

Sunday Evening News No 357

2023-12-18 – 2023-12-31

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Press Releases -Media / Presse- und Medienberichte

Presidency of EU Council abandons idea of reaching an agreement this week at EU level on new genomic techniques

<https://agenceurope.eu/en/bulletin/article/13317/12>

Jorasch P. **Resurrection of Plant Breeding Innovation in the EU?**

<https://european-seed.com/2023/12/resurrection-of-plant-breeding-innovation-in-the-eu-2/>

Shandong CYNDA (Group) Co., Ltd.: **European Union - Agriculture ministers reject compromise over GM crop regulation reform.**

<https://www.cynnda.com.cn/web/news/2023/1228/314.html>

Lebensmittelverband Deutschland: **Zwischenbilanz und Ausblick zur Strategie „Vom Hof auf den Tisch“**

<https://www.lebensmittelverband.de/de/aktuell/gruener-deal>

Informationsdienst Gentechnik: **Neue Gentechnik: NGOs feiern Etappensieg in Brüssel**

<https://www.keine-gentechnik.de/nachricht/34880?cHash=b506e50a0571a814af072c352198be37>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): December week 50

Publications – Publikationen

Ricroch A., Eriksson D., Miladinović D., Sweet J., Van Laere K., Woźniak-Gientka E. (2023): **A Roadmap for Plant Genome Editing:** <https://link.springer.com/book/10.1007/978-3-031-46150-7>

Puchta, H. (2023): Regulation of gene-edited plants in Europe: from the valley of tears into the shining sun?. *aBIOTECH* <https://doi.org/10.1007/s42994-023-00130-8>

Some 20 years ago, the EU introduced complex regulatory rules for the growth of transgenic crops, which resulted in a de facto ban to grow these plants in fields within most European countries. With the rise of novel genome editing technologies, it has become possible to improve crops genetically in a directed way without the need for incorporation of foreign genes. Unfortunately, in 2018, the European Court of Justice ruled that such gene-edited plants are to be regulated like transgenic plants. Since then, European scientists and breeders have challenged this decision and requested a revision of this outdated law. Finally, after 5 years, the European Commission has now published a proposal on how, in the future, to regulate crops produced by new breeding technologies. The proposal tries to find a balance between the different interest groups in Europe. On one side, genetically modified plants, which cannot be discerned from their natural counterparts, will exclusively be used for food and feed and are—besides a registration step—not to be regulated at all. On the other side, plants expressing herbicide resistance are to be excluded from this regulation, a concession to the strong environmental associations and NGOs in Europe. Moreover, edited crops are to be excluded from organic farming to protect the business interests of the strong organic sector in Europe. Nevertheless, if this law passes European parliament and council, unchanged, it will present a big step forward toward establishing a more sustainable European agricultural system. Thus, it might soon be possible to develop and grow crops that are more adapted to global warming and whose cultivation will require lower amounts of pesticides. However, there is still a long way to go until the law is passed. Too often, the storm of arguments raised by the opponents, based on irrational fears of mutations and a naive understanding of nature, has fallen on fruitful ground in Europe.

<https://link.springer.com/article/10.1007/s42994-023-00130-8>

Bohle, F.; Schneider, R.; Mundorf, J.; Zühl, L.; Simon, S.; Engelhard, M. (2023): **Where Does the EU-Path on NGTs Lead Us?.** *Preprints* 2023111897 |

<https://doi.org/10.20944/preprints202311.1897.v1>

The broad and rapid application of new genomic techniques (NGTs) such as CRISPR-Cas has led to a fast increase in the number of genetically modified crops. With the recently published EU Commission's (EC) regulatory proposal on plants generated with NGTs (July 5, 2023) the process of admission of such genetically

modified plants is aimed to get accelerated and simplified. NGT plant applications shall be categorized based on their molecular characteristics into category 1 NGT (NGT1) and category 2 NGT (NGT2), which is in divergence from the current legislation centered around Directive 2001/18/EC. In the regulatory proposal NGT2 plants are envisioned to undergo a reduced risk assessment while for NGT1 plants no risk assessment is foreseen at all. To demonstrate the path of the proposal leads to in practice, we applied the proposed criteria for categorization to a list of NGT plant applications that are currently in the commercialization pipeline. A key finding is that out of those plant applications affected by the EC proposal, 94% would be classified as NGT1 and thus would receive a market approval without risk assessment, monitoring and sufficient labeling provisions. The remaining 6% of applications would be classified as NGT2 plants for which, in deviation from the current regulation, an adapted risk assessment is proposed. A screening of intended traits in the pipeline highlights that certain NGT1 plants can pose similar environmental risks (e.g. invasiveness) compared to other genetically modified organisms (GMOs), as defined in Directive 2001/18/EC. For example, NGT1 applications based on RNAi technology can exhibit insecticidal effects with potential side effects on non-target organisms (i.e. other insects). Our quantitative and case-specific elaboration on how the current EC regulatory proposal would affect the environment, health or consumer protection will be informative for decision makers and politicians.

<https://www.preprints.org/manuscript/202311.1897/v1>

<https://acrobat.adobe.com/id/urn:aaid:sc:EU:074f6085-7c8b-4135-b046-bdc18638f63e>

Bhuyan S.J., Kumar M., Devde P.R., Rai A.C. et al. (2023): Progress in gene editing tools, implications and success in plants: a review. *Front. Genome Ed., Sec. Genome Editing in Plants* 5 | <https://doi.org/10.3389/fgeed.2023.1272678>

Genetic modifications are made through diverse mutagenesis techniques for crop improvement programs. Among these mutagenesis tools, the traditional methods involve chemical and radiation-induced mutagenesis, resulting in off-target and unintended mutations in the genome. However, recent advances have introduced site-directed nucleases (SDNs) for gene editing, significantly reducing off-target changes in the genome compared to induced mutagenesis and naturally occurring mutations in breeding populations. SDNs have revolutionized genetic engineering, enabling precise gene editing in recent decades. One widely used method, homology-directed repair (HDR), has been effective for accurate base substitution and gene alterations in some plant species. However, its application has been limited due to the inefficiency of HDR in plant cells and the prevalence of the error-prone repair pathway known as non-homologous end joining (NHEJ). The discovery of CRISPR-Cas has been a game-changer in this field. This system induces mutations by creating double-strand breaks (DSBs) in the genome and repairing them through associated repair pathways like NHEJ. As a result, the CRISPR-Cas system has been extensively used to transform plants for gene function analysis and to enhance desirable traits. Researchers have made significant progress in genetic engineering in recent years, particularly in understanding the CRISPR-Cas mechanism. This has led to various CRISPR-Cas variants, including CRISPR-Cas13, CRISPR interference, CRISPR activation, base editors, prime editors, and CRASPAE, a new CRISPR-Cas system for genetic engineering that cleaves proteins. Moreover, gene editing technologies like the prime editor and base editor approaches offer excellent opportunities for plant genome engineering. These cutting-edge tools have opened up new avenues for rapidly manipulating plant genomes. This review article provides a comprehensive overview of the current state of plant genetic engineering, focusing on recently developed tools for gene alteration and their potential applications in plant research. Genetic modifications are made through diverse mutagenesis techniques for crop improvement programs. Among these mutagenesis tools, the traditional methods involve chemical and radiation-induced mutagenesis, resulting in off-target and unintended mutations in the genome. However, recent advances have introduced site-directed nucleases (SDNs) for gene editing, significantly reducing off-target changes in the genome compared to induced mutagenesis and naturally occurring mutations in breeding populations. SDNs have revolutionized genetic engineering, enabling precise gene editing in recent decades. One widely used method, homology-directed repair (HDR), has been effective for accurate base substitution and gene alterations in some plant species. However, its application has been limited due to the inefficiency of HDR in plant cells and the prevalence of the error-prone repair pathway known as non-homologous end joining (NHEJ). The discovery of CRISPR-Cas has been a game-changer in this field. This system induces mutations by creating double-strand breaks (DSBs) in the genome and repairing them through associated repair pathways like NHEJ. As a result, the CRISPR-Cas system has been extensively used to transform plants for gene function analysis and to enhance desirable traits. Researchers have made significant progress in genetic engineering in recent years, particularly in understanding the CRISPR-Cas mechanism. This has led to various CRISPR-Cas variants, including CRISPR-Cas13, CRISPR interference, CRISPR activation, base editors, prime editors, and CRASPAE, a new CRISPR-Cas system for genetic engineering that cleaves proteins. Moreover, gene editing technologies like the prime editor and base editor approaches offer excellent opportunities for plant genome engineering. These cutting-edge tools have opened up new avenues for rapidly manipulating plant genomes. This review article provides a comprehensive overview of the current state of plant genetic engineering, focusing on recently developed tools for gene alteration and their potential applications in plant research.

<https://www.frontiersin.org/articles/10.3389/fgeed.2023.1272678/full>

Ying L., Grotewold E., Dudareva N. et al. (2023): Enough is enough: feedback control of specialized metabolism. *Trends in Plant Science* DOI: [10.1016/j.tplants.2023.07.012](https://doi.org/10.1016/j.tplants.2023.07.012)

Recent advances in our understanding of plant metabolism have highlighted the significance of specialized metabolites in the regulation of gene expression associated with biosynthetic networks. This opinion article focuses on the molecular mechanisms of small-molecule-mediated feedback regulation at the transcriptional level and its potential modes of action, including metabolite signal perception, the nature of the sensor, and the

signaling transduction mechanisms leading to transcriptional and post-transcriptional regulation, based on evidence available from plants and other kingdoms of life. We also discuss the challenges associated with identifying the occurrences, effects, and localization of small molecule–protein interactions. Further understanding of small-molecule-controlled metabolic fluxes will enable rational design of transcriptional regulation systems in metabolic engineering to produce high-value specialized metabolites.

[https://www.cell.com/trends/plant-science/fulltext/S1360-1385\(23\)00258-3?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS1360138523002583%3Fshowall%3Dtrue](https://www.cell.com/trends/plant-science/fulltext/S1360-1385(23)00258-3?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS1360138523002583%3Fshowall%3Dtrue)

López-Casado G., Sánchez-Raya C., Ric-Varas P.D., Paniagua C. et al. (2023): **CRISPR/Cas9 editing of the polygalacturonase *FaPG1* gene improves strawberry fruit firmness.**

Horticulture Research 10 (3), uhad011, <https://doi.org/10.1093/hr/uhad011>

Firmness is one of the most important fruit quality traits in strawberries. The postharvest shelf life of this soft fruit is highly limited by the loss of firmness, where cell wall disassembly plays an important role. Previous studies demonstrated that the polygalacturonase *FaPG1* has a key role in remodelling pectins during strawberry softening. In this study, *FaPG1* knockout strawberry plants have been generated using the CRISPR/Cas9 system delivered via *Agrobacterium tumefaciens*. Ten independent lines, cv. “Chandler”, were obtained, and all of them were successfully edited as determined by PCR amplification and T7 endonuclease assay. The targeted mutagenesis insertion and deletion rates were analyzed using targeted deep sequencing. The percentage of edited sequences varied from 47% up to almost 100%, being higher than 95% for seven of the selected lines. Phenotypic analyses showed that 7 out of the eight lines analyzed produced fruits significantly firmer than the control, ranging from 33 to 70% increase in firmness. There was a positive relationship between the degree of *FaPG1* editing and the rise in fruit firmness. Minor changes were observed in other fruit quality traits, such as colour, soluble solids, titratable acidity or anthocyanin content. Edited fruits showed a reduced softening rate during postharvest, displayed a reduced transpirational water loss, and were less damaged by *Botrytis cinerea* inoculation. The analysis of four potential off-target sites revealed no mutation events. In conclusion, editing the *FaPG1* gene using the CRISPR/Cas9 system is an efficient method for improving strawberry fruit firmness and shelf life.

<https://academic.oup.com/hr/article/10/3/uhad011/7022301?login=false>

Itam, M.O., Iohannes, S.D., Albertsen, M. et al. (2023): **Demonstrating the benefit of agricultural biotechnology in developing countries by bridging the public and private sectors.** Nat. Plants | <https://doi.org/10.1038/s41477-023-01604-9>

Currently, hunger affects nearly 12 per cent of the world’s population — 4 per cent more than in 2015, when the United Nations launched the 2030 Agenda for Sustainable Development. If all scientific knowledge and technological innovation in crop development were readily available and globally adopted, could zero hunger have been achieved by 2030? Most people recognize the potential for agricultural biotechnology to contribute to food security. However, there has been limited application and adoption of new crop varieties in countries that are disproportionately affected by malnutrition and food insecurity.

<https://www.nature.com/articles/s41477-023-01604-9>

Fradgley N. S., Gardner K.A.; Kerton M., Swarbreck S.M., Bentley A.R. (2023): **Balancing quality with quantity: A case study of UK bread wheat.** Plant People Plat PPP

<https://doi.org/10.1002/ppp3.10462>

Societal Impact Statement: Increasing crop productivity is often proposed as a key goal for meeting the food security demands of a growing global population. However, achieving high crop yields alone without meeting end-use quality requirements is counter to this objective and can lead to negative environmental and sustainability issues. High yielding feed wheat crops in the United Kingdom are a typical example of this. The historical context of UK agricultural industrialisation, developments in plant breeding and wheat end-use processing are examined. We then outline how employing innovations in plant breeding methods offer the potential to redress the balance between wheat quantity and quality.

Summary: Bread wheat (*Triticum aestivum* L.) has historically been an important crop for many human civilisations. Today, variability in wheat supply and trade has a large influence on global economies and food security. The United Kingdom is an example of an industrialised country that achieves high wheat yields through intensive cropping systems and a favourable climate. However, only a minority of the wheat grain produced is of suitable end-use quality for modern bread baking methods and most wheat produced is fed to livestock. A large agricultural land area and input use dedicated to producing grain for animal rather than human food has wide-ranging negative impacts for environmental sustainability and domestic food production. Here we present an historical perspective of agricultural and economic changes that have resulted in UK production primarily focussing on wheat quantity over quality. Agricultural intensification, liberalisation of free trade in agricultural commodities, innovations in the milling and baking sector, developments in scientific understanding of genetics and plant breeding, and geopolitical changes have all played a role. We propose that wheat breeding plays a crucial role in influencing these issues and although wheat breeders in the United Kingdom have historically applied the most-up-to-date scientific advances, recent advances in genomics tools and quantitative genetics present a unique opportunity for breeders to redress the balance between quantity and quality.

<https://nph.onlinelibrary.wiley.com/doi/10.1002/ppp3.10462>

Hernandes-Lopes J., Pinto M.S., Vieira L.R., Monteiro P.B., Gerasimov S.V. (2023): **Enabling genome editing in tropical maize lines through an improved, morphogenic regulator-assisted transformation protocol**. *Front. Genome Ed., Sec. Genome Editing in Plants*, Volume 5 | <https://doi.org/10.3389/fgeed.2023.1241035>

The recalcitrance exhibited by many maize (*Zea mays*) genotypes to traditional genetic transformation protocols poses a significant challenge to the large-scale application of genome editing (GE) in this major crop species. Although a few maize genotypes are widely used for genetic transformation, they prove unsuitable for agronomic tests in field trials or commercial applications. This challenge is exacerbated by the predominance of transformable maize lines adapted to temperate geographies, despite a considerable proportion of maize production occurring in the tropics. Ectopic expression of morphogenic regulators (MRs) stands out as a promising approach to overcome low efficiency and genotype dependency, aiming to achieve 'universal' transformation and GE capabilities in maize. Here, we report the successful GE of agronomically relevant tropical maize lines using a MR-based, *Agrobacterium*-mediated transformation protocol previously optimized for the B104 temperate inbred line. To this end, we used a CRISPR/Cas9-based construct aiming at the knockout of the *VIRESCENT YELLOW-LIKE (VYL)* gene, which results in an easily recognizable phenotype. Mutations at *VYL* were verified in protoplasts prepared from B104 and three tropical lines, regardless of the presence of a single nucleotide polymorphism (SNP) at the seed region of the *VYL* target site in two of the tropical lines. Three out of five tropical lines were amenable to transformation, with efficiencies reaching up to 6.63%. Remarkably, 97% of the recovered events presented indels at the target site, which were inherited by the next generation. We observed off-target activity of the CRISPR/Cas9-based construct towards the *VYL* paralog *VYL-MODIFIER*, which could be partly due to the expression of the *WUSCHEL (WUS)* MR. Our results demonstrate efficient GE of relevant tropical maize lines, expanding the current availability of GE-amenable genotypes of this major crop.

<https://www.frontiersin.org/articles/10.3389/fgeed.2023.1241035/full>

EFSA:

Ballester, A.R., Roqué, M., Ricci-Cabello, I., Rotger, A., Malih, N. (2023):. **Horizon scanning on microorganisms and their products obtained by new developments in biotechnology**. *EFSA supporting publication* 20 (12):EN-8503, 65 pp. doi:[10.2903/sp.efsa.2023.EN-8503](https://doi.org/10.2903/sp.efsa.2023.EN-8503)

Background: The aim of this horizon scanning is to map applications of new genomic techniques (NGTs) developed after Directive 2001/18/EC to obtain genetically modified microorganisms (GMMs) of categories 3 and 4, with an application to the agri-food and feed sectors; as well as understanding their relevant safety and risk assessment aspects.

Methods: The review comprised systematic comprehensive searches for the identification of relevant applications: i) structured electronic searches in Medline, EMBASE, and Web of Science, and ii) searches in on-line resources, including websites of companies, regulatory agencies, patents, and registries.

Results: We identified 35GMMs meeting the eligibility criteria. An evidence table (available in a separate file) offers a detailed description of their characteristics. Most of the GMMs were developed or commercialised by institutions in China or USA (14and 10cases, respectively). Of the 35GMMs identified, 11were bacteria, 22yeasts, one fungal endophyte, and one microalga. As for use, 30 GMMs were used as (or as a source of) food or food additives, three as (or as a source of) feed or feed additives, and two for agricultural purposes. Eight GMMs are already commercialized, 9 are published in patent applications, and 18 are under development. When considering the purpose of the new traits introduced, 10GMMs modify flavours in food; 10 increase the bioproduction of compounds; seven improve food profile/composition; two boost immunity/reduce toxicity in feed additives; five optimize food production processes, and one increases nitrogen-fixation as fertiliser. Only three identified GMMs have been subjected to an authorisation process by national or international authorities, and risk assessment studies are scarcely available. The findings of this horizon scan illustrate the growing worldwide adoption of NGTs in producing GMMs for application in the food and feed sectors

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/sp.efsa.2023.EN-8503>

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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