

# Sunday Evening News No 365

2024-02-19 – 2024-02-25

Compiled and edited by **BGF** Jany



Wissenschaftskreis  
Genomik und  
Gentechnik e.V.

## Meetings – Conferences / Veranstaltungen - Konferenzen

Europabüro der Konrad-Adenauer-Stiftung / EKD-Büro Brüssel

### **Zulassung neuer genomischer Techniken**

Öffnung der Büchse der Pandora oder Zukunftschance?

Dienstag, 19. März 12:30-14:00h; Online-Veranstaltung via Webex

Programm: <https://www.kas.de/documents/284153/0/Programm+2024-02-21+NGT+Planzen+%281%29.pdf/94d153e0-e5af-e662-d811-8f0e122efd41?version=1.0&t=1708529694273>

Registrierung: [https://forms.office.com/pages/responsepage.aspx?id=dbKTiaBzZ0SynsZPJF4sqU-bvM5tK-dMsTG68C7ON\\_JUQThGVFNWUUhZOUZFTzYxQVFTWIVEMVFSSy4u](https://forms.office.com/pages/responsepage.aspx?id=dbKTiaBzZ0SynsZPJF4sqU-bvM5tK-dMsTG68C7ON_JUQThGVFNWUUhZOUZFTzYxQVFTWIVEMVFSSy4u)

## Press Releases -Media / Presse- und Medienberichte

Dervinschger: **Neue Gentechnik: Sind Pflanzen patentierbar?**

<https://www.dervinschger.it/de/news/neue-gentechnik-sind-pflanzen-patentierbar-11507>

Dionglay C.: **The First Decade of CRISPR: Advances and Outlook**

<https://www.isaaa.org/blog/entry/default.asp?BlogDate=2/21/2024>

FDA: **Guidance for Industry: Foods Derived from Plants Produced Using Genome Editing**

<https://www.fda.gov/regulatory-information/search-fda-guidance-documents/guidance-industry-foods-derived-plants-produced-using-genome-editing>

**EPA clarifies GMO definition**

<https://www.epa.govt.nz/news-and-alerts/latest-news/epa-clarifies-gmo-definition/>

Le Page M.: **First gene-edited meat will come from disease-proof CRISPR pigs**

<https://www.newscientist.com/article/2418305-first-gene-edited-meat-will-come-from-disease-proof-crispr-pigs/>

Ledesma A., Van Eenennaam A.: **Global Status of Gene Edited Food Animals and their Products**

<https://www.usda.gov/sites/default/files/documents/AOF-2024-VanEenennaam.pdf>

Uduak T.: **CRISPRed Pigs: Precision Porcine Gene Editing Combats PRRS Virus Threat**

<https://www.genengnews.com/topics/genome-editing/crispred-pigs-precision-porcine-gene-editing-combats-prrs-virus-threat/>

Miller H.I. and Young S.S.: **The Validity Of Much Published Scientific Research Is Questionable (Part 1)**

<https://henrymillermd.org/27564/the-validity-of-much-published-scientific>

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 08-2024

## Publications – Publikationen

Molitorisová A. and Purnhagen K. (2024): **A Citizen Jury on New Genomic Techniques: A Format For Public Participation in Genomic Matters in Agriculture?**

<https://europeanlawblog.eu/2024/02/19/a-citizen-jury-on-new-genomic-techniques-a-format-for-public-participation-in-genomic-matters-in-agriculture/>

Wynberg R. (2024): **African Perspectives on Agroecology**

Why farmer-led seed and knowledge systems matter

<https://practicalactionpublishing.com/book/2698/african-perspectives-on-agroecology>

Clark, A., Wilcox, P., Morrison, S. et al. (2024): **Identifying Māori perspectives on gene editing in Aotearoa New Zealand.** Commun Biol 7, 221 | <https://doi.org/10.1038/s42003-024-05896-1>

Māori perspectives on gene technologies are evolving, and traditional cultural constructs continue to inform a wide diversity of views. Here we summarise a series of research activities aimed at identifying evolving Māori perspectives on gene editing and how these inform engagement at the co-innovation interface.  
<https://www.nature.com/articles/s42003-024-05896-1>

Fernandez A., Danisman E, Boroujerdi M.T., Kazemi S. Moreno F.J., Epstein M.M. (2024): **Research gaps and future needs for allergen prediction in food safety.** Front. Allergy-Sec. Food Allergy 5 | <https://doi.org/10.3389/falgy.2024.1297547>

The allergenicity and protein risk assessments in food safety are facing new challenges. Demands for healthier and more sustainable food systems have led to significant advances in biotechnology, the development of more complex foods, and the search for alternative protein sources. All this has increased the pressure on the safety assessment prediction approaches anchored into requirements defined in the late 90's. In 2022, the EFSA's Panel on Genetically Modified Organisms published a scientific opinion focusing on the developments needed for allergenicity and protein safety assessments of new products derived from biotechnology. Here, we further elaborate on the main elements described in this scientific opinion and prioritize those development needs requiring critical attention. The starting point of any new recommendation would require a focus on clinical relevance and the development of a fit-for-purpose database targeted for specific risk assessment goals. Furthermore, it is imperative to review and clarify the main purpose of the allergenicity risk assessment. An internationally agreed consensus on the overall purpose of allergenicity risk assessment will accelerate the development of fit-for-purpose methodologies, where the role of exposure should be better clarified. Considering the experience gained over the last 25 years and recent scientific developments in the fields of biotechnology, allergy, and risk assessment, it is time to revise and improve the allergenicity safety assessment to ensure the reliability of allergenicity assessments for food of the future.  
[https://www.frontiersin.org/articles/10.3389/falgy.2024.1297547/full?utm\\_source=F-NTF&utm\\_medium=EMLX&utm\\_campaign=PRD\\_FEOPS\\_20170000\\_ARTICLE](https://www.frontiersin.org/articles/10.3389/falgy.2024.1297547/full?utm_source=F-NTF&utm_medium=EMLX&utm_campaign=PRD_FEOPS_20170000_ARTICLE)

Helmsorig G., Walla A., Rütjes T., Buchmann G., Schüller R., Hensel G., von Korff M. (2024): **early maturity 7 promotes early flowering by controlling the light input into the circadian clock in barley.** Plant Physiology, 194 (2), 849–866 | <https://doi.org/10.1093/plphys/kiad551>

Breeding for variation in photoperiod response is crucial to adapt crop plants to various environments. Plants measure changes in day length by the circadian clock, an endogenous timekeeper that allows plants to anticipate changes in diurnal and seasonal light–dark cycles. Here, we describe the *early maturity 7* (*eam7*) locus in barley (*Hordeum vulgare*), which interacts with *PHOTOPERIOD 1* (*Ppd-H1*) to cause early flowering under non-inductive short days. We identify *LIGHT-REGULATED WD 1* (*LWD1*) as a putative candidate to underlie the *eam7* locus in barley as supported by genetic mapping and CRISPR-Cas9-generated *lwd1* mutants. Mutations in *eam7* cause a significant phase advance and a misregulation of core clock and clock output genes under diurnal conditions. Early flowering was linked to an upregulation of *Ppd-H1* during the night and consequent induction of the florigen *FLOWERING LOCUS T1* under short days. We propose that *EAM7* controls photoperiodic flowering in barley by controlling the light input into the clock and diurnal expression patterns of the major photoperiod response gene *Ppd-H1*.  
<https://academic.oup.com/plphys/article/194/2/849/7406703?login=false>

Slaman, E., Kottenhagen, L., de Martinez, W. et al. (2024): **Comparison of Cas12a and Cas9-mediated mutagenesis in tomato cells.** Sci Rep 14, 4508 | <https://doi.org/10.1038/s41598-024-55088-4>

Cas12a is a promising addition to the CRISPR toolbox, offering versatility due to its TTV-protospacer adjacent motif (PAM) and the fact that it induces double-stranded breaks (DSBs) with single-stranded overhangs. We characterized Cas12a-mediated genome editing in tomato using high-throughput amplicon sequencing on protoplasts. Of the three tested variants, *Lachnospiraceae* (Lb) Cas12a was the most efficient. Additionally, we developed an easy and effective Golden-Gate-based system for crRNA cloning. We compared LbCas12a to SpCas9 by investigating on-target efficacy and specificity at 35 overlapping target sites and 57 (LbCas12a) or 100 (SpCas9) predicted off-target sites. We found LbCas12a an efficient, robust addition to SpCas9, with similar overall though target-dependent efficiencies. LbCas12a induced more and larger deletions than SpCas9, which can be advantageous for specific genome editing applications. Off-target activity for LbCas12a was found at 10 out of 57 investigated sites. One or two mismatches were present distal from the PAM in all cases. We conclude that Cas12a-mediated genome editing is generally precise as long as such off-target sites can be avoided. In conclusion, we have determined the mutation pattern and efficacy of Cas12a-mediated CRISPR mutagenesis in tomato and developed a cloning system for the routine application of Cas12a for tomato genome editing.  
<https://www.nature.com/articles/s41598-024-55088-4>

Duan Z., Liang Y., Sun J., Zhu J.-K. et al: (2024): **An engineered Cas12i nuclease that is an efficient genome editing tool in animals and plants.** The Innovation 5(2): 100564, | DOI: <https://doi.org/10.1016/j.xinn.2024.100564>

The type V-I CRISPR-Cas system is becoming increasingly more attractive for genome editing. However, natural nucleases of this system often exhibit low efficiency, limiting their application. Here, we used structure-guided rational design and protein engineering to optimize an uncharacterized Cas12i nuclease, Cas12i3. As a result, we developed Cas-SF01, a Cas12i3 variant that exhibits significantly improved gene editing activity in mammalian cells. Cas-SF01 shows comparable or superior editing performance compared to SpCas9 and other Cas12 nucleases. Compared to natural Cas12i3, Cas-SF01 has an expanded PAM range and effectively recognizes NTTN and noncanonical NATN and TTVN PAMs. In addition, we identified an amino acid substitution, D876R, that markedly reduced the off-target effect while maintaining high on-target activity, leading to the development of Cas-SF01<sup>Hifi</sup> (high-fidelity Cas-SF01). Finally, we show that Cas-SF01 has high gene editing activities in mice and plants. Our results suggest that Cas-SF01 can serve as a robust gene editing platform with high efficiency and specificity for genome editing applications in various organisms.

[https://www.cell.com/the-innovation/fulltext/S2666-6758\(24\)00002-X?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS266667582400002X%3Fshowall%3Dtrue](https://www.cell.com/the-innovation/fulltext/S2666-6758(24)00002-X?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS266667582400002X%3Fshowall%3Dtrue)

Kwon D.-H., Gim G.-M., Yum S.-Y., Jang G. (2024): **Current status and future of gene engineering in livestock.** BMB Reports 57(1): 50-59 |

<https://doi.org/10.5483/BMBRep.2023-0208>

The application of gene engineering in livestock is necessary for various reasons, such as increasing productivity and producing disease resistance and biomedicine models. Overall, gene engineering provides benefits to the agricultural and research aspects, and humans. In particular, productivity can be increased by producing livestock with enhanced growth and improved feed conversion efficiency. In addition, the application of the disease resistance models prevents the spread of infectious diseases, which reduces the need for treatment, such as the use of antibiotics; consequently, it promotes the overall health of the herd and reduces unexpected economic losses. The application of biomedicine could be a valuable tool for understanding specific livestock diseases and improving human welfare through the development and testing of new vaccines, research on human physiology, such as human metabolism or immune response, and research and development of xenotransplantation models. Gene engineering technology has been evolving, from random, time-consuming, and laborious methods to specific, time-saving, convenient, and stable methods. This paper reviews the overall trend of genetic engineering technologies development and their application for efficient production of genetically engineered livestock, and provides examples of technologies approved by the United States (US) Food and Drug Administration (FDA) for application in humans.

<https://www.bmbreports.org/journal/view.html?doi=10.5483/BMBRep.2023-0208>

Shriver A.J. (2024): **Biotechnological fixes and the Big Three urgent moral challenges facing the global livestock industry.** Front. Anim. Sci. 5:1305462. |

<https://doi.org/10.3389/fanim.2024.1305462>

The current global food system, and in particular the livestock industry, has been effective at providing low-cost calories to large segments of the population, but it also causes significant harms and poses serious risks. In particular, the global food system currently likely causes billions of animals to suffer every year, significantly contributes to climate change, and threatens public health via the possibility of zoonotic disease. There are many other problems that have been identified with the livestock industry, but these three threats, which I refer to as the Big Three, are among the most urgent moral issues in the world. Significant progress could be made to address all three of these risks if the global population moved to a primarily plant-based diet. However, there are reasons to believe this possibility is unrealistic given current consumer preferences and political realities. As an alternative, one could ask whether an approach relying entirely on novel biotechnology could be used to address the urgent moral challenges of the global livestock industry without substantially changing the consumer experience or facing political backlash. In this paper I consider what such a scenario would look like, and argue that failing to address any one of these three major issues would be a serious moral failing. Though many other suggestions have been made looking at how biotechnology might address individual issues, this paper suggests that in order to avoid the need for difficult behavioral and political changes, biotechnological solutions would ultimately need to be developed that address welfare, environmental, and public health concerns.

<https://www.frontiersin.org/articles/10.3389/fanim.2024.1305462/full>

Burger B.T., Beaton B-P., Campbell M.A., Brett B.T., Melissa S. Rohrer M.S. et al. (2024): **Generation of a Commercial-Scale Founder Population of Porcine Reproductive and Respiratory Syndrome Virus Resistant Pigs Using CRISPR-Cas.** The CRISPR Journal 7 (1) DOI: 10.1089/crispr.2023.0061

Disease resistance genes in livestock provide health benefits to animals and opportunities for farmers to meet the growing demand for affordable, high-quality protein. Previously, researchers used gene editing to modify the porcine CD163 gene and demonstrated resistance to a harmful virus that causes porcine reproductive and respiratory syndrome (PRRS). To maximize potential benefits, this disease resistance trait needs to be present in commercially relevant breeding populations for multiplication and distribution of pigs. Toward this goal, a first-of-its-kind, scaled gene editing program was established to introduce a single modified CD163 allele into four genetically diverse, elite porcine lines. This effort produced healthy pigs that resisted PRRS virus infection as determined by macrophage and animal challenges. This founder population will be used for additional disease

and trait testing, multiplication, and commercial distribution upon regulatory approval. Applying CRISPR-Cas to eliminate a viral disease represents a major step toward improving animal health.  
<https://www.liebertpub.com/doi/10.1089/crispr.2023.0061>

Bernatchez, L., Ferchaud, AL., Berger, C.S. et al. (2024): **Genomics for monitoring and understanding species responses to global climate change.** Nat Rev Genet 25, 165–183 | <https://doi.org/10.1038/s41576-023-00657-y>

All life forms across the globe are experiencing drastic changes in environmental conditions as a result of global climate change. These environmental changes are happening rapidly, incur substantial socioeconomic costs, pose threats to biodiversity and diminish a species' potential to adapt to future environments. Understanding and monitoring how organisms respond to human-driven climate change is therefore a major priority for the conservation of biodiversity in a rapidly changing environment. Recent developments in genomic, transcriptomic and epigenomic technologies are enabling unprecedented insights into the evolutionary processes and molecular bases of adaptation. This Review summarizes methods that apply and integrate omics tools to experimentally investigate, monitor and predict how species and communities in the wild cope with global climate change, which is by genetically adapting to new environmental conditions, through range shifts or through phenotypic plasticity. We identify advantages and limitations of each method and discuss future research avenues that would improve our understanding of species' evolutionary responses to global climate change, highlighting the need for holistic, multi-omics approaches to ecosystem monitoring during global climate change.  
<https://www.nature.com/articles/s41576-023-00657-y>

Asadi M., Millar A.A. (2024): **Review: Plant microRNAs in pathogen defense: A panacea or a piece of the puzzle?** Plant Science 341, 111993 | <https://doi.org/10.1016/j.plantsci.2024.111993>

Plant [microRNAs](#) (miRNAs) control key [agronomic traits](#) that are associated with their conserved role(s) in development. However, despite a multitude of studies, the utility of miRNAs in plant-pathogen resistance remains less certain. Reviewing the literature identifies three general classes of miRNAs regarding [plant pathogen](#) defense. Firstly, a number of evolutionary dynamic 22 nucleotide miRNA families that repress large numbers of [plant immunity](#) genes, either directly, or through triggering the biogenesis of secondary [siRNAs](#). However, understanding of their role in defense and of their manipulation to enhance pathogen resistance are still lacking. Secondly, highly conserved miRNAs that indirectly impact disease resistance through their targets that are primarily regulating development or hormone signaling. Any alteration of these miRNAs usually results in pleiotropic impacts, which may alter disease resistance in some plant species, and against some pathogens. Thirdly, are the comparatively diverse and evolutionary dynamic set of non-conserved miRNAs, some of which contribute to pathogen resistance, but whose narrow evolutionary presence will likely restrict their utility. Therefore, reflecting the diverse and evolving nature of plant-pathogen interactions, a complex interplay of plant miRNAs with pathogen responses exists. Any miRNA-based solution for pathogen resistance will likely be highly specific, rather than a general panacea.  
<https://www.sciencedirect.com/science/article/pii/S0168945224000207>

M. Pohl, U. Hommen, S. Eilebrecht, et al. (2024): **Ants are no bees – Gaps in the assessment of relevant exposure routes to pesticides and plant incorporated protectants,** Environmental Chemistry and Ecotoxicology | <https://doi.org/10.1016/j.enceco.2024.02.00>

Ants (Formicidae) are ubiquitous in terrestrial ecosystems, including agricultural areas and forests. They are important for soil movement, decomposition, nutrient cycling, pollination, predation, scavenging and seed dispersal. Furthermore, they serve as a crucial food source for various wildlife. However, ants are no part of current ecotoxicity testing. Here, we systematically analyze whether and how ants can be exposed to active substances from plant protection products (PPPs) or genetically modified plants (GMPs). Like other arthropods, ants can be exposed via direct contact with PPPs after application, inhalation, uptake of contaminated drinking water or diet. For plant incorporated protectants (PIPs) expressed by GMPs, dietary exposure is the only relevant exposure route. Ants exhibit a diverse dietary spectrum, including plant material, honey dew collection, fungal cultivation, scavenging, and predation. Notably, foraging for dead or weakened arthropods, e.g., treated pest organisms, represents a significant exposure route because such food may be readily available in large amounts after spraying a field. Arthropods, alive or deceased, serve as the dominant protein source for numerous ant species, essential for larval development and the egg production of the queen(s). Consequently, exposure routes, via contaminated food items, can jeopardize entire ant colonies if it reaches the queen. However, effects arising from contaminated prey are not routinely assessed, neither for non-social nor for social insects such as the honey bee, which collects only nectar and pollen and is intensively tested in the assessment of PPPs. We conclude that ecotoxicity testing in ants would fill a gap and support the assessment of biodiversity effects. To achieve this, we recommend further research to explore the exposure of the different castes and developmental stages of ants in greater detail and to develop protocols allowing for ecological risk assessments of PPPs and PIPs via dietary uptake. This comprehensive approach will contribute significantly to our understanding of the potential consequences of PPP and GMP exposure to non-target ants.  
<https://www.sciencedirect.com/science/article/pii/S2590182624000043?via%3Dihub>

Wright, C.J., Stevens, L., Mackintosh, A. *et al.* (2024): **Comparative genomics reveals the dynamics of chromosome evolution in Lepidoptera.** *Nat Ecol Evol* | <https://doi.org/10.1038/s41559-024-02329-4>

Chromosomes are a central unit of genome organization. One-tenth of all described species on Earth are butterflies and moths, the Lepidoptera, which generally possess 31 chromosomes. However, some species display dramatic variation in chromosome number. Here we analyse 210 chromosomally complete lepidopteran genomes and show that the chromosomes of extant lepidopterans are derived from 32 ancestral linkage groups, which we term Merian elements. Merian elements have remained largely intact through 250 million years of evolution and diversification. Against this stable background, eight lineages have undergone extensive reorganization either through numerous fissions or a combination of fusion and fission events. Outside these lineages, fusions are rare and fissions are rarer still. Fusions often involve small, repeat-rich Merian elements and the sex-linked element. Our results reveal the constraints on genome architecture in Lepidoptera and provide a deeper understanding of chromosomal rearrangements in eukaryotic genome evolution. <https://www.nature.com/articles/s41559-024-02329-4>

## EFSA

CEP Panel (2024): Safety evaluation of the food enzyme bacillolysin from the non-genetically modified *Bacillus amyloliquefaciens* strain NZYM-NB. *EFSA Journal*, 22(2), e8615.

<https://doi.org/10.2903/j.efsa.2024.8615>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2024.8615>

CEP Panel (2024): Safety evaluation of the food enzyme asparaginase from the genetically modified *Aspergillus niger* strain AGN. *EFSA Journal*, 22(2), e8617.

<https://doi.org/10.2903/j.efsa.2024.8617>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2024.8617>

Moreno F.J. *et al.* (2024): Roadmap for the integration of gastro-intestinal (GI) tract microbiomes (human and domestic animal) in risk assessments under EFSA's remit. EFSA Supporting publication 21(2): EN-8597. 238 pp. doi:[10.2903/sp.efsa.2024.EN-8597](https://doi.org/10.2903/sp.efsa.2024.EN-8597)

<https://www.efsa.europa.eu/es/supporting/pub/en-8597>

Debode F, Caulier S, Demeter S, Dubois B, Gelhay V, Hulin J, Muhovski Y, Ninane V, Rousseau G, and Bragard C, (2024): Roadmap for the integration of environmental microbiomes in risk assessments under EFSA's remit. EFSA Supporting publication 21(2): EN-8602. 93 pp.

doi:[10.2903/sp.efsa.2024.EN-8602](https://doi.org/10.2903/sp.efsa.2024.EN-8602)

<https://www.efsa.europa.eu/es/efsajournal/pub/en-8602>

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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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