

# Sunday Evening News No 266

Week 06 (2022-07-02 – 2022-13-02)

Selected and edited by **BGF** Jany

---

## Komitologieverfahren für gv-Pflanzen

Am Donnerstag, 10.02.2022 hat der Berufungsausschuss über eine mögliche Zulassung von Raps 73496 und Baumwolle GHB811 beraten.

[https://ec.europa.eu/food/system/files/2022-01/app-comm\\_gmffer\\_20220210\\_agenda.pdf](https://ec.europa.eu/food/system/files/2022-01/app-comm_gmffer_20220210_agenda.pdf)

Über das Abstimmungsergebnis ist bislang nichts bekannt geworden. Gut so! Im Abstimmungsverhalten der Mitgliedsstaaten hat sich nicht geändert. Wahrscheinlich hatten die Mitgliedsstaaten fast wie immer hierzu keine Meinung und schoben die Entscheidung an die Kommission weiter. Das Abstimmungsverhalten von Deutschland wird sich demnächst möglicherweise ändern. Deutschland wird eine Meinung haben und sich nicht mehr ausschließlich bei den Abstimmungen enthalten (siehe Pressemeldung von Agra Europe)

Am 16.02.2022 wird der Ständige Ausschuss (SCoPAFF) über eine mögliche Zulassung der Sojabohne MON 87769 x MON 89788 beraten.

[https://ec.europa.eu/food/system/files/2022-02/sc\\_modif-genet\\_20220216\\_agenda.pdf](https://ec.europa.eu/food/system/files/2022-02/sc_modif-genet_20220216_agenda.pdf)

Ausstehende gv-Pflanzen, die noch ins Komitologieverfahren überführt werden müssen: Mais 3272, Sojabohne MON 87705 x MON 87708 X MON 89788 und Pflanzen mit abgeschlossener EFSA-Sicherheitsbewertung (<https://www.biotech-gm-food.com/eu-zulassungsverfahren-gentechnisch-veraenderter-pflanzen-gvo>)

## Agra Europe: Özdemir und Lemke wollen auch bei GVO und Pflanzenschutz eng zusammenarbeiten

Umwelt-, Ernährungs-, Artenschutz- und Agrarpolitik aus einem Guss kündigen Cem Özdemir und Steffie Lemke an. Sie wollen Glyphosat 2023 vom Markt nehmen und die Gentechnik regulieren.

<https://www.topagrar.com/management-und-politik/news/oezdemir-und-lemke-wollen-auch-bei-gvo-und-pflanzenschutz-eng-zusammenarbeiten-12845936.html>

Ausschnitt: „Das Bundeslandwirtschaftsministerium will auch bei Entscheidungen der EU zur Zulassung von Pflanzenschutzmitteln sowie zum Import von gentechnisch veränderten Organismen (GVO) einen gemeinsamen Kurs mit dem Bundesumweltressort fahren.“

Wie ein Ministeriumssprecher gegenüber Agra-Europe erklärte, hat Ressortchef Cem Özdemir bereits klargestellt, dass „es eine enge Zusammenarbeit“ mit seiner Parteikollegin, Umweltministerin Steffi Lemke, geben wird.

Die Forderung nach einer Ausgestaltung der Umwelt-, Ernährungs- und Artenschutz- sowie der Agrarpolitik „aus einem Guss“ gelte „natürlich auch für anstehende Entscheidungen auf europäischer Ebene“.

Abstimmungsverhalten der Mitgliedsstaaten siehe Abbildung unten.

## Comitology procedure for GM plants:

On Thursday, February 10, 2022, the Appeals Committee discussed a possible approval of rapeseed 73496 and cotton GHB811.

[https://ec.europa.eu/food/system/files/2022-01/app-comm\\_gmffer\\_20220210\\_agenda.pdf](https://ec.europa.eu/food/system/files/2022-01/app-comm_gmffer_20220210_agenda.pdf)

So far nothing has become known about the outcome the voting so far. Good this way! Obviously, there has been no change in the voting behaviour of the member states. As usual, the member states probably had no opinion on the matter and passed the decision on to the Commission. Germany's voting behaviour may change soon. Germany will have an opinion and will no longer exclusively abstain from voting (see Agra Europe press release).

On February 16, 2022, the Standing Committee (SCoPAFF) will discuss a possible approval of the soybean MON 87769 x MON 89788.

[https://ec.europa.eu/food/system/files/2022-02/sc\\_modif-genet\\_20220216\\_agenda.pdf](https://ec.europa.eu/food/system/files/2022-02/sc_modif-genet_20220216_agenda.pdf)

Pending GM crops that still need to be transferred to the comitology procedure: Maize 3272, soybean MON 87705 x MON 87708 X MON 89788 and plants with completed EFSA safety assessment (<https://www.biotech-gm-food.com/eu-zulassungsverfahren-gentechnisch-veraenderter-pflanzen-gvo>).

Press release

### Özdemir and Lemke also want to work closely together on GMOs and crop protection

Cem Özdemir and Steffie Lemke have announced a unified environmental, food, species protection and agricultural policy. They want to take glyphosate off the market in 2023 and regulate genetic engineering.

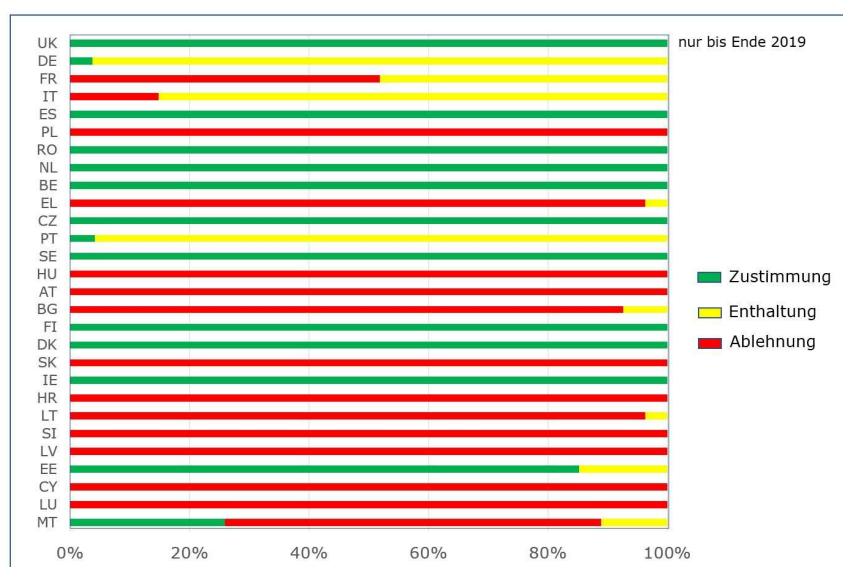
The Federal Ministry of Agriculture also wants to follow a common course with the Federal Ministry for the Environment when it comes to EU decisions on the approval of plant protection products and the import of genetically modified organisms (GMO).

As a ministry spokesman explained to Agra-Europe, minister Cem Özdemir has already made it clear that "there will be close cooperation" with his party colleague, Environment Minister Steffi Lemke.

The call for environmental, food, species protection and agricultural policies to be designed "from a single source" also applies "of course to upcoming decisions at European level".

<https://www.topagrar.com/management-und-politik/news/oezdemir-und-lemke-wollen-auch-bei-gvo-und-pflanzenschutz-eng-zusammenarbeiten-12845936.html>

### Voting behaviour of the member states (SCoAPFF) (2010 – 2020)



### Meetings – Conferences / Veranstaltungen - Tagungen

European Innovation Council and SMEs Executive Agency: EU - Webinar CPVO Coop: Constraints and opportunities for edited varieties. Is the GMO legal framework impacting the creation of new plants?

12 April 2022, 10:30 - 12 April 2022, 12:00

[https://intellectual-property-helpdesk.ec.europa.eu/news-events/events/eu-webinar-cpvo-coop-constraints-and-opportunities-edited-varieties-gmo-legal-framework-impacting\\_en](https://intellectual-property-helpdesk.ec.europa.eu/news-events/events/eu-webinar-cpvo-coop-constraints-and-opportunities-edited-varieties-gmo-legal-framework-impacting_en)

### Press Releases – Media Reports / Pressemeldungen und Medienberichte

Genome Editing – WieWasWozu?

<https://genomeediting.podcaster.de/>

idw: Gentechnik kann sich positiv aufs Klima auswirken

<https://nachrichten.idw-online.de/2022/02/08/gentechnik-kann-sich-positiv-aufs-klima-auswirken/?groupcolor=4>

University of Bonn: **Exploring how genetic engineering can have a positive effect on the climate**

<https://phys.org/news/2022-02-exploring-genetic-positive-effect-climate.html>

Van Deynze A.: **Gene Editing: A 21st Century Tool to Combat Climate Change**

<https://www.realclearpolicy.com/articles/2022/01/25/gene-editing-a-21st-century-tool-to-combat-climate-change-813480.html>

Worzews T.: **„Wir können nicht in der Bioblase vor uns her träumen“**

<https://www.faz.net/aktuell/wissen/gentechnik-und-oekoanbau-agrarwissenschaftler-im-interview-17779173.html>

Informationsdienst Gentechnik: **Europäischer Gerichtshof verhandelt über Neue Gentechnik**

<https://www.keine-gentechnik.de/nachricht/34544?cHash=1c18e7ab12c24c26ca1ad3e3d2ff3cb0>

Nur zum Teil richtig; missverständlich dargestellt. Hier handelt es sich um die gesetzliche Einordnung von Pflanzen, die durch in-vitro-Zufallsmutagenese gewonnen wurden.

<https://www.biotech-gm-food.com/kommentare/staatsrat-ruft-eugh-zur-einordnung-von-in-vivo-und-in-vitro-zufallsmutagenesen-an>

GM Watch: **More than 80 organisations call on European Commission to wait for court's clarifications on new GM**

<https://gmwatch.org/en/106-news/latest-news/19982>

<https://www.eurovia.org/wp-content/uploads/2022/02/Open-Letter-Referral-to-the-CJEU-on-the-status-of-new-genomic-techniques-under-EU-law-EN.pdf>

GM Watch: **Glyphosate and Roundup: All roads lead to cancer**

<https://gmwatch.org/en/106-news/latest-news/19980>

ECVC: **European Commission's vision of carbon farming is inadequate to achieve the Green Deal objectives**

<https://www.eurovia.org/european-commissions-vision-of-carbon-farming-is-inadequate-to-achieve-the-green-deal-objectives/>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): (February week 06)

## Publications – Publikationen

Kovak, E., Blaustein-Rejto, D., Qaim, M. (2022): **Genetically modified crops support climate change mitigation**. Trends in Plant Science, <https://doi.org/10.1016/j.tplants.2022.01.004>

Genetically modified (GM) crops can help reduce agricultural greenhouse gas (GHG) emissions. In addition to possible decreases in production emissions, GM yield gains also mitigate land-use change and related emissions. Wider adoption of already-existing GM crops in Europe could result in a reduction equivalent to 7.5% of the total agricultural GHG emissions of Europe

<https://www.cell.com/action/showPdf?pii=S1360-1385%2822%2900004-8>

Mallapaty S.: (2022): **China's approval of gene-edited crops energizes researchers**

Scientists say newly published guidelines will spur research into crops that have increased yields and greater resilience to climate change.

Nature: <https://doi.org/10.1038/d41586-022-00395-x>

Wilson, K.M., McCool, W.C., Brewer, S.C. et al. (2022): **Climate and demography drive 7000 years of dietary change in the Central Andes**. *Sci Rep* 12, 2026 |.

<https://doi.org/10.1038/s41598-022-05774-y>

Explaining the factors that influence past dietary variation is critically important for understanding changes in subsistence, health, and status in past societies; yet systematic studies comparing possible driving factors remain scarce. Here we compile the largest dataset of past diet derived from stable isotope  $\delta^{13}\text{C}\text{‰}$  and  $\delta^{15}\text{N}\text{‰}$  values in the Americas to quantitatively evaluate the impact of 7000 years of climatic and demographic change on dietary variation in the Central Andes. Specifically, we couple paleoclimatic data from a general circulation model with estimates of relative past population inferred from archaeologically derived radiocarbon dates to assess the influence of climate and population on spatiotemporal dietary variation using an ensemble machine learning model capable of accounting for interactions among predictors. Results reveal that climate and population strongly predict diet (80% of  $\delta^{15}\text{N}\text{‰}$  and 66% of  $\delta^{13}\text{C}\text{‰}$ ) and that Central Andean diets correlate much more strongly with local climatic conditions than regional population size, indicating that the past

7000 years of dietary change was influenced more by climatic than socio-demographic processes. Visually, the temporal pattern suggests decreasing dietary variation across elevation zones during the Late Horizon, raising the possibility that sociopolitical factors overrode the influence of local climatic conditions on diet during that time. The overall findings and approach establish a general framework for understanding the influence of local climate and demography on dietary change across human history.

<https://www.nature.com/articles/s41598-022-05774-y.pdf>

Zobrist J.D. Martin-Ortigosa S., Lee K., Azanu M.K., Q Ji Q., Wang K. (2021): **Transformation of Teosinte (*Zea mays* ssp. *parviglumis*) via Biolistic Bombardment of Seedling-Derived Callus Tissues**, *Frontiers in Plant Science* | [DOI: 10.3389/fpls.2021.773419](https://doi.org/10.3389/fpls.2021.773419)

Modern maize exhibits a significantly different phenotype than its wild progenitor teosinte despite many genetic similarities. Of the many subspecies of *Zea mays* identified as teosinte, *Zea mays* ssp. *parviglumis* is the most closely related to domesticated maize. Understanding teosinte genes and their regulations can provide great insights into the maize domestication process and facilitate breeding for future crop improvement. However, a protocol of genetic transformation, which is essential for gene functional analyses, is not available in teosinte. In this study, we report the establishment of a robust callus induction and regeneration protocol using whorl segments of seedlings germinated from mature seeds of *Zea parviglumis*. We also report, for the first time, the production of fertile, transgenic teosinte plants using the particle bombardment. Using herbicide resistance genes such as mutant acetolactate synthase (*Als*) or bialaphos resistance (*bar*) as selectable markers, we achieved an average transformation frequency of 4.17% (percentage of independent transgenic events in total bombarded explants that produced callus). Expression of visual marker genes of red fluorescent protein *tdTomato* and  $\beta$ -glucuronidase (*gus*) could be detected in bombarded callus culture and in T1 and T2 progeny plants. The protocol established in this work provides a major enabling technology for research toward the understanding of this important plant in crop domestication.

<https://www.frontiersin.org/articles/10.3389/fpls.2021.773419/full>

Taheri, S., Gantait, S., Azizi, P. et al. (2022): **Drought tolerance improvement in *Solanum lycopersicum*: an insight into “OMICS” approaches and genome editing**. *3 Biotech* **12**, 63 |

<https://doi.org/10.1007/s13205-022-03132-3>

*Solanum lycopersicum* (tomato) is an internationally acclaimed vegetable crop that is grown worldwide. However, drought stress is one of the most critical challenges for tomato production, and it is a crucial task for agricultural biotechnology to produce drought-resistant cultivars. Although breeders have done a lot of work on the tomato to boost quality and quantity of production and enhance resistance to biotic and abiotic stresses, conventional tomato breeding approaches have been limited to improving drought tolerance because of the intricacy of drought traits. Many efforts have been made to better understand the mechanisms involved in adaptation and tolerance to drought stress in tomatoes throughout the years. “Omics” techniques, such as genomics, transcriptomics, proteomics, and metabolomics in combination with modern sequencing technologies, have tremendously aided the discovery of drought-responsive genes. In addition, the availability of biotechnological tools, such as plant transformation and the recently developed genome editing system for tomatoes, has opened up wider opportunities for validating the function of drought-responsive genes and the generation of drought-tolerant varieties. This review highlighted the recent progresses for tomatoes improvement against drought stress through “omics” and “multi-omics” technologies including genetic engineering. We have also discussed the roles of non-coding RNAs and genome editing techniques for drought stress tolerance improvement in tomatoes.

<https://link.springer.com/article/10.1007/s13205-022-03132-3>

Mi J., Vallarino J.G., Petřík I., Novák O. (2022): **A manipulation of carotenoid metabolism influence biomass partitioning and fitness in tomato**. *Metabolic Engineering* **70**, 166-180 |

<https://doi.org/10.1016/j.ymben.2022.01.004>

Improving yield, nutritional value and tolerance to abiotic stress are major targets of current breeding and biotechnological approaches that aim at increasing crop production and ensuring food security. [Metabolic engineering](#) of [carotenoids](#), the precursor of vitamin-A and plant hormones that regulate plant growth and response to adverse growth conditions, has been mainly focusing on [provitamin A](#) biofortification or the production of high-value carotenoids. Here, we show that the introduction of a single gene of the carotenoid [biosynthetic pathway](#) in different tomato cultivars induced profound metabolic alterations in carotenoid, [apocarotenoid](#) and phytohormones pathways. Alterations in isoprenoid- (abscisic acid, gibberellins, cytokinins) and non-isoprenoid (auxin and jasmonic acid) derived hormones together with enhanced [xanthophyll](#) content influenced [biomass partitioning](#) and abiotic stress tolerance (high light, salt, and drought), and it caused an up to 77% fruit yield increase and enhanced fruit's provitamin A content. In addition, metabolic and hormonal changes led to accumulation of key [primary metabolites](#) (e.g. osmoprotectants and antiaging agents) contributing with enhanced abiotic stress tolerance and fruit shelf life. Our findings pave the way for developing a new generation of crops that combine high productivity and increased nutritional value with the capability to cope with climate change-related environmental challenges.

<https://www.sciencedirect.com/science/article/pii/S1096717622000106?via%3Dihub>

Ercoli M.F., Luu D.D., Rim E.Y., Shigenaga A., de Araujo Jr A.T. et al. (2022): **Plant immunity: Rice XA21-mediated resistance to bacterial infection**. *PNAS* **119** (8) e2121568119 |

<https://doi.org/10.1073/pnas.2121568119>

In this article, we describe the development of the plant immunity field, starting with efforts to understand the genetic basis for disease resistance, which ~30 y ago led to the discovery of diverse classes of immune receptors that recognize and respond to infectious microbes. We focus on knowledge gained from studies of the rice XA21 immune receptor that recognizes RaxX (required for activation of XA21 mediated immunity X), a sulfated microbial peptide secreted by the gram-negative bacterium *Xanthomonas oryzae* pv. *oryzae*. XA21 is representative of a large class of plant and animal immune receptors that recognize and respond to conserved microbial molecules. We highlight the complexity of this large class of receptors in plants, discuss a possible role for RaxX in *Xanthomonas* biology, and draw attention to the important role of sulfotyrosine in mediating receptor–ligand interactions.

<https://www.pnas.org/content/119/8/e2121568119>

Lin H.-Y., Liao J.-W., Chen R.-S., Chang C.-H. et al. (2022): **Food Safety Assessment of Commercial Genetically Modified Soybeans in Rats**. *Foods*, 11(4), 496 |

<https://doi.org/10.3390/foods11040496>

Although the safety of commercial genetically modified (GM) soybeans has been well evaluated and GM soybeans are legally sold under government management, some consumers still have concerns about their safety. The objective of this study was to evaluate the safety of commercial GM soybeans sold in markets as a food source. In the present study, two commercial GM (GM-1 and -2) soybeans and one non-GM soybean were randomly purchased and subjected to a whole food toxicity assessment. Rats (SD), male and female, were divided into six groups (10/sex/group). Two dosages of 1 g/kg/day and 5 g/kg/day of soybeans were selected for the low- and high-dose groups. Rats were administered the soybeans via daily oral fed for 90 days. The results indicate that the body weight, organ weight, biochemistry, hematology, and urology showed no biologically adverse effects. At necropsy, no significant differences between organ weights were noted between the non-GM- and GM soybeans-treated groups. Moreover, no gross or histopathological lesions were observed in the high-dosage (5 g/kg/day) fed groups of the non-GM and GM soybean fed rats. In conclusion, this food safety assessment revealed that commercial GM soybeans are substantially equivalent to non-GM soybeans in rats.

<https://www.mdpi.com/2304-8158/11/4/496>

Bai, Y., Yang, C., Halitschke, R., Paetz, C., Kessler, D. et al. (2022): **Natural history guided – omics reveals plant defensive chemistry against leafhopper pests**. *Science* 375, eabm2948,

| <https://doi.org/10.1126/science.abm2948>

Although much is known about plant traits that function in nonhost resistance against pathogens, little is known about nonhost resistance against herbivores, despite its agricultural importance. *Empoasca* leafhoppers, serious agricultural pests, identify host plants by eavesdropping on unknown outputs of jasmonate (JA)–mediated signaling. Forward- and reverse-genetics lines of a native tobacco plant were screened in native habitats with native herbivores using high-throughput genomic, transcriptomic, and metabolomic tools to reveal an *Empoasca*-elicited JA-JAZi module. This module induces an uncharacterized caffeoylputrescine–green leaf volatile compound, catalyzed by a polyphenol oxidase in a Michael addition reaction, which we reconstitute in vitro; engineer in crop plants, where it requires a berberine bridge enzyme-like 2 (BBL2) for its synthesis; and show that it confers resistance to leafhoppers. Natural history–guided forward genetics reveals a conserved nonhost resistance mechanism useful for crop protection.

<https://www.science.org/doi/10.1126/science.abm2948>

Reavey, C.E., Walker, A.S., Joyce, S.P. et al. (2022): **Self-limiting fall armyworm: a new approach in development for sustainable crop protection and resistance management**.

*BMC Biotechnol* 22, 5 | <https://doi.org/10.1186/s12896-022-00735-9>

Background: The fall armyworm, *Spodoptera frugiperda*, is a significant and widespread pest of maize, sorghum, rice, and other economically important crops. Successful management of this caterpillar pest has historically relied upon application of synthetic insecticides and through cultivation of genetically engineered crops expressing insecticidal proteins (*Bt* crops). Fall armyworm has, however, developed resistance to both synthetic insecticides and *Bt* crops, which risks undermining the benefits delivered by these important crop protection tools. Previous modelling and empirical studies have demonstrated that releases of insecticide- or *Bt*-susceptible insects genetically modified to express conditional female mortality can both dilute insecticide resistance and suppress pest populations.

Results: Here, we describe the first germline transformation of the fall armyworm and the development of a genetically engineered male-selecting self-limiting strain, OX5382G, which exhibits complete female mortality in the absence of an additive in the larval diet. Laboratory experiments showed that males of this strain are competitive against wild-type males for copulations with wild-type females, and that the OX5382G self-limiting transgene declines rapidly to extinction in closed populations following the cessation of OX5382G male releases. Population models simulating the release of OX5382G males in tandem with *Bt* crops and non-*Bt* ‘refuge’ crops show that OX5382G releases can suppress fall armyworm populations and delay the spread of resistance to insecticidal proteins.

Conclusions: This article describes the development of self-limiting fall armyworm designed to control this pest by suppressing pest populations, and population models that demonstrate its potential as a highly effective method of managing resistance to *Bt* crops in pest fall armyworm populations. Our results provide early promise for a potentially valuable future addition to integrated pest management strategies for fall armyworm



and other pests for which resistance to existing crop protection measures results in damage to crops and impedes sustainable agriculture.

<https://bmcbiotechnol.biomedcentral.com/articles/10.1186/s12896-022-00735-9>

<https://bmcbiotechnol.biomedcentral.com/track/pdf/10.1186/s12896-022-00735-9.pdf>

Muntaabski I., Scannapieco, A.C., Liendo M.C., Niz J.M., Russo R. & Salvador R. (2022): **Bacterially expressed dsRNA induces *Varroa destructor* gene knockdown by honey bee-mediated oral administration**, Journal of Apicultural Research,

<https://doi.org/10.1080/00218839.2022.2028967>

The ectoparasite *Varroa destructor* causes serious losses of *Apis mellifera* colonies and negatively impacts the beekeeping industry around the world. New control methods have been proposed based on the RNA interference technique. Previous reports showed that parasitized honey bees fed with double-stranded RNA (dsRNA) synthesized *in vitro* reduce the transcription levels of target genes in Varroa mites. An efficient and inexpensive alternative to produce dsRNA is the use of bacteria capable of achieving high levels of *in vivo* synthesis. In the present study, dsRNA synthesized *in vivo* was used to induce gene silencing in *V. destructor* and evaluate their effect on the survival of both honey bees and the parasitic Varroa mites. The results evidenced that dsRNA fed to the bees engendered gene silencing in mites, inhibiting expression levels of target genes by 50%. Indeed, a reduction of 50% in Varroa survival was observed when bacterially expressed dsRNAs were administered to mite-parasitized bees. Worker bees that were fed with Varroa-targeted dsRNA by oral route showed no survival differences compared to control bees, fed with sucrose or dsRNA-GFP solutions. Our results demonstrated that specific dsRNA over-expressed in bacteria is capable of reducing mite survival by bee-mediated oral administration. This study provides an efficient and low-cost method for dsRNA production to control parasites and honey bee diseases.

<https://www.tandfonline.com/doi/full/10.1080/00218839.2022.2028967>

Saleh, A.K., El-Gendi, H., Soliman, N.A. *et al.* (2022): **Bioprocess development for bacterial cellulose biosynthesis by novel *Lactiplantibacillus plantarum* isolate along with characterization and antimicrobial assessment of fabricated membrane**. Sci Rep 12, 2181 (2022). <https://doi.org/10.1038/s41598-022-06117-7>

Bacterial cellulose (BC) is an ecofriendly biopolymer with diverse commercial applications. Its use is limited by the capacity of bacterial production strains and cost of the medium. Mining for novel organisms with well-optimized growth conditions will be important for the adoption of BC. In this study, a novel BC-producing strain was isolated from rotten fruit samples and identified as *Lactiplantibacillus plantarum* from 16S rRNA sequencing. Culture conditions were optimized for supporting maximal BC production using one variable at a time, Plackett–Burman design, and Box Behnken design approaches. Results indicated that a modified Yamanaka medium supported the highest BC yield (2.7 g/l), and that yeast extract, MgSO<sub>4</sub>, and pH were the most significant variables influencing BC production. After optimizing the levels of these variables through Box Behnken design, BC yield was increased to 4.51 g/l. The drug delivery capacity of the produced BC membrane was evaluated through fabrication with sodium alginate and gentamycin antibiotic at four different concentrations. All membranes (normal and fabricated) were characterized by scanning electron microscope, Fourier transform-infrared spectroscopy, X-ray diffraction, and mechanical properties. The antimicrobial activity of prepared composites was evaluated by using six human pathogens and revealed potent antibacterial activity against *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, and *Streptococcus mutans*, with no detected activity against *Pseudomonas aeruginosa* and *Candida albicans*.

<https://www.nature.com/articles/s41598-022-06117-7.pdf>

Das, D., Paries, M., Hobecker, K. *et al.* (2022): **PHOSPHATE STARVATION RESPONSE transcription factors enable arbuscular mycorrhiza symbiosis**. Nat Commun 13, 477 | <https://doi.org/10.1038/s41467-022-27976-8>

Arbuscular mycorrhiza (AM) is a widespread symbiosis between roots of the majority of land plants and *Glomeromycotina* fungi. AM is important for ecosystem health and functioning as the fungi critically support plant performance by providing essential mineral nutrients, particularly the poorly accessible phosphate, in exchange for organic carbon. AM fungi colonize the inside of roots and this is promoted at low but inhibited at high plant phosphate status, while the mechanistic basis for this phosphate-dependence remained obscure. Here we demonstrate that a major transcriptional regulator of phosphate starvation responses in rice PHOSPHATE STARVATION RESPONSE 2 (PHR2) regulates AM. Root colonization of *phr2* mutants is drastically reduced, and PHR2 is required for root colonization, mycorrhizal phosphate uptake, and yield increase in field soil. PHR2 promotes AM by targeting genes required for pre-contact signaling, root colonization, and AM function. Thus, this important symbiosis is directly wired to the PHR2-controlled plant phosphate starvation response.

<https://www.nature.com/articles/s41467-022-27976-8.pdf>

Han Z., Sieriebriennikov B., Susoy V., Wen-Sui Lo W-S. *et al.* (2022): **Horizontally Acquired Cellulases Assist the Expansion of Dietary Range in *Pristionchus* Nematodes**, Molecular Biology and Evolution, Volume 39 (2), msab370 | <https://doi.org/10.1093/molbev/msab370>

Horizontal gene transfer (HGT) enables the acquisition of novel traits via non-Mendelian inheritance of genetic material. HGT plays a prominent role in the evolution of prokaryotes, whereas in animals, HGT is rare and its functional significance is often uncertain. Here, we investigate horizontally acquired cellulase genes in the free-

living nematode model organism *Pristionchus pacificus*. We show that these cellulase genes 1) are likely of eukaryotic origin, 2) are expressed, 3) have protein products that are secreted and functional, and 4) result in endo-cellulase activity. Using CRISPR/Cas9, we generated an octuple cellulase mutant, which lacks all eight cellulase genes and cellulase activity altogether. Nonetheless, this cellulase-null mutant is viable and therefore allows a detailed analysis of a gene family that was horizontally acquired. We show that the octuple cellulase mutant has associated fitness costs with reduced fecundity and slower developmental speed. Furthermore, by using various *Escherichia coli* K-12 strains as a model for cellulosic biofilms, we demonstrate that cellulases facilitate the procurement of nutrients from bacterial biofilms. Together, our analysis of cellulases in *Pristionchus* provides comprehensive evidence from biochemistry, genetics, and phylogeny, which supports the integration of horizontally acquired genes into the complex life history strategy of this soil nematode.  
<https://academic.oup.com/mbe/article/39/2/msab370/6493351>

Mesnage R., Ibragim M., Mandrioli D., Falcioni L. et al. (2022): **Comparative Toxicogenomics of Glyphosate and Roundup Herbicides by Mammalian Stem Cell-Based Genotoxicity Assays and Molecular Profiling in Sprague-Dawley Rats**. *Toxicological Sciences*, kfab143 | <https://doi.org/10.1093/toxsci/kfab143>

Whether glyphosate-based herbicides (GBHs) are more potent than glyphosate alone at activating cellular mechanisms, which drive carcinogenesis remain controversial. As GBHs are more cytotoxic than glyphosate, we reasoned they may also be more capable of activating carcinogenic pathways. We tested this hypothesis by comparing the effects of glyphosate with Roundup GBHs both *in vitro* and *in vivo*. First, glyphosate was compared with representative GBHs, namely MON 52276 (European Union), MON 76473 (United Kingdom), and MON 76207 (United States) using the mammalian stem cell-based ToxTracker system. Here, MON 52276 and MON 76473, but not glyphosate and MON 76207, activated oxidative stress and unfolded protein responses. Second, molecular profiling of liver was performed in female Sprague-Dawley rats exposed to glyphosate or MON 52276 (at 0.5, 50, and 175 mg/kg bw/day glyphosate) for 90 days. MON 52276 but not glyphosate increased hepatic steatosis and necrosis. MON 52276 and glyphosate altered the expression of genes in liver reflecting TP53 activation by DNA damage and circadian rhythm regulation. Genes most affected in liver were similarly altered in kidneys. Small RNA profiling in liver showed decreased amounts of miR-22 and miR-17 from MON 52276 ingestion. Glyphosate decreased miR-30, whereas miR-10 levels were increased. DNA methylation profiling of liver revealed 5727 and 4496 differentially methylated CpG sites between the control and glyphosate and MON 52276 exposed animals, respectively. Apurinic/aprimidinic DNA damage formation in liver was increased with glyphosate exposure. Altogether, our results show that Roundup formulations cause more biological changes linked with carcinogenesis than glyphosate.  
<https://academic.oup.com/toxsci/advance-article/doi/10.1093/toxsci/kfab143/6446050>

Hamdan N., Lee C.H., Wong S.L. et al. (2022): **Prevention of Enzymatic Browning by Natural Extracts and Genome-Editing: A Review on Recent Progress**. *Molecules* 27(3), 1101 | <https://doi.org/10.3390/molecules27031101>

Fresh fruits and vegetable products are easily perishable during postharvest handling due to enzymatic browning reactions. This phenomenon has contributed to a significant loss of food quality and appearance. Thus, a safe and effective alternative method from natural sources is needed to tackle enzymatic browning prevention. The capabilities of natural anti-browning agents derived from plant- and animal-based resources in inhibiting enzymatic activity have been demonstrated in the literature. Some also possess strong antioxidants properties. This review aims to summarize a recent investigation regarding the use of natural anti-browning extracts from different sources for controlling the browning. The potential applications of genome-editing in preventing browning activity and improving postharvest quality is also discussed. Moreover, the patents on the anti-browning extract from natural sources is also presented in this review. The information reviewed here could provide new insights, contributing to the development of natural anti-browning extracts and genome-editing techniques for the prevention of food browning.  
<https://www.mdpi.com/1420-3049/27/3/1101>

Forrest IS, Chaudhary K, Vy HMT, et al. (2022): **Population-Based Penetrance of Deleterious Clinical Variants**. *JAMA* 327 (4), 350–359. doi:10.1001/jama.2021.23686

Among 72 434 study participants, 43 395 were from the UK Biobank (mean [SD] age, 57 [8.0] years; 24 065 [55%] women; 2948 [7%] non-European) and 29 039 were from the BioMe Biobank (mean [SD] age, 56 [16] years; 17 355 [60%] women; 19 663 [68%] non-European). Of 5360 pathogenic/loss-of-function variants, 4795 (89%) were associated with an RD less than or equal to 0.05. Mean penetrance was 6.9% (95% CI, 6.0%-7.8%) for pathogenic variants and 0.85% (95% CI, 0.76%-0.95%) for benign variants reported in ClinVar (difference, 6.0 [95% CI, 5.6-6.4] percentage points), with a median of 0% for both groups due to large numbers of nonpenetrant variants. Penetrance of pathogenic/loss-of-function variants for late-onset diseases was modified by age: mean penetrance was 10.3% (95% CI, 9.0%-11.6%) in individuals 70 years or older and 8.5% (95% CI, 7.9%-9.1%) in individuals 20 years or older (difference, 1.8 [95% CI, 0.40-3.3] percentage points). Penetrance of pathogenic/loss-of-function variants was heterogeneous even in known disease predisposition genes, including *BRCA1* (mean [range], 38% [0%-100%]), *BRCA2* (mean [range], 38% [0%-100%]), and *PALB2* (mean [range], 26% [0%-100%]). In 2 large biobank cohorts, the estimated penetrance of pathogenic/loss-of-function variants was variable but generally low. Further research of population-based penetrance is needed to refine variant interpretation and clinical evaluation of individuals with these variant alleles.  
<https://jamanetwork.com/journals/jama/article-abstract/2788347>

Höijer, I., Emmanouilidou, A., Östlund, R. et al. (2022): **CRISPR-Cas9 induces large structural variants at on-target and off-target sites in vivo that segregate across generations.** Nat Commun 13, 627 | <https://doi.org/10.1038/s41467-022-28244-5>

CRISPR-Cas9 genome editing has potential to cure diseases without current treatments, but therapies must be safe. Here we show that CRISPR-Cas9 editing can introduce unintended mutations in vivo, which are passed on to the next generation. By editing fertilized zebrafish eggs using four guide RNAs selected for off-target activity in vitro, followed by long-read sequencing of DNA from >1100 larvae, juvenile and adult fish across two generations, we find that structural variants (SVs), i.e., insertions and deletions  $\geq 50$  bp, represent 6% of editing outcomes in founder larvae. These SVs occur both at on-target and off-target sites. Our results also illustrate that adult founder zebrafish are mosaic in their germ cells, and that 26% of their offspring carries an off-target mutation and 9% an SV. Hence, pre-testing for off-target activity and SVs using patient material is advisable in clinical applications, to reduce the risk of unanticipated effects with potentially large implications. <https://www.nature.com/articles/s41467-022-28244-5.pdf>

Lang G., Grill C., Scheibel T. (2022): **Site-Specific Functionalization of Recombinant Spider Silk Janus Fibers.** Angewandte Chemie | <https://doi.org/10.1002/anie.202115232>

Biotechnological production is a powerful tool to design materials with customized properties. The aim of this work was to apply designed spider silk proteins to produce Janus fibers with two different functional sides. First, functionalization was established through a cysteine-modified silk protein, ntag<sup>Cys</sup>eADF4( $\kappa$ 16). After fiber spinning, gold nanoparticles (AuNPs) were coupled via thiol-ene click chemistry. Significantly reduced electrical resistivity indicated sufficient loading density of AuNPs on such fiber surfaces. Then, Janus fibers were electrospun in a side-by-side arrangement, with “non-functional” eADF4(C16) on the one and “functional” ntag<sup>Cys</sup>eADF4( $\kappa$ 16) on the other side. Post-treatment was established to render silk fibers insoluble in water. Subsequent AuNP binding was highly selective on the ntag<sup>Cys</sup>eADF4( $\kappa$ 16) side demonstrating the potential of such silk-based systems to realize complex bifunctional structures with spatial resolutions in the nano scale. <https://onlinelibrary.wiley.com/doi/10.1002/anie.202115232>

#### EFSA

FEEDAP Panel (2022): Scientific Opinion on the safety of the fermentation product of *Aspergillus oryzae* NRRL 458 (Amaferm®) as a feed additive for dairy cows (Biozyme Inc.). EFSA Journal 20 (2): 6983, 10 pp. | <https://doi.org/10.2903/j.efsa.2022.6983>  
<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2022.6983>

---

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](http://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.*

Klaus-Dieter Jany  
Nelkenstrasse 36  
D-76351 Linkenheim-Hochstetten  
[jany@biotech-gm-food.com](mailto:jany@biotech-gm-food.com)

1. Vorsitzender des WGG e.V.  
Postfach 120721  
D-60114 Frankfurt/Main  
[jany@wgg-ev.de](mailto:jany@wgg-ev.de)