Sunday Evening News No 337

2023-07-31 – 2023-08-06

Compiled and edited by *BGF* Jany

Wissenschaftskreis
Genomik und
Gentechnik e.V.

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Press Releases -Media / Presse- und Medienberichte

Kaufmann D.: **Wir kennen TATSÄCHLICH den Unterschied**
https://evidenzbasierte-politik.de/2023/08/02/wir-kennen-tatsaechlich-den-unterschied/

https://www.biowisskomm.de/2023/08/wir-kennen-tatsaechlich-den-
unterschied/?fbclid=IwAR3sqX9GXkS60evozZK6cNmJOdmgnZB-6yXZOQ59B8h3_eZVWb-sImtfEj0

Testbiotech: **Übersichtstabelle zu Unterschieden zwischen Neuer Gentechnik und Züchtung veröffentlicht**
https://www.testbiotech.org/aktuelles/uebersichtstabelle-unterschiede-NGT-zuechtung

Knödler G.: **Ein Schnitt in die grüne DNA**
https://taz.de/Debatte-ueber-neue-Gentechnik/!5948071/

Kovak E.: **Viewpoint: What would the sustainability impact be if Europe approves gene-edited crops?**
https://geneticliteracyproject.org/2023/08/03/viewpoint-what-would-the-sustainability-impact-be-if-europe-
approves-gene-edited-crops/

Sustainable Pulse: **Hungary Confirms Status as GMO-Free Leader with Strong Position on Gene Edited Crops**
https://sustainablepulse.com/2023/08/01/hungary-confirms-status-as-gmo-free-leader-with-strong-position-
on-gene-edited-crops/

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ►here: July / August week 31

Publications – Publikationen

Schröder C.: **Gefahr versus Risiko - Das Dilemma in der Risikokommunikation**
Eine zuverlässige und verständliche Risikokommunikation ist beim Umgang mit Chemikalien unerlässlich. Doch gerade in der Risikokommunikation beobachten wir seit vielen Jahren, dass insbesondere die Begriffe Gefahr und Risiko oft synonym verwendet werden. Mit enormen Auswirkungen, vor allem, was die gesellschaftliche Akzeptanz so mancher Chemikalien betrifft.
https://www.chemanager-online.com/restricted-files/230175

OECD: **Safety Assessment of Transgenic Organisms in the Environment**
Volume 10OECD Consensus Document on Environmental Considerations for the Release of Transgenic Plants
https://www.oecd.org/publications/safety-assessment-of-transgenic-organisms-in-the-environment-volume-10-
62ed0e04-en.htm
pdf-file: https://www.oecd-ilibrary.org/docserver/62ed0e04-
en.pdf?expires=1690941065&id=id&accname=guest&checksum=BFAFF7DCB9454AB5B8CCF54B042FDB85

Pankaj, Y.K., Kumar, V. (2023): **CRISPR/CAS: The Beginning of a New Era in Crop Improvement.** In: Raina, A., Wani, M.R., Laskar, R.A., Tomlekova, N., Khan, S. (eds) Advanced Crop Improvement, Volume 1. Springer, Cham. https://doi.org/10.1007/978-3-031-28146-4_17
Because of the number of crop genome sequences available and the advancements in genome editing tools, it is now possible to design crops that have virtually any characteristic you choose. Using ZFNs (zinc-finger nucleases) and transcription activator-like effector nucleases, scientists may now more accurately target any gene of interest in their research. Protein editing procedures need the use of expensive and time-consuming instruments, which might be prohibitively expensive. It is far easier to clone using CRISPR/Cas9 genome editing techniques than it is to clone using first-generation genome editing techniques. It is possible to use a single Cas9 protein to target several guide RNAs in various areas of the genome using a single Cas9 protein. CRISPR-Cas9 was used to demonstrate that technology has the potential to be utilised to change agricultural crops, according to the researchers. Cas9 cassettes were then used to improve target selectivity while simultaneously

decreasing off-target cleavage (e.g. Nmcas9, Sacas9 and Stcas9). Genome editing techniques have become more varied, accurate and powerful as a result of the discovery of Cas9 enzymes from numerous bacterial species. CRISPR/Cas technology has a wide range of uses, including gene function studies and agricultural development. As explained in this chapter, this strategy may be used to help both gene function research and crop improvement research. Techniques for biotechnological crop improvement, such as CRISPR/Cas genome editing, have become increasingly popular in recent years. A few examples of how it may be used include making crops disease resistant, enhancing plant growth and appearance and creating fibre, among other things. The final section of this chapter discusses some of the most serious concerns surrounding the CRISPR/Cas system, as well as some prospective research directions for the future.
https://link.springer.com/chapter/10.1007/978-3-031-28146-4_17

Yigider, E., Taspinar, M.S. & Agar, G. **Advances in bread wheat production through CRISPR/Cas9 technology: a comprehensive review of quality and other aspects**. Planta 258, 55 (2023). https://doi.org/10.1007/s00425-023-04199-9
Wheat (*Triticum aestivum* L.), the basic nutrition for most of the human population, contributes 20% of the daily energy needed because of its, carbohydrate, essential amino acids, minerals, protein, and vitamin content. Wheat varieties that produce high yields and have enhanced nutritional quality will be required to fulfill future demands. Hexaploid wheat has A, B, and D genomes and includes three like but not identical copies of genes that influence important yield and quality. CRISPR/Cas9, which allows multiplex genome editing provides major opportunities in genome editing studies of plants, especially complicated genomes such as wheat. In this overview, we discuss the CRISPR/Cas9 technique, which is credited with bringing about a paradigm shift in genome editing studies. We also provide a summary of recent research utilizing CRISPR/Cas9 to investigate yield, quality, resistance to biotic/abiotic stress, and hybrid seed production. In addition, we provide a synopsis of the laboratory experience-based solution alternatives as well as the potential obstacles for wheat CRISPR studies. Although wheat's extensive genome and complicated polyploid structure previously slowed wheat genetic engineering and breeding progress, effective CRISPR/Cas9 systems are now successfully used to boost wheat development.
https://link.springer.com/article/10.1007/s00425-023-04199-9

Elsharawy, H., Refat, M. (2023): **CRISPR/Cas9 genome editing in wheat: enhancing quality and productivity for global food security—a review**. Funct Integr Genomics 23, 265 | https://doi.org/10.1007/s10142-023-01190-1
Wheat (*Triticum aestivum* L.) is an important cereal crop that is grown all over the world for food and industrial purposes. Wheat is essential to the human diet due to its rich content of necessary amino acids, minerals, vitamins, and calories. Various wheat breeding techniques have been utilized to improve its quality, productivity, and resistance to biotic and abiotic stress impairing production. However, these techniques are expensive, demanding, and time-consuming. Additionally, these techniques need multiple generations to provide the desired results, and the improved traits could be lost over time. To overcome these challenges, researchers have developed various genome editing tools to improve the quality and quantity of cereal crops, including wheat. Genome editing technologies evolve quickly. Nowadays, single or multiple mutations can be enabled and targeted at specific loci in the plant genome, allowing controlled removal of undesirable features or insertion of advantageous ones. Clustered, regularly interspaced short palindromic repeat (CRISPR)/CRISPR-associated protein (Cas) is a powerful genome editing tool that can be effectively used for precise genome editing of wheat and other crops. This review aims to provide a comprehensive understanding of this technology's potential applications to enhance wheat's quality and productivity. It will first explore the function of CRISPR/Cas9 in preserving the adaptive immunity of prokaryotic organisms, followed by a discussion of its current applications in wheat breeding.
https://link.springer.com/article/10.1007/s10142-023-01190-1

Daniel M., Sebastin R., Yu J.-K., Soosaimanickam M.P., Chung J.W, (2023): **Enhancing Horticultural Crops through Genome Editing: Applications, Benefits, and Considerations.** Horticulturae 9 (8), 884| https://doi.org/10.3390/horticulturae9080884
Genome editing has emerged as a powerful tool for accelerating crop improvement in horticultural crops by enabling precise modifications to their genetic makeup. This review provides an in-depth exploration of the applications, methodologies, and potential impacts of genome editing in horticulture. The review focuses on three major genome editing tools in horticulture, CRISPR-Cas9, TALENs, and ZFNs. The underlying mechanisms, applications, and potential challenges associated with each tool are discussed in detail. CRISPR-Cas9, being a versatile and widely used system, has the potential to enhance traits such as disease resistance, abiotic stress tolerance, nutritional content, and yield in horticultural crops. TALENs and ZFNs, although less commonly used, offer alternative options for targeted DNA modifications, and have demonstrated success in specific applications. We emphasize the potential benefits of genome editing in horticulture, including improved crop productivity, quality, and nutritional value. However, challenges such as off-target effects, delivery methods, and regulatory frameworks need to be addressed for the full realization of this technology's potential. This review serves as a valuable resource for researchers, policymakers, and stakeholders, providing insights into the opportunities and complexities associated with harnessing genome editing for enhanced traits in horticultural crops. By navigating these challenges, genome editing can contribute to sustainable advancements in horticulture, benefiting both producers and consumers worldwide.
https://www.mdpi.com/2311-7524/9/8/884

Cai Y., Chen L., Hou W. (2023): **Genome Editing Technologies Accelerate Innovation in Soybean Breeding. Agronomy** 13 (8), 2045; https://doi.org/10.3390/agronomy13082045
https://www.mdpi.com/2073-4395/13/8/2045

Animasaun D.A., Adedibu P.A., Yury S., Emmanuel F., Tekutyeva L., Balabanova L. (2023): **Modern Plant Biotechnology: An Antidote against Global Food Insecurity** Agronomy *13* (8), 2038 | https://doi.org/10.3390/agronomy13082038
Food insecurity has become a pressing issue on a worldwide scale as the globe plows through a food crisis. The disastrous impact of this menace has been exacerbated by climate change, frequent conflicts, pandemic outbreaks, and the global economic recession, which have been prevalent in recent years. Although food insecurity prevails globally, it is especially critical in some regions in Africa, East and Southeast Asia, and South America. Several efforts have been made to curb food insecurity; however, none have been able to curtail it sufficiently. Genetic engineering of crops is a fast-growing technology that could be a viable tool for mitigating food insecurity. Crop varieties resistant to pests and diseases, abiotic stress, spoilage, or specific herbicides have been developed using this technology. Crops have been modified for increased yield, nutritional content, essential vitamins, and micro-mineral fortification. More intriguing is the advent of plant-derived edible vaccines, which prove equally effective and significantly affordable. However, in many countries, government policies pose a limiting factor for the acceptance of this technology. This article discusses the genetic modification of crops, highlighting its origins, methods, applications, achievements, impact, acceptance, distribution, and potential as a viable antidote to global food insecurity.
https://www.mdpi.com/2073-4395/13/8/2038

Ahmed, H.I., Heuberger, M., Schoen, A. (2023): **Einkorn genomics sheds light on history of the oldest domesticated wheat.** Nature | https://doi.org/10.1038/s41586-023-06389-7
Einkorn (*Triticum monococcum*) was the first domesticated wheat species, and was central to the birth of agriculture and the Neolithic Revolution in the Fertile Crescent around 10,000 years ago[1,2]. Here we generate and analyse 5.2-Gb genome assemblies for wild and domesticated einkorn, including completely assembled centromeres. Einkorn centromeres are highly dynamic, showing evidence of ancient and recent centromere shifts caused by structural rearrangements. Whole-genome sequencing analysis of a diversity panel uncovered the population structure and evolutionary history of einkorn, revealing complex patterns of hybridizations and introgressions after the dispersal of domesticated einkorn from the Fertile Crescent. We also show that around 1% of the modern bread wheat (*Triticum aestivum*) A subgenome originates from einkorn. These resources and findings highlight the history of einkorn evolution and provide a basis to accelerate the genomics-assisted improvement of einkorn and bread wheat.
https://www.nature.com/articles/s41586-023-06389-7

Borges, C.E., Von dos Santos Veloso, R., da Conceição, C.A. et al. (2023): **Forecasting *Brassica napus* production under climate change with a mechanistic species distribution model**. Sci Rep 13, 12656 (2023). https://doi.org/10.1038/s41598-023-38910-3
Brassica napus, a versatile crop with significant socioeconomic importance, serves as a valuable source of nutrition for humans and animals while also being utilized in biodiesel production. The expansion potential of *B. napus* is profoundly influenced by climatic variations, yet there remains a scarcity of studies investigating the correlation between climatic factors and its distribution. This research employs CLIMEX to identify the current and future ecological niches of *B. napus* under the RCP 8.5 emission scenario, utilizing the Access 1.0 and CNRM-CM5 models for the time frame of 2040–2059. Additionally, a sensitivity analysis of parameters was conducted to determine the primary climatic factors affecting *B. napus* distribution and model responsiveness. The simulated outcomes demonstrate a satisfactory alignment with the known current distribution of *B. napus*, with 98% of occurrence records classified as having medium to high climatic suitability. However, the species displays high sensitivity to thermal parameters, thereby suggesting that temperature increases could trigger shifts in suitable and unsuitable areas for *B. napus*, impacting regions such as Canada, China, Brazil, and the United States.
https://www.nature.com/articles/s41598-023-38910-3

Shumbe L., Soares E., Muhovski Y., Smit I., Vanderschuren H. (2023): **Mutation of the Vinv 5' UTR regulatory region reduces acrylamide levels in processed potato to reach EU food-safety standards.** bioRxiv | https://doi.org/10.1101/2023.07.18.549223
Protein–coding regions of genes have so far been the preferred targets for trait improvement using CRISPR–Cas9 genome editing in plants. Alteration of the reading frame can result in termination of transcription or translation, hence, loss of function of the encoded protein. 5' UTR sequences also represent a practical target region to alter gene expression and protein abundance. However, editing of 5' UTRs has so far been scarcely used to engineer trait in crop plants. Here, we demonstrate that insertion of a single adenine nucleotide mediated by Cas9 in the 5' UTR region of two alleles from the *Vacuolar invertase* gene (*VInv*) of the tetraploid potato variety Lady Rosetta (LaRo) is sufficient to substantially lower the content of reducing sugars in the potato under cold–storage conditions. Moreover, the acrylamide content generated during processing of the edited potato lines into crisps was more than three folds lower than the current EU–regulated maximum level

of 750 µg/kg in crisps. This gene–editing approach represents a durable strategy to improve food safety of potatoes in varieties widely preferred by the consumers and the industry.
https://www.biorxiv.org/content/10.1101/2023.07.18.549223v1

Luo T., Li L., Wang S., Chang N, (2023): **Research Progress of Nucleic Acid Detection Technology for Genetically Modified Maize.** Int. J. Mol. Sci. *24* (15), 12247 | https://doi.org/10.3390/ijms241512247
Genetically modified (GM) maize is one of the earliest GM crops to have achieved large-scale commercial cultivation globally, and it is of great significance to excel in the development and implementation of safety policy regarding GM, and in its technical oversight. This article describes the general situation regarding genetically modified maize, including its varieties, applications, relevant laws and regulations, and so on. From a technical point of view, we summarize and critically analyze the existing methods for detecting nucleic acid levels in genetically modified maize. The nucleic acid extraction technology used for maize is explained, and the introduction of traditional detection techniques, which cover variable-temperature and isothermal amplification detection technology and gene chip technology, applications in maize are described. Moreover, new technologies are proposed, with special attention paid to nucleic acid detection methods using sensors. Finally, we review the current limitations and challenges of GM maize nucleic acid testing and share our vision for the future direction of this field.
https://www.mdpi.com/1422-0067/24/15/12247

Kroll, A., Rousset, Y., Hu, XP., Liebrand, N. & Lercher, M.J. (2023): **Turnover number predictions for kinetically uncharacterized enzymes using machine and deep learning;** Nature Communications 14, 4139 | https://www.nature.com/articles/s41467-023-39840-4
The turnover number k_{cat}, a measure of enzyme efficiency, is central to understanding cellular physiology and resource allocation. As experimental k_{cat} estimates are unavailable for the vast majority of enzymatic reactions, the development of accurate computational prediction methods is highly desirable. However, existing machine learning models are limited to a single, well-studied organism, or they provide inaccurate predictions except for enzymes that are highly similar to proteins in the training set. Here, we present TurNuP, a general and organism-independent model that successfully predicts turnover numbers for natural reactions of wild-type enzymes. We constructed model inputs by representing complete chemical reactions through differential reaction fingerprints and by representing enzymes through a modified and re-trained Transformer Network model for protein sequences. TurNuP outperforms previous models and generalizes well even to enzymes that are not similar to proteins in the training set. Parameterizing metabolic models with TurNuP-predicted k_{cat} values leads to improved proteome allocation predictions. To provide a powerful and convenient tool for the study of molecular biochemistry and physiology, we implemented a TurNuP web server.
https://www.nature.com/articles/s41467-023-39840-4

EFSA

CEP Panel (2023): Safety evaluation of the food enzyme α-amylase from the non-genetically modified *Bacillus licheniformis* strain T74. *EFSA Journal*, 21(8), 1–14.
https://doi.org/10.2903/j.efsa.2023.8160
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8160

CEP Panel (2023): Safety evaluation of the food enzyme subtilisin from the non-genetically modified *Bacillus paralicheniformis* strain DP-Dzx96. *EFSA Journal*, 21(8), 1–11.
https://doi.org/10.2903/j.efsa.2023.8155
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8155

CEP Panel (2023): Safety evaluation of the food enzyme α-amylase from the non-genetically modified *Bacillus amyloliquefaciens* strain BA. *EFSA Journal*, 21(7), 1–14.
https://doi.org/10.2903/j.efsa.2023.8157
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8157

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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. Mo*st of *the pdf files can be downloaded directly from the links.*

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