

Sunday Evening News No 272

Week 12 (2022-21-03 – 2022-27-03)

Selected and edited by **BGF** Jany



Mr. Putin stop this war - The war is barbaric and outrageous. Mr. Putin show moral greatness and end the suffering of the population and the death of civilians

Like any war, the war in Ukraine is horrific. Unlike other wars, its effects will be felt worldwide. The events of the war and the possible effects obscure almost all press reports.

Press Releases – Media Reports / Pressemeldungen und Medienberichte

Kurlemann R.: **Nobelpreis aber kein Patent: Der Rechtskrimi um die Genschere Crispr/Cas**
<https://www.riffreporter.de/de/gesellschaft/patent-gentechnik-usa-europa-crispr-nobelpreis-charpentier-doudna-zhang>

Informationsdienst Gentechnik: **Genome Editing: England erleichtert Feldversuche**
<https://www.keine-gentechnik.de/nachricht/34575?cHash=a62a6ccb974c21c87db2d9e8ec41ddca>

English C.: **Ukraine War Exposes Folly Of Anti-GMO Protectionism**

<https://www.acsh.org/news/2022/03/22/ukraine-war-exposes-folly-anti-gmo-protectionism-16199>

EC-Commission: **Safeguarding food security and reinforcing the resilience of food systems**
https://ec.europa.eu/info/sites/default/files/food-farming-fisheries/key_policies/documents/safeguarding-food-security-reinforcing-resilience-food-systems.pdf

Then C., Sharratt L.: **Unintended effects caused by techniques of new genetic engineering create a new quality of hazards and risks**

https://cban.ca/wp-content/uploads/New_GE_unintended_effects.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](#): March week 12)

Publications – Publikationen

Schindele, A., Gehrke, F., Schmidt, C. et al. (2022): **Using CRISPR-Kill for organ specific cell elimination by cleavage of tandem repeats.** Nat Commun 13, 1502 (2022).

<https://doi.org/10.1038/s41467-022-29130-w>

CRISPR/Cas has been mainly used for mutagenesis through the induction of double strand breaks (DSBs) within unique protein-coding genes. Using the SaCas9 nuclease to induce multiple DSBs in functional repetitive DNA of *Arabidopsis thaliana*, we can now show that cell death can be induced in a controlled way. This approach, named CRISPR-Kill, can be used as tool for tissue engineering. By simply exchanging the constitutive promoter of SaCas9 with cell type-specific promoters, it is possible to block organogenesis in *Arabidopsis*. By AP1-specific expression of CRISPR-Kill, we are able to restore the *apetala1* phenotype and to specifically eliminate petals. In addition, by expressing CRISPR-Kill in root-specific pericycle cells, we are able to dramatically reduce the number and the length of lateral roots. In the future, the application of CRISPR-Kill may not only help to control development but could also be used to change the biochemical properties of plants.

<https://www.nature.com/articles/s41467-022-29130-w.pdf>

Devos Y., Oberkofler L., Glandorf D.C.M. (2022): **Genetically modified plants and food/feed: Risk assessment considerations**, Reference Module in Biomedical Sciences |

<https://doi.org/10.1016/B978-0-12-824315-2.00012-9>

Genetic modification has been used for over 20 years to produce genetically modified plants (GMPs) and derived food and feed products. Recent scientific developments in molecular and [synthetic biology](#) enable the (targeted) engineering of new generation GMPs, and are widening the spectrum of [plant species](#) and traits that can be modified. While existing approaches for prospective risk assessments of contemporary GMPs are considered comprehensive and adequate for new

generation GMPs, there are instances where specific risk assessment aspects may require adjustment. For such cases the problem formulation remains an useful framework to perform case-specific and fit-for-purpose risk assessments.

<https://www.sciencedirect.com/science/article/pii/B9780128243152000129?via%3Dihub> pdf-file available

Rodríguez A.V. et al. (2022): **Myths and Realities about Genetically Modified Food: A Risk-Benefit Analysis**. Appl. Sci. 12 (6), 2861; <https://doi.org/10.3390/app12062861>

The development and consumption of genetically modified (GM) crops are surrounded by controversy. According to proponents, only molecular biology approaches and genetic engineering tools are realistic food shortage solutions for the world's ever-growing population. The main purpose of this study is to review the impact of GM products on human, animal, and environmental health. People still reject GM crops not only because of safety concerns, but also for moral reasons. Toxicity, allergies, and possible horizontal gene transfer (HGT) to the environment or to other species have been associated with the marketing of GM products. Moreover, the scarce data available about the long-term implications of using GM crops is another opponent concern. Nevertheless, science has evidenced no harm from GM crops use to date but has, instead, reported several benefits that result from their commercialization, such as economic, environmental, and health benefits for the general public. Legislation and policies about GM product labeling standards are being discussed. To overcome emerging food security challenges, considering quality scientific information is essential rather than leaving the issue and merely moving toward moral discussion. Hence, a risk-benefit analysis is necessary.

<https://www.mdpi.com/2076-3417/12/6/2861>

https://mdpi-res.com/d_attachment/applsci/applsci-12-02861/article_deploy/applsci-12-02861-v2.pdf

Ye, R.; Yang, X.; Rao, Y. (2022): **Genetic Engineering Technologies for Improving Crop Yield and Quality**. Agronomy 12, 759. | <https://doi.org/10.3390/agronomy12040759>

Genetic engineering refers to the specific molecular biological modification of DNA sequences. With the rapid development of genetic engineering methods, especially the breakthroughs in guiding endonuclease technology, gene remodeling of crops has become simpler, more precise, and efficient. Genetic engineering techniques can be used to develop crops with superior traits such as high trace elements and high plant nutrients, providing an important tool to meet the needs of nearly 7.6 billion people in the world for crop yield and quality and to achieve sustainable development. This review first introduces transgenic technology and gene editing technology and analyzes the achievements in improving the efficiency of genetic transformation and regeneration in recent years. Then, it focuses on reviewing the applications of related genetic engineering technologies in improving the yield and quality of rice, maize, and wheat. In addition, the problems of genetic engineering technology in crop applications are discussed. The aim is to provide a reference for research on the development of genetic engineering technologies and the improvement of crop yield and quality.

https://mdpi-res.com/d_attachment/agronomy/agronomy-12-00759/article_deploy/agronomy-12-00759.pdf

Mashilo J., Shimelis H., Ngwepe R.M., Thungo Z. (2022): **Genetic Analysis of Fruit Quality Traits in Sweet Watermelon (*Citrullus lanatus* var. *lanatus*): A Review**; Front. Plant Sci. | <https://doi.org/10.3389/fpls.2022.834696>

Fruit quality traits of sweet watermelon (*Citrullus lanatus* var. *lanatus*) are crucial for new product development and commercialization. Sweet watermelon fruit quality traits are affected by the compositions of phytochemical compounds, phytohormones, and fruit flesh firmness which are affected by genes, the growing environment and their interaction. These compositions determine fruit ripening, eating quality, and postharvest shelf-life. Knowledge of the genetic profile and analyses of quality traits in watermelon is vital to develop improved cultivars with enhanced nutritional compositions, consumer-preferred traits, and extended storage life. This review aims to present the opportunities and progress made on the genetic analysis of fruit quality traits in watermelon as a guide for quality breeding based on economic and end-user attributes. The first section of the review highlights the genetic mechanisms involved in the biosynthesis of phytochemical compounds (i.e., sugars, carotenoids, amino acids, organic acids, and volatile compounds), phytohormones (i.e., ethylene and abscisic acid) and fruit flesh structural components (i.e., cellulose, hemicellulose, and pectin) elicited during watermelon fruit development and ripening. The second section pinpoints the progress on the development of molecular markers and quantitative trait loci (QTL) analysis for phytochemical compounds, phytohormones and fruit quality attributes. The review presents gene-editing technology and innovations associated with fruit quality traits for selection and accelerated cultivar development. Finally, the paper discussed gene actions conditioning fruit ripening in citron watermelon (*C. lanatus* var. *citroides* [L. H. Bailey] Mansf. ex Greb.) as reference genetic resources to guide current and future breeding. Information presented in this review is useful for watermelon variety design, product profiling and development to serve the diverse value chains of the crop.

<https://www.frontiersin.org/articles/10.3389/fpls.2022.834696/full>

Chen W. et al. (2022): **Convergent selection of a WD40 protein that enhances grain yield in maize and rice**, *Science* (2022). DOI: [10.1126/science.abg7985](https://doi.org/10.1126/science.abg7985)

A better understanding of the extent of convergent selection among crops could greatly improve breeding programs. We found that the quantitative trait locus *KRN2* in maize and its rice ortholog, *OsKRN2*, experienced convergent selection. These orthologs encode WD40 proteins and interact with a gene of unknown function, *DUF1644*, to negatively regulate grain number in both crops. Knockout of *KRN2* in maize or *OsKRN2* in rice increased grain yield by ~10% and ~8%, respectively, with no apparent trade-offs in other agronomic traits.

Furthermore, genome-wide scans identified 490 pairs of orthologous genes that underwent convergent selection during maize and rice evolution, and these were enriched for two shared molecular pathways. *KRN2*, together with other convergently selected genes, provides an excellent target for future crop improvement. <https://www.science.org/doi/10.1126/science.abg7985>

Yu G., Matny O., Champouret N., Steuernagel B. et al. (2022): **Aegilops sharonensis genome-assisted identification of stem rust resistance gene Sr62**. Nature Communications 13 (1) | DOI: [10.1038/s41467-022-29132-8](https://doi.org/10.1038/s41467-022-29132-8)

The wild relatives and progenitors of wheat have been widely used as sources of disease resistance (*R*) genes. Molecular identification and characterization of these *R* genes facilitates their manipulation and tracking in breeding programmes. Here, we develop a reference-quality genome assembly of the wild diploid wheat relative *Aegilops sharonensis* and use positional mapping, mutagenesis, RNA-Seq and transgenesis to identify the stem rust resistance gene *Sr62*, which has also been transferred to common wheat. This gene encodes a tandem kinase, homologues of which exist across multiple taxa in the plant kingdom. Stable *Sr62* transgenic wheat lines show high levels of resistance against diverse isolates of the stem rust pathogen, highlighting the utility of *Sr62* for deployment as part of a polygenic stack to maximize the durability of stem rust resistance. <https://www.nature.com/articles/s41467-022-29132-8.pdf>

Li X., Zhang X., Gao S., Cui F., Chen W., Fan L., Qi Y. (2022): **Single-cell RNA sequencing reveals the landscape of maize root tips and assists in identification of cell type-specific nitrate-response genes**, The Crop Journal | DOI: [10.1016/j.cj.2022.02.004](https://doi.org/10.1016/j.cj.2022.02.004)

The root system is fundamental for maize growth and yield. Characterizing its heterogeneity and cell type-specific response to nitrate at the single-cell level will shed light on root development and nutrient uptake. We profiled the transcriptomes of more than 7000 cells derived from root tips of maize seedlings grown on media with or without nitrate, and identified 11 major cell types or tissues and 85 cell type-specific nitrate-response genes, including several known nitrate metabolic genes. A pseudotime analysis showed a continuous pseudotime series with the beginning at meristematic zone cells and showed that the root hair cell was derived by differentiation of a subset of epidermal cells. Interspecies comparison of root cells between maize and rice revealed the conservation and divergence of the root cell types and identified 57, 216, and 80 conserved orthologous genes in root hair, endodermis, and phloem cells respectively. This study provides a global view of maize root tip developmental processes and responses to nitrate at the single-cell level. The genes described in the present work could serve as targets for further genetic analyses and accurate regulation of gene expression and phenotypic variation in specific cell types or tissues.

<https://www.sciencedirect.com/science/article/pii/S2214514122000460?via%3Dihub>

Wang R. et al. (2022): **MtGSTF7, activated by the MYB transcription factor LAP1, specifically participates in anthocyanin accumulation in Medicago truncatula**, Journal of Experimental Botany (2022). DOI: [10.1093/jxb/erac112](https://doi.org/10.1093/jxb/erac112)

Anthocyanins and proanthocyanins are two end-products of the flavonoid biosynthesis pathway. They are believed to be synthesized on the ER, and then sequestered into the vacuole. In *Arabidopsis thaliana*, AtTT19 is necessary for both anthocyanin and PA accumulation. Here, we found that MtGSTF7, a homolog of AtTT19, is essential for anthocyanin accumulation but not required for PA accumulation in *Medicago truncatula*. MtGSTF7 was induced by the anthocyanin regulator LAP1 and its tissue expression pattern was correlated with anthocyanin deposition in *M. truncatula*. *Tnt1*-insertional mutants of MtGSTF7 lost anthocyanin accumulation in vegetative organs, and introducing a genomic fragment of MtGSTF7 could completely complement the mutant phenotypes. Additionally, the accumulation of anthocyanins induced by LAP1 was significantly blocked in *mtgstf7* mutants. Yeast-one-hybridization and dual-luciferase reporter assays revealed that LAP1 could bind to the MtGSTF7 promoter to activate its expression. Ectopic expression of MtGSTF7 in *tt19* mutants could rescue their anthocyanin deficiency, but not their PA defect. Furthermore, PA accumulation was not affected in the *mtgstf7* mutants. Taken together, our results show that the mechanism of anthocyanin and PA accumulation in *M. truncatula* is different from that in *A. thaliana*, and provide a new target gene for engineering anthocyanins in plants.

<https://academic.oup.com/jxb/advance-article/doi/10.1093/jxb/erac112/6549631>

Jahromi, M.G., Rahnama, H., Mousavi, A. et al. (2022): **Comparative evaluation of resistance to potato virus Y (PVY) in three different RNAi-based transgenic potato plants**. Transgenic Res | <https://doi.org/10.1007/s11248-022-00302-0>

Small interfering RNAs (siRNAs) produced from template double-stranded RNAs (dsRNAs) can activate the immune system in transgenic plants by detecting virus transcripts to degrade. In the present study, an RNA interference (RNAi) gene silencing mechanism was used for the development of transgenic potato plants resistant to potato virus Y (PVY), the most harmful viral disease. Three RNAi gene constructs were designed based on the coat protein (CP) and the untranslated region parts of the PVY genome, being highly conserved among all strains of the PVY viruses. Transgenic potato plants were generated using *Agrobacterium* containing pCAMRNAiCP, pCAMRNAiUR, and pCAMRNAiCP-UR constructs. The transgene insertions were confirmed by molecular analysis containing polymerase chain reaction (PCR) and southern blotting. The resistance of transgenic plants to PVY virus was determined using bioassay and evaluating the amount of viral RNA in plants by RT-PCR, dot blotting of PVY coating protein, and enzyme-linked immunosorbent assay (ELISA). Bioassay analysis revealed that more than 67% of transgenic potato plants were resistant to PVY compared with the

non-transgenic plants, which showed viral disease symptoms. No phenotypic abnormalities were observed in transgenic plants. Out of six lines in southern blot analysis, four lines had one copy of the transgene and two lines had two copies of the target genes. No correlation was detected between the copy number of the genes and the resistance level of the plant to PVY. Transgenic lines obtained from all three constructs indicated more or less similar levels of resistance against viral infection; however, CP-UR lines exhibited relatively high resistance followed by CP and UR expressing lines, respectively. Meanwhile, some lines showed a delay in symptoms 35 days after infection which were classified as susceptible.

<https://link.springer.com/article/10.1007/s11248-022-00302-0>

Koo C.W. et al. (2022): Recovery of particulate methane monooxygenase structure and activity in a lipid bilayer; Science 375 (6586), 1287-1291

Bacterial methane oxidation using the enzyme particulate methane monooxygenase (pMMO) contributes to the removal of environmental methane, a potent greenhouse gas. Crystal structures determined using inactive, detergent-solubilized pMMO lack several conserved regions neighboring the proposed active site. We show that reconstituting pMMO in nanodiscs with lipids extracted from the native organism restores methane oxidation activity. Multiple nanodisc-embedded pMMO structures determined by cryo-electron microscopy to 2.14- to 2.46-angstrom resolution reveal the structure of pMMO in a lipid environment. The resulting model includes stabilizing lipids, regions of the PmoA and PmoC subunits not observed in prior structures, and a previously undetected copper-binding site in the PmoC subunit with an adjacent hydrophobic cavity. These structures provide a revised framework for understanding and engineering pMMO function.

<https://www.science.org/doi/10.1126/science.abm3282>

EFSA:

GMO Panel (2022): Scientific Opinion on the assessment of genetically modified maize DP4114 x MON 810 x MIR 604 x NK 603 and subcombinations, for food and feed uses, under Regulation (EC) No 1829/2003 (application EFSA-GMO-NL-2018-150). EFSA Journal 20 (3): 7134, 38 pp. <https://doi.org/10.2903/j.efsa.2022.7134>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2022.7134>

James K., Millington A, Nicola Randal N. (2022): Food and feed safety vulnerabilities in the circular economy

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/sp.efsa.2022.EN-7226>

Wie immer wird für Hinweise und der Zusendung von Publikationen und sonstigen Informationen gedankt. pdf-Dateien können meist direkt aus den links heruntergeladen werden.

Bitte besuchen sie auch die Webseite des Wissenschaftlerkreis Grüne Gentechnik e.V. (WGG): www.wgg-ev.de.

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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