

2023-06-19 – 2023-06-25

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Press Releases -Media / Presse- und Medienberichte

Willard M.: **Draft NGT regulation: Key Elements and First Reactions**

<https://www.arc2020.eu/draft-ngt-regulation-key-elements-and-first-reactions/>

Farm Europe: **NGTs: a step in the right direction by the European Commission**

<https://www.farm-europe.eu/news/ngts-a-step-in-the-right-direction-by-the-european-commission/>

Footo N.: **EU moves towards looser rules on certain gene edited crops**

https://www.euractiv.com/section/agriculture-food/news/eu-moves-towards-looser-rules-on-certain-gene-edited-crops/?_ga=2.111926657.423797618.1687268983-314482148.1687268983

BioEco: **European organic movement resolution: No hidden GMOs, system-based approach to innovation**

<https://www.bioecoactual.com/en/2023/06/22/european-organic-movement-resolution-no-hidden-gmos-system-based-approach-to-innovation/>

Resolution of the organic movement in favour of a system-based approach of innovation and sustainability – Keep Organic GMO-free

https://www.organicseurope.bio/content/uploads/2023/06/6_IFOAMEU_GA2023_Resolution_NGTs.pdf?dd

Merlot J.: **Aus Prinzip dagegen**

<https://www.spiegel.de/wissenschaft/natur/neue-regeln-fuer-gentechnik-in-der-eu-gefaehrliche-stimmungsmache-gegen-die-gesetzesnovelle-a-a90beb23-9fd3-4fbb-af2e-60ce0ac67890>

Konrad Adenauer Stiftung: **Kein erhöhtes Risiko: Genome Editing in der Pflanzenzüchtung**

<https://www.kas.de/documents/252038/22161843/Kein+erh%C3%B6htes+Risiko+-+Genome+Editing+in+der+Pflanzenz%C3%BCchtung.+Argumente+aus+wissenschaftlicher+Sicht+gegen+eine+estriktive+Regulierung.pdf/736126e3-619b-98c2-44ff-e346893e78e1?version=1.0&t=1687271346938>

Bundesregierung Deutschland: **Wehrhaft-Resilient-Nachhaltig - Integrierte Sicherheit für Deutschland** siehe Seite 70

<https://www.nationalesicherheitsstrategie.de/Sicherheitsstrategie-DE.pdf>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): June week 25

Publications – Publikationen

Special:

I.M. Portant, R.E. Sults, (2023): **The presence of carcinogenic compounds in gene-edited NGOs causes cancer in humans.** *Arch Toxicol* (2023). <https://doi.org/10.1007/s00204-023-03535-y>

pdf-file available, a publication for April 1; an April fool hoax (?)

Testbiotech (2023): ‘Gene Scissors’ cause chaotic disturbance in plant genome

<https://www.testbiotech.org/en/content/gene-scissors-cause-chaotic-disturbance-plant-genome>

Gen-Schere verursacht Chaos im Erbgut von Pflanzen

<https://www.testbiotech.org/sites/default/files/CRISPRthrispis%20bei%20Pflanzen.pdf>

GM Watch: Gene editing found to cause chaos in the genome of tomatoes

<https://www.gmwatch.org/en/106-news/latest-news/20239-gene-editing-found-to-cause-chaos-in-the-genome-of-tomatoes>

Samach A., Mafessoni F., Gross O., Melamed-Bessudo C., Filler-Hayut S., Dahan-Meir T., Amsellem Z., Pawlowski W.P., Levy A.A. (2023) A CRISPR-induced DNA break can trigger crossover, chromosomal loss and chromothripsis-like rearrangements. *bioRxiv*.
<https://doi.org/10.1101/2023.05.22.541757>
<https://www.biorxiv.org/content/10.1101/2023.05.22.541757v1.full.pdf>

Ojha A., Zhang F., Patil G.B. (2023): **Genome editing and chromosome engineering in plants.** *Plant Genome* 16:e20352. <https://doi.org/10.1002/tpg2.20352>
<https://access.onlinelibrary.wiley.com/doi/epdf/10.1002/tpg2.20352>
<https://access.onlinelibrary.wiley.com/doi/full/10.1002/tpg2.20352>

Ukhatova, Y.V., Erastenkova, M.V., Korshikova, E.S. et al. (2023): **Improvement of Crops Using the CRISPR/Cas System: New Target Genes.** *Mol Biol* 57, 375–397 |
<https://doi.org/10.1134/S0026893323030135>

The success of genome editing of crops using the CRISPR/Cas system largely depends on the correct choice of target genes, for which directed changes will increase yield and improve the quality of plant raw materials and resistance to biotic and abiotic stress factors. This work systematizes and catalogs data on target genes used to improve cultivated plants. The latest systematic review examined articles indexed in the Scopus database and published before August 17, 2019. Our work covers the period from August 18, 2019 to March 15, 2022. A search according to the given algorithm allowed us to identify 2090 articles, among which only 685 contain the results of gene editing of 28 species of cultivated plants (the search was carried out for 56 crops). A significant part of these papers considered either editing of target genes, which was previously carried out in similar works, or studies related to the field of reverse genetics, and only 136 articles contain data on editing of new target genes, whose modification is aimed at improving plant traits important for breeding. In total, 287 target genes of cultivated plants were subjected to editing in order to improve properties significant for breeding over the entire period of the CRISPR/Cas system application. This review presents a detailed analysis of the editing of new target genes. The studies were most often aimed at increasing productivity and disease resistance, as well as improving the properties of plant materials. It was noted whether it was possible to obtain stable transformants at the time of publication and whether editing was applied to nonmodel cultivars. The range of modified cultivars of a number of crops has been significantly expanded, in particular, for wheat, rice, soybean, tomato, potato, rapeseed, grape, and maize. In the vast majority of cases, editing constructs were delivered using agrobacterium-mediated transformation, less commonly, using biolistics, protoplast transfection, and haploinducers. The desired change in traits was most often achieved by gene knockout. In some cases, knockdown and nucleotide substitutions in the target gene were carried out. To obtain nucleotide substitutions in the genes of cultivated plants, base-editing and prime-editing technologies are increasingly used. The emergence of a convenient CRISPR/Cas editing system has contributed to the development of specific molecular genetics of many crop species.
<https://link.springer.com/article/10.1134/S0026893323030135>

Van Schepler-Luu , Sciallano C., Stiebner M., Ji C. et al. (2023): **Genome editing of an African elite rice variety confers resistance against endemic and emerging *Xanthomonas oryzae* pv. *oryzae* strains.** *eLife*, 20.06.2023. | DOI: 10.7554/eLife.84864

Bacterial leaf blight (BB) of rice, caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), threatens global food security and the livelihood of small-scale rice producers. Analyses of *Xoo* collections from Asia, Africa and the Americas demonstrated complete continental segregation, despite robust global rice trade. Here, we report unprecedented BB outbreaks in Tanzania. The causative strains, unlike endemic African *Xoo*, carry Asian-type TAL effectors targeting the sucrose transporter *SWEET11a* and iTALes suppressing *Xa1*. Phylogenomics clustered these strains with *Xoo* from Southern-China. African rice varieties do not carry effective resistance. To protect African rice production against this emerging threat, we developed a hybrid CRISPR-Cas9/Cpf1 system to edit all known TALE-binding elements in three *SWEET* promoters of the East African elite variety Komboka. The edited lines show broad-spectrum resistance against Asian and African strains of *Xoo*, including strains recently discovered in Tanzania. The strategy could help to protect global rice crops from BB pandemics.
<https://elifesciences.org/articles/84864>

Ahmad N., Fatima S., Mehmood M.A., Zaman Q.U., Atif R.M. et al. (2023): **Targeted genome editing in polyploids: lessons from *Brassica*.** *Front. Plant Sci./ Sec. Functional and Applied Plant Genomics* Volume 14 | <https://doi.org/10.3389/fpls.2023.1152468>

CRISPR-mediated genome editing has emerged as a powerful tool for creating targeted mutations in the genome for various applications, including studying gene functions, engineering resilience against biotic and abiotic stresses, and increasing yield and quality. However, its utilization is limited to model crops for which well-annotated genome sequences are available. Many crops of dietary and economic importance, such as wheat, cotton, rapeseed-mustard, and potato, are polyploids with complex genomes. Therefore, progress in these crops has been hampered due to genome complexity. Excellent work has been conducted on some species of *Brassica* for its improvement through genome editing. Although excellent work has been conducted

on some species of *Brassica* for genome improvement through editing, work on polyploid crops, including U's triangle species, holds numerous implications for improving other polyploid crops. In this review, we summarize key examples from genome editing work done on *Brassica* and discuss important considerations for deploying CRISPR-mediated genome editing more efficiently in other polyploid crops for improvement.

<https://www.frontiersin.org/articles/10.3389/fpls.2023.1152468/full>

Leland L. Glenna L.L. (2023): **Are intellectual property policies for gene-edited crops fit for purpose?** The perspectives of German scientists. PPP | <https://doi.org/10.1002/ppp3.10397>

Societal Impact Statement: A growing body of research indicates that intellectual property policies for agricultural biotechnologies are hindering research and limiting the use of the technologies. Research also indicates that public resistance to agricultural biotechnologies, including transgenic and gene-edited crops, is at least in part motivated by concerns about intellectual property restrictions. Therefore, changing the policies governing agricultural biotechnologies promises to reduce public resistance and to enhance the diffusion of research outputs. Because so many patents related to gene editing are held by universities and because so much cutting-edge research is conducted by public scientists, exploring the scientists' perspectives on these policies offers insights into possibilities for policy changes.

Summary

- After the European Court of Justice's ruling that gene-edited crops would be regulated the way transgenic crops are regulated, the European Commission consulted with stakeholders and concluded that policies governing gene-edited crops are not fit for purpose. This research explores whether public scientists in Germany also consider intellectual property policies not fit for purpose.
- The data come from intensive interviews with 10 scientists working at German universities and research institutes.
- The interviewed scientists describe how intellectual property policies limited the use of transgenic breeding techniques and how they now limit applications of gene-editing techniques. They overwhelmingly support policy changes that facilitate the use of their scientific breakthroughs to solve problems in the world, and they do not want to see large companies use the technologies to consolidate economic power or to profit at the expense of solving problems.
- Because intellectual property policies are often cited as a key reason for the resistance to agricultural biotechnologies and because research indicates that current policies are not enhancing crop innovations or social welfare, a change in intellectual property policies is likely to reduce resistance to the new crop breeding technologies and yield more social benefits.

<https://nph.onlinelibrary.wiley.com/doi/full/10.1002/ppp3.10397>

Machnicka, A.A. (2023). **Gene Editing Technology Patents or Monopolization of Scientific Knowledge and Health Care?**. In: Godt, C., Lamping, M. (eds) A Critical Mind. MPI Studies on Intellectual Property and Competition Law, vol 30. Springer, Berlin, Heidelberg.

https://doi.org/10.1007/978-3-662-65974-8_24

This contribution deals with gene editing technology from the perspective of patent law. The monopolization of scientific knowledge and its effects on health care are under scrutiny. The contribution is based on the premise that the gene editing sector and its peculiarities require a reassessment of patent law principles, and this challenge is undertaken by reference to Hanns Ullrich's academic legacy. Various aspects of the controversial—but at the same time promising—domain of genome editing are discussed from the perspective of its monopolization, availability for research and commercial downstream development.

https://link.springer.com/chapter/10.1007/978-3-662-65974-8_24

Li, Y., Mamonova, E., Köhler, N. et al. (2023): **Breakdown of self-incompatibility due to genetic interaction between a specific S-allele and an unlinked modifier.** Nat Commun **14**, 3420 | <https://doi.org/10.1038/s41467-023-38802-0>

Breakdown of self-incompatibility has frequently been attributed to loss-of-function mutations of alleles at the locus responsible for recognition of self-pollen (i.e. the S-locus). However, other potential causes have rarely been tested. Here, we show that self-compatibility of S_1S_1 -homozygotes in selfing populations of the otherwise self-incompatible *Arabidopsis lyrata* is not due to S-locus mutation. Between-breeding-system cross-progeny are self-compatible if they combine S_1 from the self-compatible cross-partner with recessive S_1 from the self-incompatible cross-partner, but self-incompatible with dominant S-alleles. Because S_1S_1 homozygotes in outcrossing populations are self-incompatible, mutation of S_1 cannot explain self-compatibility in S_1S_1 cross-progeny. This supports the hypothesis that an S_1 -specific modifier unlinked to the S-locus causes self-compatibility by functionally disrupting S_1 . Self-compatibility in $S_{19}S_{19}$ homozygotes may also be caused by an S_{19} -specific modifier, but we cannot rule out a loss-of-function mutation of S_{19} . Taken together, our findings indicate that breakdown of self-incompatibility is possible without disruptive mutations at the S-locus.

<https://www.nature.com/articles/s41467-023-38802-0>

Burch C.L., Romanchuk A., Kelly M., Wu Y., Jones C.D. (2023): **Empirical Evidence That Complexity Limits Horizontal Gene Transfer.** Genome Biology and Evolution **15** (6), evad089 | <https://doi.org/10.1093/gbe/evad089>

Horizontal gene transfer (HGT) is a major contributor to bacterial genome evolution, generating phenotypic diversity, driving the expansion of protein families, and facilitating the evolution of new phenotypes, new metabolic pathways, and new species. Comparative studies of gene gain in bacteria suggest that the frequency with which individual genes successfully undergo HGT varies considerably and may be associated with the number of protein–protein interactions in which the gene participates, that is, its connectivity. Two nonexclusive hypotheses have emerged to explain why transferability should decrease with connectivity: the complexity hypothesis (Jain R, Rivera MC, Lake JA. 1999. Horizontal gene transfer among genomes: the complexity hypothesis. *Proc Natl Acad Sci U S A*. 96:3801–3806.) and the balance hypothesis (Papp B, Pál C, Hurst LD. 2003. Dosage sensitivity and the evolution of gene families in yeast. *Nature* 424:194–197.). These hypotheses predict that the functional costs of HGT arise from a failure of divergent homologs to make normal protein–protein interactions or from gene misexpression, respectively. Here we describe genome-wide assessments of these hypotheses in which we used 74 existing prokaryotic whole genome shotgun libraries to estimate rates of horizontal transfer of genes from taxonomically diverse prokaryotic donors into *Escherichia coli*. We show that 1) transferability declines as connectivity increases, 2) transferability declines as the divergence between donor and recipient orthologs increases, and that 3) the magnitude of this negative effect of divergence on transferability increases with connectivity. These effects are particularly robust among the translational proteins, which span the widest range of connectivities. Whereas the complexity hypothesis explains all three of these observations, the balance hypothesis explains only the first one.
<https://academic.oup.com/gbe/article/15/6/evad089/7180211>

Hoang N.T., Taherzadeh O., Ohash H. et al. (2023): **Mapping potential conflicts between global agriculture and terrestrial conservation**. *PNAS* 120 (23) e2208376120 | <https://doi.org/10.1073/pnas.2208376120>

Demand for food products, often from international trade, has brought agricultural land use into direct competition with biodiversity. Where these potential conflicts occur and which consumers are responsible is poorly understood. By combining conservation priority (CP) maps with agricultural trade data, we estimate current potential conservation risk hotspots driven by 197 countries across 48 agricultural products. Globally, a third of agricultural production occurs in sites of high CP (CP > 0.75, max = 1.0). While cattle, maize, rice, and soybean pose the greatest threat to very high-CP sites, other low-conservation risk products (e.g., sugar beet, pearl millet, and sunflower) currently are less likely to be grown in sites of agriculture–conservation conflict. Our analysis suggests that a commodity can cause dissimilar conservation threats in different production regions. Accordingly, some of the conservation risks posed by different countries depend on their demand and sourcing patterns of agricultural commodities. Our spatial analyses identify potential hotspots of competition between agriculture and high-conservation value sites (i.e., 0.5° resolution, or ~367 to 3,077km², grid cells containing both agriculture and high-biodiversity priority habitat), thereby providing additional information that could help prioritize conservation activities and safeguard biodiversity in individual countries and globally. A web-based GIS tool at <https://agriculture.spatialfootprint.com/biodiversity/> systematically visualizes the results of our analyses.
<https://www.pnas.org/doi/10.1073/pnas.2208376120>

Wyckhuys, K.A.G., Tang, F.H.M. & Hadi, B.A.R. (2023): **Pest management science often disregards farming system complexities**. *Commun Earth Environ* 4, 223 | <https://doi.org/10.1038/s43247-023-00894-3>

Since the 1940s, pesticide-intensive crop protection has sustained food security but also caused pervasive impacts on biodiversity, environmental integrity and human health. Here, we employ a systematic literature review to structurally analyze pest management science in 65 developing countries. Within a corpus of 3,407 publications, we find that taxonomic coverage is skewed towards a subset of 48 herbivores. Simplified contexts are commonplace: 48% of studies are performed within laboratory confines. 80% treat management tactics in an isolated rather than integrated fashion. 83% consider no more than two out of 15 farming system variables. Limited attention is devoted to pest-pathogen or pest-pollinator interplay, trophic interactions across ecosystem compartments or natural pest regulation. By overlooking social strata, the sizable scientific progress on agroecological management translates into slow farm-level uptake. We argue that the scientific enterprise should integrate system complexity to chart sustainable trajectories for global agriculture and achieve transformative change on the ground.
<https://www.nature.com/articles/s43247-023-00894-3>

Azizi-Dargahlou, S., Pouresmaeil, M. (2023): **Agrobacterium tumefaciens-Mediated Plant Transformation: A Review**. *Mol Biotechnol* | <https://doi.org/10.1007/s12033-023-00788-x>

Agrobacterium tumefaciens-mediated plant transformation is the most dominant technique for the transformation of plants. It is used to transform monocotyledonous and dicotyledonous plants. *A. tumefaciens* apply for stable and transient transformation, random and targeted integration of foreign genes, as well as genome editing of plants. The Advantages of this method include cheapness, uncomplicated operation, high reproducibility, a low copy number of integrated transgenes, and the possibility of transferring larger DNA fragments. Engineered endonucleases such as CRISPR/Cas9 systems, TALENs, and ZFNs can be delivered with this method. Nowadays, *Agrobacterium*-mediated transformation is used for the Knock in, Knock down, and Knock out of genes. The transformation effectiveness of this method is not always desirable. Researchers applied various strategies to improve the effectiveness of this method. Here, a general overview of the characteristics and mechanism of gene transfer with *Agrobacterium* is presented. Advantages, updated data on the factors involved in optimizing this method, and other useful materials that lead to maximum exploitation as

well as overcoming obstacles of this method are discussed. Moreover, the application of this method in the generation of genetically edited plants is stated. This review can help researchers to establish a rapid and highly effective Agrobacterium-mediated transformation protocol for any plant species.
<https://link.springer.com/article/10.1007/s12033-023-00788-x>

Delhomme, T.M., Munteanu, M., Buonanno, M. et al. (2023): **Proton and alpha radiation-induced mutational profiles in human cells.** *Sci Rep* **13**, 9791 |

<https://doi.org/10.1038/s41598-023-36845-3>

Ionizing radiation is known to be DNA damaging and mutagenic, however less is known about which mutational footprints result from exposures of human cells to different types of radiation. We were interested in the mutagenic effects of particle radiation exposures on genomes of various human cell types, in order to gauge the genotoxic risks of galactic cosmic radiation, and of certain types of tumor radiotherapy. To this end, we exposed cultured cell lines from the human blood, breast and lung to fractionated proton and alpha particle (helium nuclei) beams at doses sufficient to considerably affect cell viability. Whole-genome sequencing revealed that mutation rates were not overall markedly increased upon proton and alpha exposures. However, there were modest changes in mutation spectra and distributions, such as the increases in clustered mutations and of certain types of indels and structural variants. The spectrum of mutagenic effects of particle beams may be cell-type and/or genetic background specific. Overall, the mutational effects of repeated exposures to proton and alpha radiation on human cells in culture appear subtle, however further work is warranted to understand effects of long-term exposures on various human tissues.

<https://www.nature.com/articles/s41598-023-36845-3>

Matsuzaki, R., Gunnigle, E., Geissen, V. et al. (2023): **Pesticide exposure and the microbiota-gut-brain axis.** *ISME J* | <https://doi.org/10.1038/s41396-023-01450-9>

The gut microbiota exist within a dynamic ecosystem shaped by various factors that includes exposure to xenobiotics such as pesticides. It is widely regarded that the gut microbiota plays an essential role in maintaining host health, including a major influence on the brain and behaviour. Given the widespread use of pesticides in modern agriculture practices, it is important to assess the long-term collateral effects these xenobiotic exposures have on gut microbiota composition and function. Indeed, exposure studies using animal models have shown that pesticides can induce negative impacts on the host gut microbiota, physiology and health. In tandem, there is a growing body of literature showing that the effects of pesticide exposure can be extended to the manifestation of behavioural impairments in the host. With the increasing appreciation of the microbiota-gut-brain axis, in this review we assess whether pesticide-induced changes in gut microbiota composition profiles and functions could be driving these behavioural alterations. Currently, the diversity of pesticide type, exposure dose and variation in experimental designs hinders direct comparisons of studies presented. Although many insights presented, the mechanistic connection between the gut microbiota and behavioural changes remains insufficiently explored. Future experiments should therefore focus on causal mechanisms to examine the gut microbiota as the mediator of the behavioural impairments observed in the host following pesticide exposure.

<https://www.nature.com/articles/s41396-023-01450-9>

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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