-a-waterhemp-amaranthus-tuberculatus-population-from-central-illinois/4A0A4F199E3BFA876BF2501814784C2D

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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