Sunday Evening News No 346

2023-10-02 – 2023-10-08

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

Endlich das Brot mit „Frei von allem“ Now, finally the bread with free of everything

Meetings – Conferences / Tagungen - Konferenzen

VBIO: 24. Oktober um 17.00 Uhr: **„Forschung - Ethik - Relevanz: Tierversuche in Deutschland aus Sicht eines Forschenden“**.
Registrierung: https://us06web.zoom.us/webinar/register/WN_OeXXZDhCSh6TXwM0f2iSJA

Infoday: Food Proteins from Biotechnology
30.November 2023 - DECHEMA-Haus, Frankfurt am Main
https://dechema.de/Food23.html

Press Releases -Media / Presse- und Medienberichte

Christiane Nüsslein-Volhard: „Grenzen und Potentiale der modernen Genforschung“
https://www.tagblatt.de/Nachrichten/Christiane-Nuesslein-Volhard-Grenzen-und-Potentiale-der-modernen-Genforschung-605143.html

Nobelpreis für Medizin für die Entwicklung von mRNA-Impfstoffen
https://www.forschung-und-lehre.de/forschung/nobelpreis-fuer-medizin-geht-an-katalin-kariko-und-drew-weissman-5940

Nobel Prize goes to scientists behind mRNA Covid vaccines
https://www.bbc.com/news/health-66983060

Bertioli D.J. and Miller H.I: **The Inhibition of Innovation** - Fall 2023 Regulation
https://www.cato.org/regulation/fall-2023/inhibition-innovation

Liboreiro J.: **These are the four technologies the EU wants to protect, especially from China**
https://www.euronews.com/my-europe/2023/10/03/these-are-the-four-technologies-the-eu-wants-to-protect-especially-from-china

POINT NEWSLETTER NR. 255 – SEPTEMBER 2023 - Aktuelle Biotechnologie
https://www.scienceindustries.ch/_file/34630/point-2023-09-255-d.pdf?utm_source=POINT+Newsletter&utm_campaign=d021f0fcaf-POINT_September_2023_live&utm_medium=email&utm_term=0_19eef28c92-d021f0fcaf-1210937714

Commission: **Commission Recommendation of 03 October 2023 on critical technology areas for the EU's economic security for further risk assessment with Member States**

https://defence-industry-space.ec.europa.eu/commission-recommendation-03-october-2023-critical-technology-areas-eus-economic-security-further_en

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ▶here: October week 40

Publications – Publikationen

Fischer, K., Rock, J.S. (2023): **The scientific narrative around new food technologies needs to change**. Nat Rev Bioeng | https://doi.org/10.1038/s44222-023-00128-3
The scientific narrative around food biotechnologies, such as genetically modified crops, is ineffective at predicting their role in the development and change of agricultural practices and food. Here, we suggest placing the scientific discussion of new food technologies in the context of the political and economic forces that shape agriculture.
https://www.nature.com/articles/s44222-023-00128-3

Tuncel, A., Pan, C., Sprink, T. et al. (2023): **Genome-edited foods.** Nat Rev Bioeng | https://doi.org/10.1038/s44222-023-00115-8
Genome editing can transform agriculture and shape the future of food by improving crop yields and animal productivity, which in turn can help to achieve food security for the growing world population. CRISPR–Cas-based technologies are powerful gene editing tools that are applied to various food products. In this Review, we discuss the applications of CRISPR–Cas aimed at increasing the nutritional value of crops through macronutrient engineering and biofortification or the reduction of the amount of antinutrients. We examine the role of CRISPR–Cas in improving the flavour of crops and reducing post-harvest losses to increase consumer acceptance and decrease food waste. We also highlight the gene editing of animal food products and probiotics. We summarize the regulations for approval of gene-edited foods worldwide and the progressively evolving public view. Finally, we explore the strategies that can help to enhance the efficiency of genome editing techniques and the acceptance of genome-edited foods in the global market, and extend the technology to low-resource settings.
https://www.nature.com/articles/s44222-023-00115-8

Shahiba A M; Jayalekshmy V G; Arun Chacko (2023): **Traditional Plant Breeding Techniques - Exploring Crossbreeding and Selection Methods** | DOI:10.5281/zenodo.8406082

Khaipho-Burch M., Cooper M., Crossa J., de Leon N, et al. (2023): **Scale up trials to validate modified crops' benefits.** Nature 621, 470-473
With a changing climate and a growing population, the world increasingly needs more-productive and resilient crops. But improving them requires a knowledge of what actually works in the field.
https://www.nature.com/articles/d41586-023-02895-w.pdf

Huang, Y., He, J., Xu, Y. et al. (2023): **Pangenome analysis provides insight into the evolution of the orange subfamily and a key gene for citric acid accumulation in citrus fruits.** Nat Genet | https://doi.org/10.1038/s41588-023-01516-6
The orange subfamily (Aurantioideae) contains several *Citrus* species cultivated worldwide, such as sweet orange and lemon. The origin of *Citrus* species has long been debated and less is known about the Aurantioideae. Here, we compiled the genome sequences of 314 accessions, de novo assembled the genomes of 12 species and constructed a graph-based pangenome for Aurantioideae. Our analysis indicates that the ancient Indian Plate is the ancestral area for *Citrus*-related genera and that South Central China is the primary center of origin of the *Citrus* genus. We found substantial variations in the sequence and expression of the *PH4* gene in *Citrus* relative to *Citrus*-related genera. Gene editing and biochemical experiments demonstrate a central role for *PH4* in the accumulation of citric acid in citrus fruits. This study provides insights into the origin and evolution of the orange subfamily and a regulatory mechanism underpinning the evolution of fruit taste.
https://www.nature.com/articles/s41588-023-01516-6

Raimondeau P., Bianconi M.E., Pereira L., Parisod C., Christin P.-A., Dunning L.T. (2023): **Lateral gene transfer generates accessory genes that accumulate at different rates within a grass lineage.** New Phytologist | https://doi.org/10.1111/nph.19272
Lateral gene transfer (LGT) is the movement of DNA between organisms without sexual reproduction. The acquired genes represent genetic novelties that have independently evolved in the donor's genome. Phylogenetic methods have shown that LGT is widespread across the entire grass family, although we know little about the underlying dynamics.
We identify laterally acquired genes in five *de novo* reference genomes from the same grass genus (four *Alloteropsis semialata* and one *Alloteropsis angusta*). Using additional resequencing data for a further 40 *Alloteropsis* individuals, we place the acquisition of each gene onto a phylogeny using stochastic character mapping, and then infer rates of gains and losses
We detect 168 laterally acquired genes in the five reference genomes (32–100 per genome). Exponential decay models indicate that the rate of LGT acquisitions (6–28 per Ma) and subsequent losses (11–24% per Ma) varied

significantly among lineages. Laterally acquired genes were lost at a higher rate than vertically inherited loci (0.02–0.8% per Ma).
This high turnover creates intraspecific gene content variation, with a preponderance of them occurring as accessory genes in the *Alloteropsis* pangenome. This rapid turnover generates standing variation that can ultimately fuel local adaptation.
https://nph.onlinelibrary.wiley.com/doi/10.1111/nph.19272

Sulli, M., Dall'Osto, L., Ferrante, P. et al. (2023**): Generation and physiological characterization of genome-edited *Nicotiana benthamiana* plants containing zeaxanthin as the only leaf xanthophyll.** Planta 258, 93 | https://doi.org/10.1007/s00425-023-04248-3
Plant carotenoids act both as photoreceptors and photoprotectants in photosynthesis and as precursors of apocarotenoids, which include signaling molecules such as abscisic acid (ABA). As dietary components, the xanthophylls lutein and zeaxanthin have photoprotective functions in the human macula. We developed transient and stable combinatorial genome editing methods, followed by direct LC–MS screening for zeaxanthin accumulation, for the simultaneous genome editing of the two homeologous *Lycopene Epsilon Cyclase* (*LCYe*) and the two *Zeaxanthin Epoxidase* (*ZEP*) genes present in the allopolyploid *Nicotiana benthamiana* genome. Editing of the four genes resulted in plants in which all leaf xanthophylls were substituted by zeaxanthin, but with different ABA levels and growth habits, depending on the severity of the *ZEP1* mutation. In high-zeaxanthin lines, the abundance of the major photosystem II antenna LHCII was reduced with respect to wild-type plants and the LHCII trimeric state became unstable upon thylakoid solubilization. Consistent with the depletion in LHCII, edited plants underwent a compensatory increase in PSII/PSI ratios and a loss of the large-size PSII supercomplexes, while the level of PSI-LHCI supercomplex was unaffected. Reduced activity of the photoprotective mechanism NPQ was shown in high-zeaxanthin plants, while PSII photoinhibition was similar for all genotypes upon exposure to excess light, consistent with the antioxidant and photoprotective role of zeaxanthin in vivo.
https://link.springer.com/article/10.1007/s00425-023-04248-3

Kiranmai, B., Vasantha, S.V., Jyoshna, B., Suvarna Mukhi, B. (2023). **Detection of Accurate Gene Location for Modification or Replacement of DNA and True Guide Synthetic gRNA for CRISPR.** In: Kumar, A., Ghinea, G., Merugu, S. (eds) Proceedings of the 2nd International Conference on Cognitive and Intelligent Computing. ICCIC 2022. Cognitive Science and Technology. Springer, Singapore. https://doi.org/10.1007/978-981-99-2746-3_49
One of the most important aspects of bioinformatics is locating genes within a long DNA sequence. Until the development of bioinformatics, the only way to locate genes along the chromosome was to study their behavior in the organism or isolate the DNA and study in a test laboratory. Bioinformatics allow scientists to make educated guesses about where genes are located simply by analyzing sequence data using a computer. The CRISPR/CAS9 system has been rapidly adopted for genome editing. In a typical CRISPR, a SgRNA is designed to have a guide sequence domain designated. However, one major time with this system is the lack of robust bioinformatics tools for design of single guide RNA which determines the efficiency and specificity of genome editing.
https://link.springer.com/chapter/10.1007/978-981-99-2746-3_49

Wu K., Xu C., Li T., Ma H. et al. (2023): **Application of Nanotechnology in Plant Genetic Engineering.** *Int. J. Mol. Sci.* 2023, *24*(19), 14836; https://doi.org/10.3390/ijms241914836
The ever-increasing food requirement with globally growing population demands advanced agricultural practices to improve grain yield, to gain crop resilience under unpredictable extreme weather, and to reduce production loss caused by insects and pathogens. To fulfill such requests, genome engineering technology has been applied to various plant species. To date, several generations of genome engineering methods have been developed. Among these methods, the new mainstream technology is clustered regularly interspaced short palindromic repeats (CRISPR) with nucleases. One of the most important processes in genome engineering is to deliver gene cassettes into plant cells. Conventionally used systems have several shortcomings, such as being labor- and time-consuming procedures, potential tissue damage, and low transformation efficiency. Taking advantage of nanotechnology, the nanoparticle-mediated gene delivery method presents technical superiority over conventional approaches due to its high efficiency and adaptability in different plant species. In this review, we summarize the evolution of plant biomolecular delivery methods and discussed their characteristics as well as limitations. We focused on the cutting-edge nanotechnology-based delivery system, and reviewed different types of nanoparticles, preparation of nanomaterials, mechanism of nanoparticle transport, and advanced application in plant genome engineering. On the basis of established methods, we concluded that the combination of genome editing, nanoparticle-mediated gene transformation and de novo regeneration technologies can accelerate crop improvement efficiently in the future.
https://www.mdpi.com/1422-0067/24/19/14836

Raudstein, M., Kjærner-Semb, E., Barvik, M. et al. (2023): **In vivo CRISPR/LbCas12a-mediated knock-in and knock-out in Atlantic salmon (*Salmo salar* L.).** Transgenic Res | https://doi.org/10.1007/s11248-023-00368-4
Genome editing using the CRISPR/Cas system offers the potential to enhance current breeding programs and introduce desirable genetic traits, including disease resistance, in salmon aquaculture. Several nucleases are available using this system, displaying differences regarding structure, cleavage, and PAM requirement. Cas9 is

well established in Atlantic salmon, but Cas12a has yet to be tested in vivo in this species. In the present work, we microinjected salmon embryos with LbCas12a ribonucleoprotein complexes targeting the pigmentation gene *solute carrier family 45 member 2* (*slc45a2*). Using CRISPR/LbCas12a, we were able to knock-out *slc45a2* and knock-in a FLAG sequence element by providing single-stranded DNA templates. High-throughput sequencing revealed perfect HDR rates up to 34.3% and 54.9% in individual larvae using either target or non-target strand template design, respectively. In this work, we demonstrate the in vivo application of CRISPR/LbCas12a in Atlantic salmon, expanding the toolbox for editing the genome of this important aquaculture species.
https://link.springer.com/article/10.1007/s11248-023-00368-4

Pascher K, Hainz-Renetzeder C, Jagersberger M, Kneissl K, Gollmann G, Schneeweiss GM (2023): **Contamination of imported kernels by unapproved genome-edited varieties poses a major challenge for monitoring and traceability during transport and handling on a global scale: inferences from a study on feral oilseed rape in Austria.** Front. Genome Ed. 5,1176290. | doi: 10.3389/fgeed.2023.1176290
Novel techniques such as CRISPR/Cas are increasingly being applied for the development of modern crops. However, the regulatory framework for production, labelling and handling of genome-edited organisms varies worldwide. Currently, the European Commission is raising the question whether genome-edited organisms should still be regulated as genetically modified organisms in the future or whether a deregulation should be implemented. In our paper, based on the outcome of a 2-year case study on oilseed rape in Austria, we show that seed spillage during import and subsequent transport and handling activities is a key factor for the unintended dispersal of seeds into the environment, the subsequent emergence of feral oilseed rape populations and their establishment and long-term persistence in natural habitats. These facts must likewise be considered in case of genome-edited oilseed rape contaminants that might be accidentally introduced with conventional kernels. We provide evidence that in Austria a high diversity of oilseed rape genotypes, including some with alleles not known from cultivated oilseed rape in Austria, exists at sites with high seed spillage and low weed management, rendering these sites of primary concern with respect to possible escape of genome-edited oilseed rape varieties into the environment. Since appropriate detection methods for single genome-edited oilseed rape events have only recently started to be successfully developed and the adverse effects of these artificial punctate DNA exchanges remain largely unknown, tracing the transmission and spread of these genetic modifications places high requirements on their monitoring, identification, and traceability.
https://www.frontiersin.org/articles/10.3389/fgeed.2023.1176290/full

Ahmed, A.I., Abou-Taleb, K.A.A. & Abd-Elhalim, B.T. (2023): **Characterization and application of tannase and gallic acid produced by co-fungi of *Aspergillus niger* and *Trichoderma viride* utilizing agro-residues substrates.** *Sci Rep* 13, 16755 | https://doi.org/10.1038/s41598-023-43955-5
Bioconversion using fungi, as natural factory of many applicable bioactive compounds, as enzymes utilizing agro-residue substrates as a solid, abundant, low-cost growth and enzyme production media. This study characterized and applied a tannase enzyme (308 U/mg) from *Aspergillus niger* A8 + *Trichoderma viride* co-cultures utilizing pomegranate peels. The partially purified enzyme showed maximal relative activity at 37–65 °C for 10 min and kinetics of thermal inactivation energy at a high point at 60 °C for 0.040/min. The half-life was 37 °C for 58.6 min, temperature coefficient Q_{10} of tannase was maximal for 1.38 between 40 and 50 °C, and the activation energy was 17.42 kJ/mol. The enzyme activity peaked in the pH range of 4–8, and the maximum relative activity (100.6%) for tannase was achieved at pH 6. The K_m and V_{max} values for purified enzymes using tannic acid were 7.3 mg/mL and 3333.33 U/mL, respectively. The enzyme reduced the total tannin content in all tannin-rich substrates after 12h. The gallic acid (GA) had total phenols of 77.75 ppm and antioxidant activity of 82.91%. It was observed that the GA as antimicrobial influencer exhibited the largest inhibitory zone diameter (IZD) of 31 ± 1.0 mm against *Pseudomonas aeruginosa* ATCC27853. The GA minimum inhibitory concentration value was ranged from 7770.0–121.41 µg/mL. The obtained GA showed a bactericidal effect against all bacterial strains except *Shigella sonnei* DSM5570 and *Salmonella typhi* DSM17058, which showed bacteriostatic behavior.
https://www.nature.com/articles/s41598-023-43955-5

Tanaka, M., Zhang, S., Sato, S. et al. (2023): **Physiological ER stress caused by amylase production induces regulated Ire1-dependent mRNA decay in *Aspergillus oryzae*.** Commun Biol 6, 1009 | https://doi.org/10.1038/s42003-023-05386-w
Regulated Ire1-dependent decay (RIDD) is a feedback mechanism in which the endoribonuclease Ire1 cleaves endoplasmic reticulum (ER)-localized mRNAs encoding secretory and membrane proteins in eukaryotic cells under ER stress. RIDD is artificially induced by chemicals that generate ER stress; however, its importance under physiological conditions remains unclear. Here, we demonstrate the occurrence of RIDD in filamentous fungus using *Aspergillus oryzae* as a model, which secretes copious amounts of amylases. α-Amylase mRNA was rapidly degraded by IreA, an Ire1 ortholog, depending on its ER-associated translation when mycelia were treated with dithiothreitol, an ER-stress inducer. The mRNA encoding maltose permease MalP, a prerequisite for the induction of amylolytic genes, was also identified as an RIDD target. Importantly, RIDD of *malP* mRNA is triggered by inducing amylase production without any artificial ER stress inducer. Our data provide the evidence that RIDD occurs in eukaryotic microorganisms under physiological ER stress.
https://www.nature.com/articles/s42003-023-05386-w

EFSA
CEP Panel (2023): **Safety evaluation of the food enzyme glucose oxidase from the genetically modified *Saccharomyces cerevisiae* strain LALL-GO.** EFSA Journal, 21 (10), 1–14; | https://doi.org/10.2903/j.efsa.2023.8257
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8257

CEP Panel (2023): **Safety evaluation of the food enzyme triacylglycerol lipase from the pregastric tissues of calves, young goats and lambs.** EFSA Journal 21 (9), 1–10. | https://doi.org/10.2903/j.efsa.2023.8253
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8253

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.*

Prof. Dr. Klaus-Dieter Jany
Nelkenstrasse 36
D-76351 Linkenheim-Hochstetten
jany@biotech-gm-food.com

Wissenschaftskreis Genomik und Gentechnik
1.Vorsitzender: Prof. Dr. Kl.-D. Jany
jany@wgg-ev.de