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

Wissenschaftskreis
Genomik und
Gentechnik e.V.

Meeting - Veranstaltungen

Kraft der Ideen – Das Wissenssymposium Fischer´s EM-Tage
83071 STEPHANSKIRCHEN (ROSENHEIM), 05.06.08.2023
GASTBEITRAG | Auf dem Wissenssymposium Fischer´s EM-Tage in Stephanskirchen dreht sich dieses Jahr alles um effektive Mikroorganismen und eine grüne Zukunft.
https://www.lifeverde.de/nachhaltigkeitsmagazin/gruene-wirtschaft/kraft-der-ideen-das-wissenssymposium-fischers-em-tage

Das Programm: https://shop.em-chiemgau.de/wp-content/uploads/2023/06/EM-Tage-Programm-30-06-23-Stephanskirchen-EM-Chiemgau.pdf

Press Releases -Media / Presse- und Medienberichte

DFG und Leopoldina unterstützen Vorschlag der EU-Kommission zum Umgang mit neuen Gentechnikmethoden in Pflanzenzucht
https://idw-online.de/de/news818063
www.dfg.de/download/pdf/dfg_im_profil/geschaeftsstelle/publikationen/stellungnahmen_papiere/2023/statement_genomic_techniques.pdf

Jötten F.: **»Wir sollten die moderne Technik nutzen«**
https://www.spektrum.de/news/bio-und-gentechnik-wir-sollten-die-moderne-technik-nutzen/2159721

Focus: **Bei der Gentechnik stehen die Grünen ihren eigenen Zielen im Weg**
https://www.focus.de/politik/deutschland/bei-der-gentechnik-stehen-die-gruenen-ihren-eigenen-zielen-im-weg_id_199748475.html

GM Watch: **Testbiotech: First recommendations with regard to the EU Commission proposal on new GMOs**
https://gmwatch.org/en/106-news/latest-news/20262
Background 18-7-2023:
https://www.testbiotech.org/sites/default/files/Backgrounder%20NGT%20risk%20assessment_EU%20proposal.pdf

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ►here: June week 29

Publications – Publikationen

Mehta D.: **EU proposal on CRISPR-edited crops is welcome — but not enough**
https://www.nature.com/articles/d41586-023-02328-8

Većkalov, B., van Stekelenburg, A., van Harreveld, F., & Rutjens, B. T. (2023). **Who Is Skeptical About Scientific Innovation? Examining Worldview Predictors of Artificial Intelligence, Nanotechnology, and Human Gene Editing Attitudes**. Science Communication, *0*(0).
https://doi.org/10.1177/10755470231184203
This work examines worldview predictors of attitudes toward nanotechnology, human gene editing (HGE), and artificial intelligence. By simultaneously assessing the relative predictive value of various worldview variables in two Dutch samples (total *N* = 614), we obtained evidence for spirituality as a key predictor of skepticism across domains. Religiosity consistently predicted HGE skepticism only. Lower faith in science contributed to these relationships. Aversion to tampering with nature predicted skepticism across domains. These results speak to the importance of religiosity and spirituality for scientific innovation attitudes.
https://journals.sagepub.com/doi/10.1177/10755470231184203

Alastair Matheson (2023) **The "Monsanto papers" and the nature of ghostwriting and related practices in contemporary peer review scientific literature**, Accountability in Research,| DOI: 10.1080/08989621.2023.2234819
The Monsanto company – now acquired by Bayer – has been accused of ghostwriting articles within peer review literature, with the goal of using influential names to front its content in defence of the herbicide

Roundup. Here, I conduct a detailed analysis of three Monsanto review articles and a five-article journal supplement for which detailed information from company emails is publicly available following litigation over Roundup. All the articles had external, but not Monsanto authors, and ghostly practices including ghost authorship, corporate ghost authorship and ghost management were evident in their development. There was clear evidence of ghostwriting – that is, drafting of the manuscript by non-authors – in only two cases. I found no evidence of undeserving authorship among the external authors. The articles complied with the disclosure requirements of their journals, save for the journal supplement. While crude ghostwriting did occur, much of the literature involved subtler practices through which Monsanto exercised control over content, while the attribution of the articles downplayed the company's role – and correspondingly aggrandized that of the external authors. Such practices are widespread within industry journal literature and are the responsibility of byline authors and journals as well as corporations. I discuss these cultural problems and consider remedies.
https://www.tandfonline.com/doi/full/10.1080/08989621.2023.2234819#:~:text=View%20EPUB-,ABSTRACT,well%20as%20corporations.%20I%20discuss%20these%20cultural%20problems%20and%20consider%20remedies.,-KEYWORDS%3A

Riesenberg, S., Kanis, P., Macak, D. et al. (2023): **Efficient high-precision homology-directed repair-dependent genome editing by HDRobust.** Nat Methods | https://doi.org/10.1038/s41592-023-01949-1
Homology-directed repair (HDR), a method for repair of DNA double-stranded breaks can be leveraged for the precise introduction of mutations supplied by synthetic DNA donors, but remains limited by low efficiency and off-target effects. In this study, we report HDRobust, a high-precision method that, via the combined transient inhibition of nonhomologous end joining and microhomology-mediated end joining, resulted in the induction of point mutations by HDR in up to 93% (median 60%, s.e.m. 3) of chromosomes in populations of cells. We found that, using this method, insertions, deletions and rearrangements at the target site, as well as unintended changes at other genomic sites, were largely abolished. We validated this approach for 58 different target sites and showed that it allows efficient correction of pathogenic mutations in cells derived from patients suffering from anemia, sickle cell disease and thrombophilia.
https://www.nature.com/articles/s41592-023-01949-1

Sulis D.B, Jiang X., Yang C., Marques B.M. et al. (2023): **Multiplex CRISPR editing of wood for sustainable fiber production.** Science 381 (6654), 216-221 | DOI: 10.1126/science.add4514
The domestication of forest trees for a more sustainable fiber bioeconomy has long been hindered by the complexity and plasticity of lignin, a biopolymer in wood that is recalcitrant to chemical and enzymatic degradation. Here, we show that multiplex CRISPR editing enables precise woody feedstock design for combinatorial improvement of lignin composition and wood properties. By assessing every possible combination of 69,123 multigenic editing strategies for 21 lignin biosynthesis genes, we deduced seven different genome editing strategies targeting the concurrent alteration of up to six genes and produced 174 edited poplar variants. CRISPR editing increased the wood carbohydrate-to-lignin ratio up to 228% that of wild type, leading to more-efficient fiber pulping. The edited wood alleviates a major fiber-production bottleneck regardless of changes in tree growth rate and could bring unprecedented operational efficiencies, bioeconomic opportunities, and environmental benefits.
https://www.science.org/doi/10.1126/science.add4514

Long Y., Xu W., Liu C., Dong M., Liu W. et al. (2023): **Genetically modified soybean lines exhibit less transcriptomic variation compared to natural varieties**, GM Crops & Food, 14:1, 1-11, | 10.1080/21645698.2023.2233122
Genetically modified (GM) soybeans provide a huge amount of food for human consumption and animal feed. However, the possibility of unexpected effects of transgenesis has increased food safety concerns. High-throughput sequencing profiling provides a potential approach to directly evaluate unintended effects caused by foreign genes. In this study, we performed transcriptomic analyses to evaluate differentially expressed genes (DEGs) in individual soybean tissues, including cotyledon (C), germ (G), hypocotyl (H), and radicle (R), instead of using the whole seed, from four GM and three non-GM soybean lines. A total of 3,351 DEGs were identified among the three non-GM soybean lines. When the GM lines were compared with their non-GM parents, 1,836 to 4,551 DEGs were identified. Furthermore, Gene Ontology (GO) analysis of the DEGs showed more abundant categories of GO items (199) among non-GM lines than between GM lines and the non-GM natural varieties (166). Results of Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis showed that most KEGG pathways were the same for the two types of comparisons. The study successfully employed RNA sequencing to assess the differences in gene expression among four tissues of seven soybean varieties, and the results suggest that transgenes do not induce massive transcriptomic alterations in transgenic soybeans compared with those that exist among natural varieties. This work offers empirical evidence to investigate the genomic-level disparities induced by genetic modification in soybeans, specifically focusing on seed tissues.
https://www.tandfonline.com/doi/full/10.1080/21645698.2023.2233122

Byrt, C.S., Millar, A.H. & Munns, R. (2023): **Staple crops equipped for alkaline soils**. ***Nat Biotechnol*** 41, 911–912 | https://doi.org/10.1038/s41587-023-01832-6
Gene editing boosts the yields of sorghum, rice and millet grown in alkaline soils.
https://www.nature.com/articles/s41587-023-01832-6

Choi, H.-Y.; Kim, E.-G.; Park, J.-R.; Jang, Y.-H. et al. (2023): **Volunteer Plants' Occurrence and the Environmental Adaptability of Genetically Modified Fodder Corn upon Unintentional Release into the Environment.** Plants 12, 2653 | https://doi.org/10.3390/plants12142653

The number of corn cultivars that have been improved using genetically modified technology continues to increase. However, concerns about the unintentional release of living-modified organisms (LMOs) into the environment still exist. Specifically, there are cases where LMO crops grown as fodder are released into the environment and form a volunteer plant community, which raises concerns about their safety. In this study, we analyzed the possibility of weediness and volunteer plants' occurrence when GMO fodder corn grains distributed in Korea are unintentionally released into the environment. Volunteer plants' occurrence was investigated by directly sowing grains in an untreated field. The results showed that the germination rate was extremely low, and even if a corn seed germinated, it could not grow into an adult plant and would die due to weed competition. In addition, the germination rate of edible and fodder grains was affected by temperature (it was high at 20 °C and 30 °C but low at 40 °C and extremely low at 10 °C), and it was higher in the former than in the latter. And the germination rate was higher in Daehakchal (edible corn grains) than in Gwangpyeongok (fodder corn grains). The environmental risk assessment data obtained in this study can be used for future evaluations of the weediness potential of crops and the development of volunteer plant suppression technology in response to unintentional GMO release.
https://www.mdpi.com/2223-7747/12/14/2653

Yow, A.G., Bostan, H., Young, R. et al. (2023): **Identification of bromelain subfamily proteases encoded in the pineapple genome**. *Sci Rep* 13, 11605 | https://doi.org/10.1038/s41598-023-38907-y

Papain (aka C1A) family proteases, including bromelain enzymes, are widespread across the plant kingdom and play critical regulatory functions in protein turnover during development. The proteolytic activity exhibited by papain family proteases has led to their increased usage for a wide range of cosmetic, therapeutic, and medicinal purposes. Bromelain enzymes, or bromelains in short, are members of the papain family that are specific to the bromeliad plant family. The only major commercial extraction source of bromelain is pineapple. The importance of C1A family and bromelain subfamily proteases in pineapple development and their increasing economic importance led several researchers to utilize available genomic resources to identify protease-encoding genes in the pineapple genome. To date, studies are lacking in screening bromelain genes for targeted use in applied science studies. In addition, the bromelain genes coding for the enzymes present in commercially available bromelain products have not been identified and their evolutionary origin has remained unclear. Here, using the newly developed MD2 v2 pineapple genome, we aimed to identify bromelain-encoding genes and elucidate their evolutionary origin. Orthologous and phylogenetic analyses of all papain-family proteases encoded in the pineapple genome revealed a single orthogroup (189) and phylogenetic clade (XIII) containing the bromelain subfamily. Duplication mode and synteny analyses provided insight into the origin and expansion of the bromelain subfamily in pineapple. Proteomic analysis identified four bromelain enzymes present in two commercially available bromelain products derived from pineapple stem, corresponding to products of four putative bromelain genes. Gene expression analysis using publicly available transcriptome data showed that 31 papain-family genes identified in this study were up-regulated in specific tissues, including stem, fruit, and floral tissues. Some of these genes had higher expression in earlier developmental stages of different tissues. Similar expression patterns were identified by RT-qPCR analysis with leaf, stem, and fruit. Our results provide a strong foundation for future applicable studies on bromelain, such as transgenic approaches to increase bromelain content in pineapple, development of bromelain-producing bioreactors, and studies that aim to determine the medicinal and/or therapeutic viability of individual bromelain enzymes.
https://www.nature.com/articles/s41598-023-38907-y

EFSA

CEP Panel (2023). Safety evaluation of the food enzyme pectinesterase from the genetically modified *Aspergillus niger* strain PME. *EFSA Journal*, 21(7), , 1–16.
https://doi.org/10.2903/j.efsa.2023.8152
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8152

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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