

# Sunday Evening News No 281

Week 21 (2022-05-23 – 2022-05-29)

Selected and edited by **BGF** Jany

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## Press Releases – Media Reports / Pressemeldungen und Medienberichte

**Mathys-Squire: European Commission launches public consultation on genetically engineered plants**

<https://www.mathys-squire.com/insights-and-events/news/european-commission-launches-public-consultation-on-genetically-engineered-plants/>

**Beamen E.: Genetic editing spliced into UK law**

<https://theecologist.org/2022/may/25/genetic-editing-spliced-uk-law>

**UK: Genetic Technology (Precision Breeding) Bill**

<https://publications.parliament.uk/pa/bills/cbill/58-03/0011/220011.pdf>

**Devlin H.: Britain is paving the way for gene-edited food – will the public stomach it?**

<https://www.theguardian.com/environment/2022/may/27/gene-edited-food-britain-gm-public-mood>

**GM Watch: The public wants gene editing regulated – the government should listen**

<https://www.gmwatch.org/en/106-news/latest-news/20041-the-public-wants-gene-editing-regulated-the-government-should-listen>

**Ghulam din: Scientists Create Tomatoes Genetically Engineered**

Tomatoes that have been gene-edited to produce vitamin D, known as the sunshine vitamin, could be a simple and sustainable innovation to address a worldwide health problem.

<https://technologytimes.pk/2022/05/26/scientists-create-tomatoes-genetically-engineered/>

**Vaughn A: Genetic Technology Bill: Gentechnisch veränderte Lebensmittel sollen in Großbritannien grünes Licht geben**

<https://germanic.news/genetic-technology-bill-gentechnisch-veranderte-lebensmittel-sollen-in-grosbritannien-grunes-licht-geben/>

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 21

## Publications – Publikationen

**UK: Genetic Technology (Precision Breeding) Bill**

<https://publications.parliament.uk/pa/bills/cbill/58-03/0011/220011.pdf>

**Dima O., Heyvaert Y., Inzé D. (2022): Interactive database of genome editing applications in crops and future policy making in the European Union.** Trends in Plant Science |

<https://doi.org/10.1016/j.tplants.2022.05.002>

European R&D in plant breeding is lagging behind, bound by strict genetically modified organism (GMO) regulations, applied to all crop varieties obtained with genome editing techniques. We developed an online database of worldwide genome editing applications in crops to support conclusions and to facilitate science-based policy making for this plant breeding innovation.

[https://www.cell.com/trends/plant-science/fulltext/S1360-1385\(22\)00140-](https://www.cell.com/trends/plant-science/fulltext/S1360-1385(22)00140-6?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS1360138522001406%3Fshowa)

[6?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS1360138522001406%3Fshowa](https://www.cell.com/trends/plant-science/fulltext/S1360-1385(22)00140-6?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS1360138522001406%3Fshowa)  
ll%3Dtrue pdf-file available

**OECD: Safety Assessment of Transgenic Organisms in the Environment, Volume 9**

OECD Consensus Documents on the Biology of Crops: Apple, Safflower, Rice

<https://www.oecd.org/chemicalsafety/safety-assessment-of-transgenic-organisms-in-the-environment-volume-9-e49bd2e8-en.htm>

**Liu A. (2022): Regulating Genetically Modified Crops in View of Environmental Risks**

## China's Implementation of International Obligations

This book analyzes international and Chinese regulatory approaches addressing environmental risks that may be caused by GM crops and examines how China implements its international obligations in its policies and laws. Using the legal doctrinal method, the book discusses the precautionary principle and the public involvement principle, as well as several legal measures at the international law level and in Chinese law. It observes that legal principles and measures as provided for in China's GMO legal framework have generally implemented the international obligations regarding the prevention of environmental risks that may be caused by the cultivation of GM crops and related activities. However, the book argues that Chinese law lacks an explicit codification of the precautionary principle, and the same is true with regard to public participation; the regulatory framework lacks specific obligations. It concludes that future research should focus on the application and enforcement of the relevant Chinese legislation, and that it is also important to investigate how the environmental risks that may be caused by new techniques, such as genome-editing techniques, could be prevented, given the experience gained by regulating the cultivation of GM crops and related activities.  
<https://www.springerprofessional.de/regulating-genetically-modified-crops-in-view-of-environmental-r/23083196>

Linacero, R.; Cuadrado, C.(2022): **New Research in Food Allergen Detection**. Foods 11, 1520. | <https://doi.org/10.3390/foods11101520>  
[https://mdpi-res.com/d\\_attachment/foods/foods-11-01520/article\\_deploy/foods-11-01520.pdf?version=1653301414](https://mdpi-res.com/d_attachment/foods/foods-11-01520/article_deploy/foods-11-01520.pdf?version=1653301414)

Ashley S.E., Jones A.C., Anderson D., Holt P.D. et al. (2022): **Remission of peanut allergy is associated with rewiring of allergen-driven T helper 2-related gene networks**, Allergy | <https://doi.org/10.1111/all.15324>  
<https://onlinelibrary.wiley.com/doi/epdf/10.1111/all.15324>

Reardon S.: (2022). **First pig kidneys transplanted into people: what scientists think** *Nature* **605**, 597-598 | doi: <https://doi.org/10.1038/d41586-022-01418-3>  
The genetically modified organs seemed to function for more than two days but some researchers are sceptical that the experiments had value.  
<https://www.nature.com/articles/d41586-022-01418-3>

Li, J., Scarano, A., Gonzalez, N.M. et al. (2022): **Biofortified tomatoes provide a new route to vitamin D sufficiency**. Nat. Plants | <https://doi.org/10.1038/s41477-022-01154-6>  
Poor vitamin D status is a global health problem; insufficiency underpins higher risk of cancer, neurocognitive decline and all-cause mortality. Most foods contain little vitamin D and plants are very poor sources. We have engineered the accumulation of provitamin D<sub>3</sub> in tomato by genome editing, modifying a duplicated section of phytosterol biosynthesis in Solanaceous plants, to provide a biofortified food with the added possibility of supplement production from waste material.  
<https://www.nature.com/articles/s41477-022-01154-6>  
<https://www.nature.com/articles/s41477-022-01154-6.pdf>

Chandrasekharan, N., Ramanathan, N., Pukalenty, B. et al. (2022): **Development of  $\beta$ -carotene, lysine, and tryptophan-rich maize (*Zea mays*) inbreds through marker-assisted gene pyramiding**. Sci Rep 12, 8551 | <https://doi.org/10.1038/s41598-022-11585-y>  
Maize (*Zea mays* L.) is the leading cereal crop and staple food in many parts of the world. This study aims to develop nutrient-rich maize genotypes by incorporating *crTRB1* and *o2* genes associated with increased  $\beta$ -carotene, lysine, and tryptophan levels. UMI1200 and UMI1230, high quality maize inbreds, are well-adapted to tropical and semi-arid regions in India. However, they are deficient in  $\beta$ -carotene, lysine, and tryptophan. We used the concurrent stepwise transfer of genes by marker-assisted backcross breeding (MABB) scheme to introgress *crTRB1* and *o2* genes. In each generation (from F<sub>1</sub>, BC<sub>1</sub>F<sub>1</sub>–BC<sub>3</sub>F<sub>1</sub>, and ICF<sub>1</sub>–ICF<sub>3</sub>), foreground and background selections were carried out using gene-linked (*crTRB1* 3'TE and *umc1066*) and genome-wide simple sequence repeats (SSR) markers. Four independent BC<sub>3</sub>F<sub>1</sub> lines of UMI1200 × CE477 (Cross-1), UMI1200 × VQL1 (Cross-2), UMI1230 × CE477 (Cross-3), and UMI1230 × VQL1 (Cross-4) having *crTRB1* and *o2* genes and 87.45–88.41% of recurrent parent genome recovery (RPGR) were intercrossed to generate the ICF<sub>1</sub>–ICF<sub>3</sub> generations. Further, these gene pyramided lines were examined for agronomic performance and the  $\beta$ -carotene, lysine, and tryptophan contents. Six ICF<sub>3</sub> lines (DBT-IC- $\beta$ <sub>1</sub> $\sigma$ <sub>4</sub>-4-8-8, DBT-IC- $\beta$ <sub>1</sub> $\sigma$ <sub>4</sub>-9-21-21, DBT-IC- $\beta$ <sub>1</sub> $\sigma$ <sub>4</sub>-10-1-1, DBT-IC- $\beta$ <sub>2</sub> $\sigma$ <sub>5</sub>-9-51-51, DBT-IC- $\beta$ <sub>2</sub> $\sigma$ <sub>5</sub>-9-52-52 and DBT-IC- $\beta$ <sub>2</sub> $\sigma$ <sub>5</sub>-9-53-53) possessing *crTRB1* and *o2* genes showed better agronomic performance (77.78–99.31% for DBT-IC- $\beta$ <sub>1</sub> $\sigma$ <sub>4</sub> population and 85.71–99.51% for DBT-IC- $\beta$ <sub>2</sub> $\sigma$ <sub>5</sub> population) like the recurrent parents and  $\beta$ -carotene (14.21–14.35  $\mu$ g/g for DBT-IC- $\beta$ <sub>1</sub> $\sigma$ <sub>4</sub> and 13.28–13.62  $\mu$ g/g for DBT-IC- $\beta$ <sub>2</sub> $\sigma$ <sub>5</sub>), lysine (0.31–0.33% for DBT-IC- $\beta$ <sub>1</sub> $\sigma$ <sub>4</sub> and 0.31–0.34% for DBT-IC- $\beta$ <sub>2</sub> $\sigma$ <sub>5</sub>), and tryptophan (0.079–0.082% for DBT-IC- $\beta$ <sub>1</sub> $\sigma$ <sub>4</sub> and 0.078–0.083% for DBT-IC- $\beta$ <sub>2</sub> $\sigma$ <sub>5</sub>) levels on par with that of the donor parents. In the future, these improved lines could be developed as a cultivar for various agro-climatic zones and also as good genetic materials for maize nutritional breeding programs.  
<https://www.nature.com/articles/s41598-022-11585-y>  
<https://www.nature.com/articles/s41598-022-11585-y.pdf>

Pan, C., Li, G., Malzahn, A.A. et al. (2022): **Boosting plant genome editing with a versatile CRISPR-Combo system.** Nat. Plants 8, 513–525 | <https://doi.org/10.1038/s41477-022-01151-9>  
CRISPR-Cas9, its derived base editors and CRISPR activation systems have greatly aided genome engineering in plants. However, these systems are mostly used separately, leaving their combinational potential largely untapped. Here we develop a versatile CRISPR-Combo platform, based on a single Cas9 protein, for simultaneous genome editing (targeted mutagenesis or base editing) and gene activation in plants. We showcase the powerful applications of CRISPR-Combo for boosting plant genome editing. First, CRISPR-Combo is used to shorten the plant life cycle and reduce the efforts in screening transgene-free genome-edited plants by activation of a florigen gene in *Arabidopsis*. Next, we demonstrate accelerated regeneration and propagation of genome-edited plants by activation of morphogenic genes in poplar. Furthermore, we apply CRISPR-Combo to achieve rice regeneration without exogenous plant hormones, which is established as a new method to predominately enrich heritable targeted mutations. In conclusion, CRISPR-Combo is a versatile genome engineering tool with promising applications in crop breeding.  
<https://www.nature.com/articles/s41477-022-01151-9>  
[www.nature.com/articles/s41477-022-01151-9.epdf](https://www.nature.com/articles/s41477-022-01151-9.epdf)

Kouhen M., García-Caparrós P., Twyman R.M. et al. (2022): **Improving environmental stress resilience in crops by genome editing: insights from extremophile plants,** Critical Reviews in Biotechnology, DOI: [10.1080/07388551.2022.2042481](https://doi.org/10.1080/07388551.2022.2042481)

In basic and applied sciences, genome editing has become an indispensable tool, especially the versatile and adaptable CRISPR/Cas9 system. Using CRISPR/Cas9 in plants has enabled modifications of many valuable traits, including environmental stress tolerance, an essential aspect when it comes to ensuring food security under climate change pressure. The CRISPR toolbox enables faster and more precise plant breeding by facilitating: multiplex gene editing, gene pyramiding, and *de novo* domestication. In this paper, we discuss the most recent advances in CRISPR/Cas9 and alternative CRISPR-based systems, along with the technical challenges that remain to be overcome. A revision of the latest proof-of-concept and functional characterization studies has indeed provided more insight into the quantitative traits affecting crop yield and stress tolerance. Additionally, we focus on the applications of CRISPR/Cas9 technology in regard to extremophile plants, due to their significance on: industrial, ecological and economic levels. These still unexplored genetic resources could provide the means to harden our crops against the threat of climate change, thus ensuring food security over the next century.  
<https://www.tandfonline.com/doi/abs/10.1080/07388551.2022.2042481?src=&journalCode=ibty20&>

Silva F, D.A., and Elizabeth P. B. Fontes E.P.B. (2022): **Clustered Regularly Interspaced Short Palindromic Repeats-Associated Protein System for Resistance Against Plant Viruses: Applications and Perspectives.** Front. Plant Sci. | <https://doi.org/10.3389/fpls.2022.904829>

Different genome editing approaches have been used to engineer resistance against plant viruses. The clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein (Cas; CRISPR/Cas) systems to create pinpoint genetic mutations have emerged as a powerful tool for molecular engineering of plant immunity and increasing resistance against plant viruses. This review presents (i) recent advances in engineering resistance against plant viruses by CRISPR/Cas and (ii) an overview of the potential host factors as targets for the CRISPR/Cas system-mediated broad-range resistance and immunity. Applications, challenges, and perspectives in enabling the CRISPR/Cas system for crop protection are also outlined.  
<https://www.frontiersin.org/articles/10.3389/fpls.2022.904829/full>

Caradus J. (2022): **Impacts of growing and utilising genetically modified crops and forages – a New Zealand perspective,** New Zealand Journal of Agricultural Research, DOI: [10.1080/00288233.2022.2077380](https://doi.org/10.1080/00288233.2022.2077380)

In New Zealand, a genetically modified (GM) organism means any organism where genes or other genetic material have been modified by *in vitro* techniques. This includes New Breeding Technologies (NBT) such as gene editing. The aim here is to (a) examine the importance of consumer attitudes towards food produced from GM plants or from animals fed GM feed and (b) consider whether consumer attitudes would reduce the demand and acceptance of food produced by New Zealand pastoral farmers if GM forages were included in animal feed. Published surveys indicate that consumers were willing to purchase GM foods if they cost less than non-GM foods, although the magnitude of this discount varies across countries, the type of genetic modification and how it affects the food product. While there will always be a proportion of consumers against the use of GM in food production, the published evidence would suggest that the use of GM plants in New Zealand for food production will have no long-term deleterious effects in overseas markets. From a regulatory view point, the focus should be on regulating the benefit-risk issues associated with the end-product of genetic modification rather than the processes used in their development.  
<https://www.tandfonline.com/doi/full/10.1080/00288233.2022.2077380?src=&>  
<https://www.tandfonline.com/doi/epub/10.1080/00288233.2022.2077380?needAccess=true>

## Industrial Biotechnology – White gene engineering

Bai, F., Cai, C., Zhang, T. et al. (2022): **Genome-Based Analysis of *Aspergillus niger* Aggregate Species from China and Their Potential for Fumonisin B<sub>2</sub> and Ochratoxin A Production.** Curr Microbiol 79, 193 (2022). <https://doi.org/10.1007/s00284-022-02876-8>

Based on entire genome sequencing, this study focused on the classification of *Aspergillus niger* aggregation species and investigated their potential for fumonisin B<sub>2</sub> (FB<sub>2</sub>) and ochratoxin A (OTA) production. In the current study, 22 strains were used, namely 17 *A. niger* strains, four *A. welwitschiae* strains, and one *A. lacticoffeatus* (a synonym of *A. niger*) strain. Traditional multigene phylogenetic analysis, average nucleotide identity analysis (ANI), and the whole-genome single-nucleotide polymorphism (SNP) analyses were used to reconfirm the taxonomic status of *A. niger*, *A. welwitschiae*, and *A. lacticoffeatus*. The ability of *A. niger* to produce FB<sub>2</sub> and OTA on five culture substrates was determined, and the association between FB<sub>2</sub> and OTA gene clusters and toxin-producing abilities was explored. The results revealed that the ANI method could distinguish *A. niger* from *A. welwitschiae*, with an ANI value of < 98%. The SNP-based phylogenetic analysis suggested that *A. niger* and *A. welwitschiae* were two independent phylogenetic species. The ANI, SNP, and multigene phylogenetic analysis supported previous findings that *A. lacticoffeatus* was a synonymous species of *A. niger*. *Aspergillus niger* strains exhibited the varied potential of producing FB<sub>2</sub> and OTA on different culture media. The *A. niger* genome sequence analysis revealed no significant difference in fumonisin gene clusters between FB<sub>2</sub>-nonproducing isolates and FB<sub>2</sub>-producing isolates, and the integrity of the ochratoxin biosynthesis genes cluster was clearly associated with OTA production. In conclusion, gene sequencing can be useful in assessing *A. niger*'s ability to produce OTA, but it cannot reliably predict its ability to produce FB<sub>2</sub>.  
<https://link.springer.com/article/10.1007/s00284-022-02876-8>

Wan, H., Ouyang, X., Yang, T. et al. (2022): **A 4- $\alpha$ -Glucanotransferase from *Thermus thermophilus* HB8: Secretory Expression and Characterization.** *Curr Microbiol* 79, 202 | <https://doi.org/10.1007/s00284-022-02856-y>

4- $\alpha$ -glucanotransferase (4GT, EC 2.4.1.25) catalyzes the breakdown of the  $\alpha$ -1,4 glycosidic bonds of the starch main chain and forms new  $\alpha$ -1,4 glycosidic bonds in the side chain, which is often used to optimize the physical and chemical properties of starch and to improve the quality of starch-based food. However, the low enzyme activity of 4GT limits its production and widespread application. Herein, the 4GT gene encoding 500 amino acids from *Thermus thermophilus* HB8 was cloned and expressed in *Escherichia coli*. The purified 4GT exhibited maximum activity at pH 7.0 and 60 °C and had a good stability at pH 6.0–8.0 and 30–60 °C. It was confirmed that 4GT possessed the catalytic function of extending the branch length of potato starch. Furthermore, the 4GT gene was successfully expressed extracellularly in *Bacillus subtilis*. Then, the enzyme yield of 4GT increased by 4.1 times through screening of different plasmids and hosts. Additionally, the fermentation conditions were optimized to enhance 4GT extracellular enzyme yield. Finally, a recombinant *Bacillus subtilis* with 299.9 U/mL enzyme yield of 4GT was obtained under the optimized fermentation process. In conclusion, this study provides a valuable reference for characterization and expression of food-grade enzymes.  
<https://link.springer.com/article/10.1007/s00284-022-02856-y>

Haile, S., Masi, C. & Tafesse, M. (2022): **Isolation and characterization of pectinase-producing bacteria (*Serratia marcescens*) from avocado peel waste for juice clarification.** *BMC Microbiol* 22, 145 | <https://doi.org/10.1186/s12866-022-02536-8>

Background: Bacterial pectinase is an enzyme that could be employed in numerous sectors to break down pectin polysaccharide compounds. The goal of this study is to find pectinase-producing bacteria in avocado peel waste and see if the pectinase enzyme produced can be used to make fruit juice clarification. Results: The researchers isolated four different bacterial strains from avocado peel waste samples. The potential two bacterial isolates that were identified as being *Serratia marcescens* and *Lysinibacillus macrolides*. Finally, the analysis of pectinase production and its application in fruit juice clarification were performed using one of the bacterial strains of *Serratia marcescens*. The clear apple, lemon, and mango juices were further processed to assess each juice's properties. The highest antioxidant activity was recorded in lemon juice samples. The lemon juice showed the highest total titratable acidity and total phenol content. Apple juices contained the highest total soluble solids, reducing sugar content, and viscosity and the mango juices have the maximum pH value recorded. Conclusions: The pectinase isolated from the bacterium *Serratia marcescens* could clear fruit juices. This pectinase needs to be studied more to make sure it works better in the fruit industry and other businesses.  
<https://bmcmicrobiol.biomedcentral.com/track/pdf/10.1186/s12866-022-02536-8.pdf>

## EFSA:

Mombert P., Guijarro D. Diaz-Otero B. and Alonso-Prados J.L. (2022): **Study of the different evaluation areas in the pesticide risk assessment process.** *EFSA Journal* 20 (S1): e200412, 14 pp. | <https://doi.org/10.2903/j.efsa.2022.e200412>

Both chemical and microbial active substances can currently be approved as pesticides in the EU, the provisions of their approval being set under Regulation (EC) No 1107/2009. Although sharing the same legal framework, chemicals and microorganisms used as pesticides have different risk profiles especially because once released into the environment, microbial active substances may produce secondary metabolites, multiply, spread and possibly genetically adapt or transfer antimicrobial resistance genes to other microorganisms. Consequently, the risk assessment process must adjust to the specificities ensuing from the chemical or microbial nature of the active substance. This specific programme focused on the risk assessment of microorganisms used as pesticides, especially on the low-risk criteria linked to antimicrobial resistance and the risk assessment of secondary metabolites. The use of microorganisms in integrated pest management (IPM) programmes was also investigated. In 2020, the recently adopted Farm to Fork Strategy and the Biodiversity Strategy for 2030, two important action plans of the European Green Deal, called for a 50% reduction in the use of and risk from

chemical and more hazardous pesticides. Many microorganisms are likely to be approved as low-risk active substances, thus representing important tools to achieve this goal. Given the central role that microbial active substances could play towards a more sustainable food system, a need for information regarding the actual production of secondary metabolites by the microorganisms of interest and projects investigating IPM programmes at national and EU levels was identified.

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2022.e200412>

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

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