

Sunday Evening News No 364

2024-02-12 – 2024-02-18

Compiled and edited by **BGF** Jany



Meetings – Conferences / Veranstaltungen - Konferenzen

Enter Science - Die Zukunft der Ernährung

Mittwoch, 20. März 2024 19:00 Uhr–21:30 Uhr, Bundeskunsthalle, Bonn, Helmut-Kohl-Allee 4
<https://www.bonn.de/veranstaltungenkalender/veranstaltungen/hauptkalender/extern/Enter-Science-Die-Zukunft-der-Ernaehrung.php>

Press Releases -Media / Presse- und Medienberichte

Australian agencies announced approvals for commercial cultivation and food use of GM disease resistant banana.

Office of the Gene Technology Regulator (environmental assessment and approval) - <https://www.ogtr.gov.au/gmo-dealings/dealings-involving-intentional-release/dir-199>

Food Standards Australia New Zealand (food approval) - <https://www.foodstandards.gov.au/food-standards-code/applications/A1274-Food-derived-from-disease-resistant-banana-line-QCAV-4>

Le Page M.: Genetically modified banana approved by regulators for first time

<https://www.newscientist.com/article/2417568-genetically-modified-banana-approved-by-regulators-for-first-time/>

BAFU: BAFU bewilligt Freisetzungversuch mit gentechnisch veränderter Gerste

<https://www.bafu.admin.ch/bafu/de/home/dokumentation/medienmitteilungen/anzeige-nsb-unter-medienmitteilungen.msg-id-100058.html>

Schuller J.: Erstmals testet Agroscope Crispr-Cas-Gerste – ohne Fremdgene

<https://www.bauernzeitung.ch/artikel/pflanzen/erstmals-testet-agroscope-crispr-cas-gerste-ohne-fremdgene-509126>

Bourzac K.: Glow way! Bioluminescent houseplant hits US market for first time

<https://www.nature.com/articles/d41586-024-00383-3>

Meunier E.: Few micro-organisms modified by Crispr are already on the market

<https://www.infogm.org/7976-few-micro-organisms-modified-by-Crispr-already-on-the-market?lang=fr>

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 07-2024

Publications – Publikationen

Yu D., Zhou T., Xu N., Sun X., Son S. et al. (2024): **Novel CRISPR/Cas9 system assisted by fluorescence marker and pollen killer for high-efficiency isolation of transgene-free edited plants in rice.** Plant Biotechnol. J. | <https://doi.org/10.1111/pbi.1429>
<https://onlinelibrary.wiley.com/doi/epdf/10.1111/pbi.14293>

Sun S., Han X., Jin R., Jiao J. et al. (2024): **Generation of CRISPR-edited birch plants without DNA integration using Agrobacterium-mediated transformation technology.** Plant Science 342, 112029 | <https://doi.org/10.1016/j.plantsci.2024.112029>

CRISPR/Cas9 system has emerged as a powerful tool in genome editing; however, generation of CRISPR-edited DNA-free plants is still challenging. In this study, *Betula platyphylla* (birch) was used to build a method to generate CRISPR-edited plant without foreign DNA integration using Agrobacterium-mediated transformation (CPDAT method). This technique utilizes transient genetic transformation to introduce T-DNA coding gRNA and Cas9 into birch cells, and T-DNA will express to synthesize gRNA and Cas9 protein, which will form a complex to cleave the target DNA site. The genome may be mutated due to DNA repair, and these mutations will be preserved and accumulated not dependent on whether T-DNA is integrated into the genome or not. After transient transformation, birch plants were cut into explants to induce adventitious buds without antibiotic selection pressure. Each adventitious bud can be considered as an independent potentially CRISPR-edited line

for mutation detection. CRISPR-edited birch plants without foreign DNA integration are further selected by screening CRISPR-edited lines without T-DNA integration. Among 65 randomly chosen independent lines, the mutation rate was 80.00% including 40.00% of lines with both alleles mutated. In addition, 5 lines out of 65 studied lines (7.69%) were CRISPR-edited birch plants without DNA integration. In conclusion, this innovative method presents a novel strategy for generating CRISPR-edited birch plants, thereby significantly enhancing the efficiency of generating common CRISPR-edited plants. These findings offer considerable potential to develop plant genome editing techniques further.

<https://www.sciencedirect.com/science/article/abs/pii/S0168945224000566>

McFadden B.R., Rumble J.N., Stofer K.A., Folta K.M. (2024): **U.S. public opinion about the safety of gene editing in the agriculture and medical fields and the amount of evidence needed to improve opinions.** Front. Bioeng. Biotechnol. 12: 1340398. | doi: [10.3389/fbioe.2024.1340398](https://doi.org/10.3389/fbioe.2024.1340398)

Introduction: Implementation of gene editing in agriculture and medicine hinges on public acceptance. The objectives of this study were to explore U.S. public opinion about gene editing in agricultural and medical fields and to provide more insight into the relationship between opinions about the safety of gene editing and the potential impact of evidence to improve opinions about safety.

Methods: Data were from two samples of U.S. respondents: 1,442 respondents in 2021 and 3,125 respondents in 2022. Survey respondents provided their opinions about the safety of gene editing in the agricultural and medical fields and answered questions about the number of studies or length of time without a negative outcome to improve opinions about the safety of gene editing in the agricultural and medical fields.

Results: Results indicated that respondents in both samples were more familiar, more likely to have an opinion about safety, and more positive about the safety of gene editing in the agricultural field than in the medical field. Also, familiarity was more closely associated with opinions about safety than the strength of opinions.

Discussion: These findings add to the literature examining perceptions of gene editing in the agricultural or medical fields separately. Opinions about the safety of gene editing were generally more favorable for respondents who were aware of the use of gene editing. These results support a proactive approach for effective communication strategies to inform the public about the use of gene editing in the agricultural and medical fields.

<https://www.frontiersin.org/articles/10.3389/fbioe.2024.1340398/full>

H. J. Park H.-J., Kim M., Lee D., Kim H.-J., Jung H.W. (2024): **CRISPR-Cas9 and beyond: identifying target genes for developing disease-resistant plants.** Plant Biology | <https://doi.org/10.1111/plb.13625>

Throughout the history of crop domestication, desirable traits have been selected in agricultural products. However, such selection often leads to crops and vegetables with weaker vitality and viability than their wild ancestors when exposed to adverse environmental conditions. Considering the increasing human population and climate change challenges, it is crucial to enhance crop quality and quantity. Accordingly, the identification and utilization of diverse genetic resources are imperative for developing disease-resistant plants that can withstand unexpected epidemics of plant diseases. In this review, we provide a brief overview of recent progress in genome-editing technologies, including zinc-finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and clustered regularly interspaced short palindromic repeats (CRISPR)-associated protein 9 (Cas9) technologies. In particular, we classify disease-resistant mutants of *Arabidopsis thaliana* and several crop plants based on the roles or functions of the mutated genes in plant immunity and suggest potential target genes for molecular breeding of genome-edited disease-resistant plants. Genome-editing technologies are resilient tools for sustainable development and promising solutions for coping with climate change and population increases.

<https://onlinelibrary.wiley.com/doi/10.1111/plb.13625>

Baniya; A, Subkrasae C., Ardpairin J., Anesko K. et al. (2024): **STEINERNEMA ADAMSI N. SP. (RHABDITIDA: STEINERNEMATIDAE), A NEW ENTOMOPATHOGENIC NEMATODE FROM THAILAND.** J Parasitol (2024) 110 (1): 22–39 | <https://doi.org/10.1645/23-60>

A new species of entomopathogenic nematode, *Steinernema adamsi* n. sp., was recovered from the soil of a longan tree (*Dimocarpus* sp.) in Mueang Lamphun District, Thailand, using baiting techniques. Upon analysis of the nematode's morphological traits, we found it to be a new species of *Steinernema* and a member of the *Longicaudatum* clade. Molecular analyses of the ITS rDNA and D2D3 of 28S rDNA sequences further confirmed that *S. adamsi* n. sp. is a new species of the *Longicaudatum* clade, which is closely related to *Steinernema guangdongense* and *Steinernema longicaudum*. Using morphometric analysis, the infective juveniles measure between 774.69 and 956.96 µm, males have a size range of 905.44 to 1,281.98 µm, and females are within the range of 1,628.21 to 2,803.64 µm. We also identified the symbiotic bacteria associated with the nematode based on 16S sequences as *Xenorhabdus* spp. closely related to *Xenorhabdus griffiniae*. Furthermore, we have successfully assessed a cryopreservation method for the long-term preservation of *S. adamsi* n. sp. Successful cryopreservation of this new species will allow for the longer preservation of its traits and will be valuable for its future use. The discovery of this new species has significant implications for the development of effective biological control agents in Thailand, and our work contributes to our understanding of the diversity and evolution of entomopathogenic nematodes.

<https://meridian.allenpress.com/journal-of-parasitology/article/110/1/22/498907/STEINERNEMA-ADAMSI-N-SP-RHABDITIDA>

Koralesky, K.E., Tworek, H.J.S., von Keyserlingk, M.A.G. et al. "(2024).: **Frequently Asked Questions" About Genetic Engineering in Farm Animals: A Frame Analysis.** Food ethics 9, 7 <https://doi.org/10.1007/s41055-024-00143-z>

Calls for public engagement on emerging agricultural technologies, including genetic engineering of farm animals, have resulted in the development of information that people can interact and engage with online, including "Frequently Asked Questions" (FAQs) developed by organizations seeking to inform or influence the debate. We conducted a frame analysis of FAQs webpages about genetic engineering of farm animals developed by different organizations to describe how questions and answers are presented. We categorized FAQs as having a regulatory frame (emphasizing or challenging the adequacy of regulations), an efficiency frame (emphasizing precision and benefits), a risks and uncertainty frame (emphasizing unknown outcomes), an animal welfare frame (emphasizing benefits for animals) or an animal dignity frame (considering the inherent value of animals). Animals were often featured as the object of regulations in FAQs, and questions about animals were linked to animal welfare regulations. The public were represented using a variety of terms (public, consumer) and pronouns (I, we). Some FAQs described differences between technology terms (gene editing, genetic modification) and categorized technologies as either well-established or novel. This framing of the technology may not respond to actual public concerns on the topic. Organizations seeking to use FAQs as a public engagement tool might consider including multiple viewpoints and actual questions people have about genetic engineering.

<https://link.springer.com/article/10.1007/s41055-024-00143-z>

Luo X., Guo L., Tagliere E., Yang Z., Liu Z. (2024): **Leaf dissection and margin serration are independently regulated by two regulators converging on the CUC2-auxin module in strawberry**, Current Biology (2024). DOI: [10.1016/j.cub.2024.01.010](https://doi.org/10.1016/j.cub.2024.01.010)

The remarkable diversity of leaf forms allows plants to adapt to their living environment. In general, leaf diversity is shaped by leaf complexity (compound or simple) and leaf margin pattern (entire, serrated, or lobed). Prior studies in multiple species have uncovered a conserved module of *CUC2*-auxin that regulates both leaf complexity and margin serration. How this module is regulated in different species to contribute to the species-specific leaf form is unclear. Furthermore, the mechanistic connection between leaf complexity and leaf serration regulation is not well studied. Strawberry has trifoliate compound leaves with serrations at the margin. In the wild strawberry *Fragaria vesca*, a mutant named *salad* was isolated that showed deeper leaf serrations but normal leaf complexity. *SALAD* encodes a single-Myb domain protein and is expressed at the leaf margin. Genetic analysis showed that *cuc2a* is epistatic to *salad*, indicating that *SALAD* normally limits leaf serration depth by repressing *CUC2a* expression. When both *Arabidopsis* homologs of *SALAD* were knocked out, deeper serrations were observed in *Arabidopsis* rosette leaves, supporting a conserved function of *SALAD* in leaf serration regulation. We incorporated the analysis of a third strawberry mutant *simple leaf 1 (sl1)* with reduced leaf complexity but normal leaf serration. We showed that *SL1* and *SALAD* independently regulate *CUC2a* at different stages of leaf development to, respectively, regulate leaf complexity and leaf serration. Our results provide a clear and simple mechanism of how leaf complexity and leaf serration are coordinately as well as independently regulated to achieve diverse leaf forms.

[https://www.cell.com/current-biology/abstract/S0960-9822\(24\)00010-1?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0960982224000101%3Fshowall%3Dtrue](https://www.cell.com/current-biology/abstract/S0960-9822(24)00010-1?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0960982224000101%3Fshowall%3Dtrue)

Miedaner, T., Garbelotto, M. (2024): **Human-mediated migration of plants, their pathogens and parasites.** J Plant Pathol <https://doi.org/10.1007/s42161-024-01589-0>

The adoption of agriculture in several parts of the world during the early Neolithic period led to a fundamental change in human migration. By introducing newly domesticated crops into new environments, pathogens and parasites were also inadvertently transferred from their regions of origin and underwent a considerable population growth. In the newly settled regions, some pests of indigenous plants adapted to new crops by host switching. This review is limited to three basic migration events and mainly to agricultural crops of the temperate zone: (1) the migration of the first farmers from SE Asia to Europe, (2) European expansion from the 16th century onward, (3) modern globalization since the 20th century. Molecular analyses offer the opportunity to study the evolutionary history of pest populations, their origin and dynamics and their spread around the world. Cereals' rusts and powdery mildew, storage insects were the first to spread with wheat species, barley, and pulses from the Levant across Eurasia. The Columbian exchange of crops to and from the Americas brought entirely new pests to Europe while old world pathogens spread to the Americas and subsequently to all other regions colonized by Europeans. Modern globalization further facilitated the spread of pathogens and insects worldwide, as previously inconceivable amounts of agricultural products, business travelers, and maybe tourists have elevated global accessibility. This is illustrated by case studies based on fungi and insects. In the near future, pests will have colonized all crops in all countries where they can exist according to their agro-climatic requirements.

<https://link.springer.com/article/10.1007/s42161-024-01589-0>

De Miguel Beriain I., Rueda J., Villalba A. (2024): Re-defining the human embryo: A legal perspective on the creation of embryos in research. EMBO Rep 25: 467 – 470 |

<https://doi.org/10.1038/s44319-023-00034-0>

EFSA

CEP Panel (2024). Safety evaluation of the food enzyme rennet containing chymosin and pepsin A from the abomasum of suckling calves, goats, lambs and buffaloes. EFSA Journal 22 (2), e8607. <https://doi.org/10.2903/j.efsa.2024.8607>
<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2024.8607>

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.

Prof. Dr. Klaus-Dieter Jany
Nelkenstrasse 36
D-76351 Linkenheim-Hochstetten
jany@biotech-gm-food.com

Wissenschaftskreis Genomik und Gentechnik
1.Vorsitzender: Prof. Dr. Kl.-D. Jany
jany@wgg-ev.de