

Sunday Evening News No 361

2024-01-22 – 2024-01-28

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► [WGG-Pressemitteilung](#): EU-Umweltausschuss stimmt für eine evidenzbasierte Regulierung von Pflanzen aus den neuen genomischen Techniken

► [WGG-AFBV Press release](#): EU Environment Committee votes in favour of an evidence-based regulation of plants derived from new genomic techniques

► [AFBV-EU-SAGE-WGG](#): Offener Brief an die Mitglieder des ENVI-Ausschusses zur Regulierung von Pflanzen aus den neuen genomischen Techniken

► [AFBV-EU-SAGE-WGG](#): Open letter to the members of the ENVI Committee on the regulation of plants derived from new genomic techniques

Press Releases -Media / Presse- und Medienberichte

Stellungnahme des Kommissariats der deutschen Bischöfe – Katholisches Büro in Berlin: Kommissionsvorschlag einer EU-Verordnung über mit bestimmten neuen genomischen Techniken gewonnene Pflanzen und die aus ihnen gewonnenen Lebens- und Futtermittel sowie zur Änderung der Verordnung (EU) 2017/625

https://www.kath-buero.de/files/Kath_theme/Stellungnahmen/2023/231215%20KB%20Stellungnahme%20NGT-Verordnungsentwurf.pdf

EU-Commission: Commission authorises and renews GMOs for food and animal feed

EU-Kommission lässt neue Sorte von gentechnisch verändertem Mais zu, verlängert Zulassung für zwei Rapsorten

https://ec.europa.eu/commission/presscorner/detail/en/mex_24_446

(Anmerkung: Mais Bt 11 x MIR 162 x MIR 604 x MON 89034 x 5307 x GA 21; Raps Ms8 Rf3 und Ms8 x Rf3)

EU-Parliament: New Genomic Techniques: MEPs want to ban all patents for NGT plants

<https://www.europarl.europa.eu/news/de/press-room/20240122IPR17027/new-genomic-techniques-meps-want-to-ban-all-patents-for-ngt-plants>

Result of votes and roll-call votes: <https://www.europarl.europa.eu/cmsdata/280266/2024-01-24%20roll-call%20votes.pdf>

Note: LEGISLATIVE TRAIN 12.2023 - 1 A EUROPEAN GREEN DEAL - LEGISLATIVE TRAIN 12.2023

1 A EUROPEAN GREEN DEAL PLANTS PRODUCED BY CERTAIN NEW GENOMIC TECHNIQUES - Q3 2023

<https://www.europarl.europa.eu/legislative-train/carriage/plants-produced-by-certain-new-genomic-techniques/report?sid=7601>

Arboleas M.S.: **EU Parliament gives first green light to new rules for gene-edited plants**

<https://www.euractiv.com/section/agriculture-food/news/eu-parliament-gives-first-green-light-to-new-rules-for-gene-edited-plants/>

Bio Eco Actual: **Vote on NGTs: A rushed outcome jeopardizing biosafety and freedom of choice**

<https://www.bioecoactual.com/en/2024/01/24/plenary-vote-on-ngts-a-rushed-outcome-jeopardizing-biosafety-and-freedom-of-choice/>

Koch J.: **Mehrheit stimmt für EU-Gentechniknovelle: Ökolandbau bleibt außen vor**

<https://www.agrarheute.com/politik/mehrheit-stimmt-fuer-eu-gentechniknovelle-oekolandbau-bleibt-aussen-615696>

BUND: **Kommentar: EU-Umweltausschuss für Aufweichung von Gentechnik-Regeln**

<https://www.bund.net/service/presse/pressemitteilungen/detail/news/kommentar-eu-umweltausschuss-fuer-aufweichung-von-gentechnik-regeln/>

VLOG: **Pro-Gentechnik-Votum: Europaabgeordnete sollten sich nicht beirren lassen**

<https://www.ohnegentechnik.org/artikel/pro-gentechnik-votum-europaabgeordnete-sollten-sich-nicht-beirren-lassen>

Pro GMO vote: MEPs should not be deterred

<https://www.ohnegentechnik.org/en/news/article/pro-gmo-vote-meps-should-not-be-deterred>

Euractiv: **Members of the European Parliament, give our agriculture the means to face up to the challenges of performance and sustainability**

<https://www.euractiv.com/section/agriculture-food/opinion/members-of-the-european-parliament-give-our-agriculture-the-means-to-face-up-to-the-challenges-of-performance-and-sustainability/>

tg: **Deregulation of new genomic techniques before decision**

<https://european-biotechnology.com/up-to-date/latest-news/news/deregulation-of-new-genomic-techniques-before-decision.html>

Roth K., Kaufmann D. – Grünes Netzwerk evidenzbasierte-Politik: **Faktencheck: Neue Gentechniken in der Landwirtschaft**

<https://evidenzbasierte-politik.de/2024/01/23/faktencheck-neue-gentechniken-in-der-landwirtschaft/>

President von der Leyen launches Strategic Dialogue on the Future of EU Agriculture

https://ec.europa.eu/commission/presscorner/detail/en/ip_24_417

Griera M. and Alipour N.: **EU Greens’ manifesto: A ‘Social’ Green Deal and embrace of NATO**

https://www.euractiv.com/section/politics/news/eu-greens-manifesto-a-social-green-deal-and-embrace-of-nato/?utm_source=Euractiv&utm_campaign=80ae19e5f2-EMAIL_CAMPAIGN_2024_01_18_11_19_COPY_01&utm_medium=email&utm_term=0_40c1abb0f8-%5BLIST_EMAIL_ID%5D

Hefferon K.L. and Miller H.I.: **Here’s how we can genetically modify soil microbiomes to reduce use of synthetic fertilizers and improve yields**

<https://geneticliteracyproject.org/2024/01/24/heres-how-we-can-genetically-modify-the-soil-microbiome-to-reduce-the-use-of-synthetic-fertilizers-and-improve-yields/>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): January week 04-2024

Publications – Publikationen

Ledford H.: **CRISPR-edited crops break new ground in Africa**

Scientists in the global south use the popular technique to protect local crops against local threats.

<https://www.nature.com/articles/d41586-024-00176-8>

Ríos D.F., Candia N. B., Soerensen M.C., Goberna M.F., Arrúa A.A. (2024): **Regulatory landscape for new breeding techniques (NBTs): insights from Paraguay.** Front. Bioeng. Biotechnol. 12 | <https://doi.org/10.3389/fbioe.2024.1332851>

https://www.frontiersin.org/articles/10.3389/fbioe.2024.1332851/full?utm_source=F-NTF&utm_medium=EMLX&utm_campaign=PRD_FEOPS_20170000_ARTICLE

Teufel T., López V., Greiter A, Kampffmeyer N. et al. (2024): **Strategies for traceability to prevent unauthorised GMOs (including NGTs) in the EU: State of the art and possible alternative approaches.** Foods 13 (3), 369 | <https://doi.org/10.3390/foods13030369>

The EU's regulatory framework for genetically modified organisms (GMOs) was developed for "classical" transgenic GMOs, yet advancements in so-called "new genomic techniques (NGTs)" have led to implementation challenges regarding detection and identification. As traceability can complement detection and identification strategies, improvements to the existing traceability strategy for GMOs are investigated in this study. Our results are based on a comprehensive analysis of existing traceability systems for globally traded agricultural products, with a focus on soy. Alternative traceability strategies in other sectors were also analysed. One focus was on traceability strategies for products with characteristics for which there are no analytical verification methods. Examples include imports of "conflict minerals" into the EU. The so-called EU Conflict Minerals Regulation requires importers of certain raw materials to carry out due diligence in the supply chain. Due diligence regulations, such as the EU's Conflict Minerals Regulation, can legally oblige companies to take responsibility for certain risks in their supply chains. They can also require the importer to prove the regional origin of imported goods. The insights from those alternative traceability systems are transferred to products that might contain GMOs. When applied to the issue of GMOs, we propose reversing the burden of proof: All companies importing agricultural commodities must endeavour to identify risks of unauthorised GMOs (including NGTs) in their supply chain and, where appropriate, take measures to minimise the risk to raw material imports. The publication concludes that traceability is a means to an end and serves as a prerequisite for due diligence in order to minimise the risk of GMO contamination in supply chains. The exemplary transfer of due diligence to a company in the food industry illustrates the potential benefits of mandatory due diligence, particularly for stakeholders actively managing non-GMO supply chains.

<https://www.mdpi.com/2304-8158/13/3/369>

Keeling, P.J. (2024): **Horizontal gene transfer in eukaryotes: aligning theory with data.** Nat Rev Genet | <https://doi.org/10.1038/s41576-023-00688-5>

Horizontal gene transfer (HGT), or lateral gene transfer, is the non-sexual movement of genetic information between genomes. It has played a pronounced part in bacterial and archaeal evolution, but its role in eukaryotes is less clear. Behaviours unique to eukaryotic cells — phagocytosis and endosymbiosis — have been proposed to increase the frequency of HGT, but nuclear genomes encode fewer HGTs than bacteria and archaea. Here, I review the existing theory in the context of the growing body of data on HGT in eukaryotes, which suggests that any increased chance of acquiring new genes through phagocytosis and endosymbiosis is offset by a reduced need for these genes in eukaryotes, because selection in most eukaryotes operates on variation not readily generated by HGT.

<https://www.nature.com/articles/s41576-023-00688-5>

Nizampatnam N.R., Sharma K., Gupta P., Pamei I., Sarma S., Sreelakshmi Y, Sharma R. (2023): **Introgression of a dominant phototropin1 mutant enhances carotenoids and boosts flavour-related volatiles in genome-edited tomato *RIN* mutants.** New Phytologist (2023) | doi: 10.1111/nph.19510

The tomato (*Solanum lycopersicum*) ripening inhibitor (*rin*) mutation is known to completely repress fruit ripening. The heterozygous (*RIN/rin*) fruits have extended shelf life, ripen normally, but have inferior taste/flavour. To address this, we used genome editing to generate newer alleles of *RIN* (*rin^{CR}*) by targeting the K-domain.

Unlike previously reported CRISPR alleles, the *rin^{CR}* alleles displayed delayed onset of ripening, suggesting that the mutated K-domain represses the onset of ripening. The *rin^{CR}* fruits had extended shelf life and accumulated carotenoids at an intermediate level between *rin* and progenitor line. Besides, the metabolites and hormonal levels in *rin^{CR}* fruits were more akin to *rin*. To overcome the negative attributes of *rin*, we crossed the *rin^{CR}* alleles with *Nps1*, a dominant-negative phototropin1 mutant, which enhances carotenoid levels in tomato fruits. The resulting *Nps1/rin^{CR}* hybrids had extended shelf life and 4.4–7.1-fold higher carotenoid levels than the wild-type parent.

The metabolome of *Nps1/rin^{CR}* fruits revealed higher sucrose, malate, and volatiles associated with tomato taste and flavour. Notably, the boosted volatiles in *Nps1/rin^{CR}* were only observed in fruits bearing the homozygous *Nps1* mutation. The *Nps1* introgression into tomato provides a promising strategy for developing cultivars with extended shelf life, improved taste, and flavour.

<https://nph.onlinelibrary.wiley.com/doi/10.1111/nph.19510>

Chen, Y.; Meissle, M.; Xue, J.; Zhang, N.; Ma, S. et al. (2023): **Expression of Cry1Ab/2Aj Protein in Genetically Engineered Maize Plants and Its Transfer in the Arthropod.** FoodWeb. Plants 12, 4057 | <https://doi.org/10.3390/plants12234057>

While transgenic *Bacillus thuringiensis* (Bt) maize provides pest resistance and a reduced application of chemical pesticides, a comprehensive environmental risk assessment is mandatory before its field release. This research determined the concentrations of Bt protein in plant tissue and in arthropods under field conditions in Gongzhuling City, northeastern China, to provide guidance for the selection of indicator species for non-target risk assessment studies. Bt maize expressing Cry1Ab/2Aj and non-transformed near-isoline were grown under identical environmental and agricultural conditions. Cry1Ab/2Aj was detected in plant tissues and arthropods collected from Bt maize plots during pre-flowering, flowering, and post-flowering. The expression of Cry1Ab/2Aj varied across growth stages and maize tissues, as well as in the collected arthropods at the three growth stages.

Therefore, representative species should be chosen to cover the whole growing season and to represent different habitats and ecological functions. *Dalbulus maidis* (Hemiptera: Cicadellidae), *Rhopalosiphum padi* (Hemiptera: Aphididae), *Heteronychus arator* (Coleoptera: Scarabaeidae), and *Somaticus angulatus* (Coleoptera: Tenebrionidae) are suitable non-target herbivores. *Propylea japonica* (Coleoptera: Coccinellidae), *Paederus fuscipes* (Coleoptera: Staphylinidae), *Chrysoperla nipponensis* (Neuroptera: Chrysopidae), and spiders are suggested predators. *Apis cerana* and *Apis mellifera ligustica* (both Hymenoptera: Apidae) represent pollinators and *Folsomia candida* (Collembola: Isotomidae) decomposers.

<https://www.mdpi.com/2223-7747/12/23/4057>

Ma F., Xu Q., Wang A., +17 , and Zhang G. (2024): **A universal design of restructured dimer antigens: Development of a superior vaccine against the paramyxovirus in transgenic rice.** PNAS 121 (4), e2305745121 | <https://doi.org/10.1073/pnas.2305745121>

The development of vaccines, which induce effective immune responses while ensuring safety and affordability, remains a substantial challenge. In this study, we proposed a vaccine model of a restructured “head-to-tail” dimer to efficiently stimulate B cell response. We also demonstrate the feasibility of using this model to develop a paramyxovirus vaccine through a low-cost rice endosperm expression system. Crystal structure and small-angle X-ray scattering data showed that the restructured hemagglutinin–neuraminidase (HN) formed tetramers with fully exposed quadruple receptor binding domains and neutralizing epitopes. In comparison with the original HN antigen and three traditional commercial whole virus vaccines, the restructured HN facilitated critical epitope exposure and initiated a faster and more potent immune response. Two-dose immunization with 0.5 µg of the restructured antigen (equivalent to one-127th of a rice grain) and one-dose with 5 µg completely protected chickens against a lethal challenge of the virus. These results demonstrate that the restructured HN from transgenic rice seeds is safe, effective, low-dose useful, and inexpensive. We provide a plant platform and a simple restructured model for highly effective vaccine development.

<https://www.pnas.org/doi/abs/10.1073/pnas.2305745121>

Fraiture M.-A., Gobbo A., Guillitte, C. Marchesi E., Verginelli D. et al. (2024): **Pilot market surveillance of GMM contaminations in alpha-amylase food enzyme products: A detection strategy strengthened by a newly developed qPCR method targeting a GM *Bacillus licheniformis* producing alpha-amylase.** Food Chemistry: Molecular Sciences 8 , 100186 |

<https://doi.org/10.1016/j.fochms.2023.100186>

Using high-throughput metagenomics on commercial microbial fermentation products, DNA from a new unauthorized genetically modified microorganism (GMM), namely the GM *B. licheniformis* strain producing alpha-amylase (GMM alpha-amylase2), was recently discovered and characterized. On this basis, a new qPCR method targeting an unnatural association of sequences specific to the GMM alpha-amylase2 strain was designed and developed in this study, allowing to strengthen the current GMM detection strategy. The performance of the newly developed qPCR method was assessed for its specificity and sensitivity to comply with the minimum performance requirements established by the European Network of GMO Laboratories for GMO analysis. Moreover, the transferability of the *in house* validated qPCR method was demonstrated. Finally, its applicability was confirmed by a pilot market surveillance of GMM contaminations conducted for the first time on 40 alpha-amylase food enzyme products labelled as containing alpha-amylase. This pilot market surveillance allowed also to highlight numerous contaminations with GMM alpha-amylase2, including frequent cross-contaminations with other GMM strains previously characterized. In addition, the presence of full-length AMR genes, raising health concerns, was also reported.

<https://www.sciencedirect.com/science/article/pii/S2666566223000266>

Jones, E.M., Marken, J.P. & Silver, P.A. (2024): **Synthetic microbiology in sustainability applications.** Nat Rev Microbiol | <https://doi.org/10.1038/s41579-023-01007-9>

Microorganisms are a promising means to address many societal sustainability challenges owing to their ability to thrive in diverse environments and interface with the microscale chemical world via diverse metabolic capacities. Synthetic biology can engineer microorganisms by rewiring their regulatory networks or introducing new functionalities, enhancing their utility for target applications. In this Review, we provide a broad, high-level overview of various research efforts addressing sustainability challenges through synthetic biology, emphasizing foundational microbiological research questions that can accelerate the development of these efforts. We introduce an organizational framework that categorizes these efforts along three domains — factory, farm and field — that are defined by the extent to which the engineered microorganisms interface with the natural external environment. Different application areas within the same domain share many fundamental challenges, highlighting productive opportunities for cross-disciplinary collaborations between researchers working in historically disparate fields.

<https://www.nature.com/articles/s41579-023-01007-9>

Baltar, F., Martínez-Pérez, C., Amano, C. et al. (2023): **A ubiquitous gammaproteobacterial clade dominates expression of sulfur oxidation genes across the mesopelagic ocean.** Nat Microbiol 8, 1137–1148 | <https://doi.org/10.1038/s41564-023-01374-2>

The deep ocean (>200 m depth) is the largest habitat on Earth. Recent evidence suggests sulfur oxidation could be a major energy source for deep ocean microbes. However, the global relevance and the identity of the major players in sulfur oxidation in the oxygenated deep-water column remain elusive. Here we combined single-cell genomics, community metagenomics, metatranscriptomics and single-cell activity measurements on samples

collected beneath the Ross Ice Shelf in Antarctica to characterize a ubiquitous mixotrophic bacterial group (UBA868) that dominates expression of RuBisCO genes and of key sulfur oxidation genes. Further analyses of the gene libraries from the 'Tara Oceans' and 'Malaspina' expeditions confirmed the ubiquitous distribution and global relevance of this enigmatic group in the expression of sulfur oxidation and dissolved inorganic carbon fixation genes across the global mesopelagic ocean. Our study also underscores the unrecognized importance of mixotrophic microbes in the biogeochemical cycles of the deep ocean.
<https://www.nature.com/articles/s41564-023-01374-2>

Breyer E., Baltar F. (2023): **The largely neglected ecological role of oceanic pelagic fungi.** Trends in Ecology & Evolution | <https://doi.org/10.1016/j.tree.2023.05.002>

Most investigations into ocean ecology and biogeochemistry have tended to focus on marine bacteria, archaea, and protists, while pelagic fungi (mycoplankton) have traditionally been neglected and considered to reside only in association with benthic solid substrates. Nevertheless, recent studies have revealed that pelagic fungi are distributed ubiquitously throughout the water column in every ocean basin and play an active role in the degradation of organic matter and the cycling of nutrients. We review the current status of knowledge on the ecology of mycoplankton and highlight knowledge gaps and challenges. These findings underscore the need to recognize this neglected kingdom as significant contributors to the organic matter cycling and ecology of the oceans.

[https://www.cell.com/trends/ecology-evolution/fulltext/S0169-5347\(23\)00125-8?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0169534723001258%3Fshowa%3Dtrue](https://www.cell.com/trends/ecology-evolution/fulltext/S0169-5347(23)00125-8?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0169534723001258%3Fshowa%3Dtrue)

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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