

Sunday Evening News No 326

2023-05-08 – 2023-05-14

Compiled and edited by **BGF** Jany



Erinnerung:

Vor 40 Jahren, am 19.05.1983 erschien die grundlegende Publikation zum Transfer funktioneller Gene in Pflanzen mit Hilfe des Ti-Plasmids. Hierdurch wurde letztlich der Grundstein für die moderne Pflanzenbiotechnologie gelegt, den Anwendungen eines erfolgreichen Gentransfers bei Pflanzen. Der WGG gratuliert den Autoren zu diesem Jubiläum.

Herrera-Estrella, L., Depicker, A., Van Montagu, M. *et al.* **Expression of chimaeric genes transferred into plant cells using a Ti-plasmid-derived vector.** *Nature* **303**, 209–213 (1983).
<https://doi.org/10.1038/303209a0>

A reminder

40 years ago, on May 19, 1983, the fundamental publication on the transfer of functional genes in plants using the Ti plasmid was published in *Nature*. This ultimately laid the foundation for modern plant biotechnology, the applications of successful gene transfer in plants. The WGG congratulates the authors on this anniversary.

Herrera-Estrella, L., Depicker, A., Van Montagu, M. *et al.* **Expression of chimaeric genes transferred into plant cells using a Ti-plasmid-derived vector.** *Nature* **303**, 209–213 (1983).
<https://doi.org/10.1038/303209a0>

Meetings – Conferences / Veranstaltungen - Konferenzen

Datum bitte vormerken:

FGV-WGG-Pressekonferenz „40 Jahre Grüne Gentechnik“

02.06.2023, Berlin

Redner werden die beiden Nobelpreisträger R. J. Roberts und C. Nüsslein-Vollhard sein.

Theodor-Billroth-Lectures: **Regulation of new genomic techniques in the EU**

Presented by Prof. Dr. Detlef Bartsch

July, 5th 2023 Registration:

https://us02web.zoom.us/webinar/register/WN_cgqcdJAQRW2OtGaBFF2sw#/registration

<https://www.theodor-billroth-lectures.com/webinars/regulation-of-new-genomic-techniques-in-the-eu-1-cme-point>

GBM Compact: **Focus on Proteomics**

Frankfurt/Main; September 5. -6., 2023

<https://gbm-compact.org/gbm-compact-2.html>

Press Releases -Media / Presse- und Medienberichte

Schadwinkel A.: Der Spiegel: **Der genetische Masterplan für die gesamte Menschheit**

<https://www.spiegel.de/wissenschaft/ein-bauplan-fuer-die-gesamte-menschheit-a-8ef1264c-7592-42e8-9287-733aa83dc705>

umwelt.nrw: **Ergebnisse der 100. Umweltministerkonferenz in Königswinter**

<https://www.umwelt.nrw.de/presse/detail/ergebnisse-der-100-umweltministerkonferenz-in-koenigswinter-1683894197>

Bender: **Ko-Existenz von Ökoanbau und Gentechnik sicherstellen**

<https://www.agra.de/age-kompakt/ansicht/news/bender-ko-existenz-von-oekoanbau-und-gentechnik-sicherstellen>

Euroseeds: **Farming and producing more sustainably is not a scientific problem – it’s a regulatory problem**

<https://euroseeds.eu/news/farming-and-producing-more-sustainably-is-not-a-scientific-problem-its-a-regulatory-problem/>

Dahm J.: **Berlin split on gene editing ahead of Commission proposal**

<https://www.euractiv.com/section/agriculture-food/news/berlin-split-on-gene-editing-ahead-of-commission-proposal/>

Foote N.: **Öko-Landbau und Gentechnik: Ist ein Nebeneinander möglich?**

<https://www.euractiv.de/section/landwirtschaft-und-ernahrung/news/oeko-landbau-und-gentechnik-ist-ein-nebeneinander-moeglich/>

Organic farming and gene editing: Is coexistence possible?

https://www.euractiv.com/section/agriculture-food/news/organic-farming-and-gene-editing-is-coexistence-possible/?_ga=2.259541954.91224437.1683641028-1448792024.1683641028

GM Watch: **Corteva says it will label new GM seeds**

<https://gmwatch.org/en/106-news/latest-news/20225>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): May week 19

Publications – Publikationen

Liverpool L.: **First human ‘pangenome’ aims to catalogue genetic diversity**

Researchers release draft results from an ongoing effort to capture the entirety of human genetic variation.

<https://www.nature.com/articles/d41586-023-01576-y>

Häcker I., Bartsch D., Choo A. and Marec F. (2023): **Editorial: Genetic control of insect pest species—achievements, challenges, and perspectives.** Front. Bioeng. Biotechnol.

11:1208677. | doi: 10.3389/fbioe.2023.1208677

<https://www.frontiersin.org/articles/10.3389/fbioe.2023.1208677/full>

Jenkins, D., Juba, N., Crawford, B. et al. (2023): **Regulation of plants developed through new breeding techniques must ensure societal benefits.** Nat. Plants |

<https://doi.org/10.1038/s41477-023-01403-2>

Genome editing provides a unique opportunity to create produce benefiting consumers, but success depends on risk-proportional regulation. Existing seedless fruit varieties such as watermelon, mandarin oranges and grape are strongly preferred by consumers and support healthy diets without pre-market regulatory approvals required for commercialization. Replicating the seedless trait in other fruits is a promising way to increase consumption. Here we compare the differential treatment by various regulatory systems of identical products made by inserting an ancient seedless allele into muscadine grape (*Vitis rotundifolia*) using traditional breeding or templated or non-templated genome editing tools.

<https://www.nature.com/articles/s41477-023-01403-2>

Ijaz M., Khan F., Zaki H.E.M., Khan M.M. et al. (2023): **Recent Trends and Advancements in CRISPR-Based Tools for Enhancing Resistance against Plant Pathogens .** Plants 12 (9), 1911 |

<https://doi.org/10.3390/plants12091911>

Targeted genome editing technologies are becoming the most important and widely used genetic tools in studies of phytopathology. The “clustered regularly interspaced short palindromic repeats (CRISPR)” and its accompanying proteins (Cas) have been first identified as a natural system associated with the adaptive immunity of prokaryotes that have been successfully used in various genome-editing techniques because of its flexibility, simplicity, and high efficiency in recent years. In this review, we have provided a general idea about different CRISPR/Cas systems and their uses in phytopathology. This review focuses on the benefits of knock-down technologies for targeting important genes involved in the susceptibility and gaining resistance against viral, bacterial, and fungal pathogens by targeting the negative regulators of defense pathways of hosts in crop plants via different CRISPR/Cas systems. Moreover, the possible strategies to employ CRISPR/Cas system for improving pathogen resistance in plants and studying plant–pathogen interactions have been discussed.

<https://www.mdpi.com/2223-7747/12/9/1911/htm>

Baloch F.S., Altaf M.T., Waqas Liaqat W., Mehmet Bedir M. et al. (2023) **Recent advancements in the breeding of sorghum crop: current status and future strategies for marker-assisted breeding.** Front. Genet., Sec. Plant Genomics Volume 14 | <https://doi.org/10.3389/fgene.2023.1150616>

Sorghum is emerging as a model crop for functional genetics and genomics of tropical grasses with abundant uses, including food, feed, and fuel, among others. It is currently the fifth most significant primary cereal crop. Crops are subjected to various biotic and abiotic stresses, which negatively impact on agricultural production. Developing high-yielding, disease-resistant, and climate-resilient cultivars can be achieved through marker-assisted breeding. Such selection has considerably reduced the time to market new crop varieties adapted to challenging conditions. In the recent years, extensive knowledge was gained about genetic markers. We are providing an overview of current advances in sorghum breeding initiatives, with a special focus on early breeders who may not be familiar with DNA markers. Advancements in molecular plant breeding, genetics, genomics selection, and genome editing have contributed to a thorough understanding of DNA markers, provided various proofs of the genetic variety accessible in crop plants, and have substantially enhanced plant breeding technologies. Marker-assisted selection has accelerated and precised the plant breeding process, empowering plant breeders all around the world.

<https://www.frontiersin.org/articles/10.3389/fgene.2023.1150616/full>

Drapal, M., Enfissi, E.M.A., Almeida, J. et al. (2023): **The potential of metabolomics in assessing global compositional changes resulting from the application of CRISPR/Cas9 technologies.** Transgenic Res | <https://doi.org/10.1007/s11248-023-00347-9>

Exhaustive analysis of genetically modified crops over multiple decades has increased societal confidence in the technology. New Plant Breeding Techniques are now emerging with improved precision and the ability to generate products containing no foreign DNA and mimic/replicate conventionally bred varieties. In the present study, metabolomic analysis was used to compare (i) tobacco genotypes with and without the CRISPR associated protein 9 (Cas9), (ii) tobacco lines with the edited and non-edited DE-ETIOLATED-1 gene without phenotype and (iii) leaf and fruit tissue from stable non-edited tomato progeny with and without the Cas9. In all cases, multivariate analysis based on the difference test using LC-HRMS/MS and GC-MS data indicated no significant difference in their metabolomes. The variations in metabolome composition that were evident could be associated with the processes of tissue culture regeneration and/or transformation (e.g. interaction with *Agrobacterium*). Metabolites responsible for the variance included quantitative changes of abundant, well characterised metabolites such as phenolics (e.g. chlorogenic acid) and several common sugars such as fructose. This study provides fundamental data on the characterisation of gene edited crops, that are important for the evaluation of the technology and its assessment. The approach also suggests that metabolomics could contribute to routine product-based analysis of crops/foods generated from New Plant Breeding approaches.

<https://link.springer.com/article/10.1007/s11248-023-00347-9>

Jabran M., Ali M.A., Zahoor A., Muhae-Ud-Din G. (2023): **Intelligent reprogramming of wheat for enhancement of fungal and nematode disease resistance using advanced molecular techniques.** Front. Plant Sci. 14 - 2023 |

<https://doi.org/10.3389/fpls.2023.1132699>

Wheat (*Triticum aestivum* L.) diseases are major factors responsible for substantial yield losses worldwide, which affect global food security. For a long time, plant breeders have been struggling to improve wheat resistance against major diseases by selection and conventional breeding techniques. Therefore, this review was conducted to shed light on various gaps in the available literature and to reveal the most promising criteria for disease resistance in wheat. However, novel techniques for molecular breeding in the past few decades have been very fruitful for developing broad-spectrum disease resistance and other important traits in wheat. Many types of molecular markers such as SCAR, RAPD, SSR, SSCP, RFLP, SNP, and DaRT, etc., have been reported for resistance against wheat pathogens. This article summarizes various insightful molecular markers involved in wheat improvement for resistance to major diseases through diverse breeding programs. Moreover, this review highlights the applications of marker assisted selection (MAS), quantitative trait loci (QTL), genome wide association studies (GWAS) and the CRISPR/Cas-9 system for developing disease resistance against most important wheat diseases. We also reviewed all reported mapped QTLs for bunts, rusts, smuts, and nematode diseases of wheat. Furthermore, we have also proposed how the CRISPR/Cas-9 system and GWAS can assist breeders in the future for the genetic improvement of wheat. If these molecular approaches are used successfully in the future, they can be a significant step toward expanding food production in wheat crops.

<https://www.frontiersin.org/articles/10.3389/fpls.2023.1132699/full>

Wuddineh, W.A., Xu, X. & Zhong, GY. (2023): **Amino acid substitutions in grapevine (*Vitis vinifera*) acetolactate synthase conferring herbicide resistance.** *Plant Cell Tiss Organ Cult* (2023). <https://doi.org/10.1007/s11240-023-02512-8>

Acetolactate synthase genes (ALS) have successfully been modified for providing resistance to ALS-inhibiting herbicides in many plant species. Based on sequence and expression analyses, we confirmed *VvALS1* as the best functional ALS candidate in grapevine. To develop an ALS-based herbicide selection system for facilitating grape transformation, we firstly evaluated the responses of *Vitis vinifera* cv Chardonnay callus and young in vitro shoots of *Vitis vinifera* cv Thompson Seedless to several representative ALS-inhibiting herbicides and found a typical linear response curves to some of the herbicides, including chlorsulfuron and imazapyr belonging to the

sulfonylurea or imidazolinone families, respectively. Secondly, we created constructs containing amino acid substitutions in the domains which are known to be critical to herbicide resistance and generated transgenic plants for 3 amino acid substitutions using Agrobacterium-mediated transformation of meristematic bulk tissues of Thompson Seedless. Finally, we showed that ectopic expression of two amino acid substitutions (P191S and P191T) at the N-terminal region and another (W568L) at C-terminal region in *VvALS* resulted in high resistance to chlorsulfuron or imazapyr herbicides in transgenic in vitro shoots. Our work highlighted the potential use of *VvALS* mutations imparting herbicide resistance as a selectable marker in grapevine transformation research and as a means in fostering grapevine improvement via cisgenesis, paving the way for developing a selectable co-editing system to facilitate transgene-free gene-editing.

<https://link.springer.com/article/10.1007/s11240-023-02512-8>

Ghasemi, H.I., Bacal, J., Yoon, A.C. et al. (2023): **Interstrand crosslinking of homologous repair template DNA enhances gene editing in human cells.** *Nat Biotechnol* |

<https://doi.org/10.1038/s41587-022-01654-y>

We describe a strategy to boost the efficiency of gene editing via homology-directed repair (HDR) by covalently modifying the template DNA with interstrand crosslinks. Crosslinked templates (xHDRTs) increase Cas9-mediated editing efficiencies by up to fivefold in K562, HEK293T, U2OS, iPS and primary T cells. Increased editing from xHDRTs is driven by events on the template molecule and requires ataxia telangiectasia and Rad3-related (ATR) kinase and components of the Fanconi anemia pathway.

<https://www.nature.com/articles/s41587-022-01654-y>

Shakweer, W.M.E., Krivoruchko, A.Y., Dessouki, S. et al. (2023): **A review of transgenic animal techniques and their applications.** *J Genet Eng Biotechnol* 21, 55 (2023) |

<https://doi.org/10.1186/s43141-023-00502-z>

Nowadays, breakthroughs in molecular biology are happening at an unprecedented rate. One of them is the ability to engineer transgenic animals. A transgenic animal is one whose genome has been changed to carry genes from another species or to use techniques for animal genome editing for specific traits. Animal features can be changed by purposefully altering the gene (or genes). A mouse was the first successful transgenic animal. Then pigs, sheep, cattle, and rabbits came a few years later. The foreign-interested genes that will be used in animal transgenic techniques are prepared using a variety of methods. The produced gene of interest is placed into a variety of vectors, including yeast artificial chromosomes, bacterial plasmids, and cosmids. Several techniques, including heat shock, electroporation, viruses, the gene gun, microinjection, and liposomes, are used to deliver the created vector, which includes the interesting gene, into the host cell. Transgenesis can be carried out in the gonads, sperm, fertilized eggs, and embryos through DNA microinjection, retroviruses, stem cells, and cloning. The most effective transgenic marker at the moment is fluorescent protein. Although transgenesis raises a number of ethical concerns, this review concentrates on the fundamentals of animal transgenesis and its usage in industry, medicine, and agriculture. Transgenesis success is confirmed by the integration of an antibiotic resistance gene, western and southern blots, PCR, and ELISA. If technology solves social and ethical problems, it will be the most promising in the future

<https://jgeb.springeropen.com/articles/10.1186/s43141-023-00502-z>

Richter, P.K., Blázquez-Sánchez, P., Zhao, Z. et al. (2023): **Structure and function of the metagenomic plastic-degrading polyester hydrolase PHL7 bound to its product.** *Nat Commun* 14, 1905 |

<https://doi.org/10.1038/s41467-023-37415-x>

The recently discovered metagenomic-derived polyester hydrolase PHL7 is able to efficiently degrade amorphous polyethylene terephthalate (PET) in post-consumer plastic waste. We present the cocrystal structure of this hydrolase with its hydrolysis product terephthalic acid and elucidate the influence of 17 single mutations on the PET-hydrolytic activity and thermal stability of PHL7. The substrate-binding mode of terephthalic acid is similar to that of the thermophilic polyester hydrolase LCC and deviates from the mesophilic *IsPETase*. The subsite I modifications L93F and Q95Y, derived from LCC, increased the thermal stability, while exchange of H185S, derived from *IsPETase*, reduced the stability of PHL7. The subsite II residue H130 is suggested to represent an adaptation for high thermal stability, whereas L210 emerged as the main contributor to the observed high PET-hydrolytic activity. Variant L210T showed significantly higher activity, achieving a degradation rate of 20 $\mu\text{m h}^{-1}$ with amorphous PET films.

<https://www.nature.com/articles/s41467-023-37415-x>

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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