

# Sunday Evening News No 329

2023-05-29 – 2023-06-11

Compiled and edited by **BGF** Jany



## Meetings - Veranstaltungen

### Klima wandelt Landwirtschaft - Herausforderung und Chance

Event von [The Future of Food and Farming](#)

Mi, 21. Juni 2023, 16:30 bis 19:00 (Ihre Ortszeit)

Deutsche Bank Quartier Zukunft, Friedrichstr. 181, Berlin, DE, 10117

Event-Link <https://foodandfarming.net/anmeldung/>

### The revolution of CRISPR genome editing: An expert panel discussion

<https://www.selectscience.net/webinars/the-revolution-of-crispr-genome-editing-an-expert-panel-discussion?WebinarID=2068>

## Press Releases -Media / Presse- und Medienberichte

### POINT NEWSLETTER NR. 251 – MAI 2023 Aktuelle Biotechnologie

[https://www.scienceindustries.ch/file/33962/point-2023-05-251-](https://www.scienceindustries.ch/file/33962/point-2023-05-251-d.pdf?utm_source=POINT+Newsletter&utm_campaign=0a45f48c5b-)

[d.pdf?utm\\_source=POINT+Newsletter&utm\\_campaign=0a45f48c5b-](https://www.scienceindustries.ch/file/33962/point-2023-05-251-d.pdf?utm_source=POINT+Newsletter&utm_campaign=0a45f48c5b-)

[POINT 251&utm\\_medium=email&utm\\_term=0\\_19eef28c92-0a45f48c5b-1210937714](https://www.scienceindustries.ch/file/33962/point-2023-05-251-d.pdf?utm_source=POINT+Newsletter&utm_campaign=0a45f48c5b-)

### BMEL: Erstmals alle gesellschaftlichen Gruppen in Kommission vertreten

<https://www.bmel.de/SharedDocs/Pressemitteilungen/DE/2023/077-zkbs.html>

#### ZKBS-Zusammensetzung – berufende Persönlichkeiten

[https://www.zkbs-online.de/ZKBS/DE/UeberZKBS/Zusammensetzung/zusammensetzung\\_node.html](https://www.zkbs-online.de/ZKBS/DE/UeberZKBS/Zusammensetzung/zusammensetzung_node.html)

### Noisette C.: Illegal GMO rice in Europe again

<https://www.infogm.org/7786-illegal-gmo-rice-in-europe-again?lang=fr>

### Redaktion LZ: BNN verabschiedet Resolution gegen neue Gentechnik

<https://www.lebensmittelzeitung.net/handel/nachrichten/naturkostfachhandel-bnn-verabschiedet-resolution-gegen-neue-gentechnik-171571?crefresh=1>

### DNR: Parlamentsausschüsse gegen EU-Renaturierungsgesetz

<https://www.dnr.de/aktuelles-terminen/aktuelles/parlamentsausschuesse-gegen-eu-renaturierungsgesetz>

### Dahm J.: Renaturierungsgesetz: Kommission drängt auf Einigung

<https://www.euractiv.de/section/landwirtschaft-und-ernaehrung/news/renaturierungsgesetz-kommission-draengt-auf-einigung/>

### Moore O.: How will Environment Committee vote on Nature Restoration Law?

<https://www.arc2020.eu/how-will-environment-committee-vote-on-nature-restoration-law/>

### Foote N.: Agrifood Brief: The great gene editing gamble

<https://www.euractiv.com/section/agriculture-food/news/agrifood-brief-the-great-gene-editing-gamble/>

### Biotech in the fields, Italy pressing on Europe

<https://www.breakinglatest.news/business/biotech-in-the-fields-italy-pressing-on-europe/>

### EU's next food fight – laws on gene-edited crops

<https://www.thestar.com.my/news/focus/2023/06/05/eus-next-food-fight---laws-on-gene-edited-crops>

### Golub R.: Neue Gentechnik – eine Chance ohne Risiko?

<https://www.faz.net/aktuell/wirtschaft/unternehmen/neue-gentechnik-als-chance-ohne-risiko-in-deutschland-bleibt-skepsis-18938477.html>

### Woher M., Rosenberger, J.: Diese Grafiken zeigen den weltweiten Umgang mit grüner Gentechnik

[https://www.handelsblatt.com/infografiken/grafik/infografiken-diese-grafiken-zeigen-den-weltweiten-umgang-mit-gruener-gentechnik/v\\_detail\\_tab\\_comments/29171928.html](https://www.handelsblatt.com/infografiken/grafik/infografiken-diese-grafiken-zeigen-den-weltweiten-umgang-mit-gruener-gentechnik/v_detail_tab_comments/29171928.html)

Fischer, J.A.: **Europa könnte sich für grüne Gentechnik öffnen**

[https://www.rnz.de/politik/hintergrund\\_artikel,-Berlin-Europa-koennte-sich-fuer-gruene-Gentechnik-oeffnen-arid,1125902.html](https://www.rnz.de/politik/hintergrund_artikel,-Berlin-Europa-koennte-sich-fuer-gruene-Gentechnik-oeffnen-arid,1125902.html)

Lange, M.; Brose, M.: **Verbraucher sorgen sich, aber Wissenschaftler sind optimistisch**

<https://www.deutschlandfunk.de/gruene-gentechnik-diskussion-gewinnt-an-neuer-schaerfe-dlf-b7b6496d-100.html>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): May /Juneweek 22 and June 23

## **Publications – Publikationen**

Guertler P., Pallarz S., Belter A., Eckermann K.N, Grohmann L. (2023): **Detection of commercialized plant products derived from new genomic techniques (NGT) - Practical examples and current perspectives.** Food Control 152 109869 |

<https://doi.org/10.1016/j.foodcont.2023.109869>

New genomic techniques (NGT) are increasingly applied in plant research and development in many countries due to their simplicity in introducing genetic modifications that alter specific traits. First NGT products are on the market in several countries where no specific regulatory approval is required. In the European Union (EU), however, all NGT derived products are subject to the existing genetically modified organism (GMO) authorization regulations. This nourishes the discussion on the technical and analytical feasibility of detecting, identifying and differentiating plants produced by targeted mutagenesis from conventional breeding products and spontaneous mutations in routine food/feed and seed/grain testing by enforcement laboratories. The anticipated difficulties are currently based mainly on theoretical considerations, particularly with regard to single nucleotide or very limited sequence changes.

Against that background, this brief review examines concrete and practical approaches for the detection and identification of market-relevant NGT plants. Four early commercialized NGT plants have been examined as real examples to verify the feasibility of detection method design and development using routinely applied analytical approaches. In addition, we searched for potential new screening approaches and show, how a common and well conserved genetic element used in CRISPR/Cas9 applications may serve as a potential target, if this foreign DNA element is still integrated in the host genome.

The conclusions to be drawn from the considered theoretical approaches and the practical examples are described in the context of key differences to the current GMO testing practice, in particular regarding the difficulty to develop methods specifically identifying NGT applications. Finally, we discuss whether the consideration of such factors could facilitate a resolution of the current dilemma between detection and the ability to identify plant NGT events.

<https://www.sciencedirect.com/science/article/pii/S0956713523002694?via%3Dihub>

Menary J. and Fuller S.S. (2023): **New genomic techniques, old divides: stakeholder attitudes towards new biotechnology regulation in the EU and UK**

The European Union and United Kingdom are in the process of establishing new regulation regarding the use of new genomic techniques in crop and animal breeding. As part of this process, consultations have been launched to understand the views of stakeholders and the wider public towards the use of new genomic techniques in plant and animal breeding. The responsible research and innovation framework emphasises the importance of dialogue between technology developers and stakeholders, including the public, but what are the opinions of stakeholders towards the regulation of NGTs in Europe and do they view these consultations as opportunities to engage with technology governance? We conducted semi-structured interviews with experts from a range of agri-food stakeholder groups in the European Union and United Kingdom to understand current attitudes towards new biotechnology regulation, how they viewed the process of consultation in both places and what influence they felt they had in shaping regulations. We found that the discussion is similar in both EU and UK, with predictable and fixed opinions determined by attitudes towards the perceived risks associated with direct mutagenesis. Both UK and EU consultations were considered to have the same weaknesses and stakeholders discussed a desire for more dialogic forms of engagement. We highlight several options for new forms of involvement in biotechnology regulation by exploring relevant responsible research and innovation literature.

<https://doi.org/10.1101/2023.06.04.543624> doi:bioRxiv preprint

Cortés A.J. and Du H. (2023): **Molecular Genetics Enhances Plant Breeding**

Int. J. Mol. Sci. 24 (12), 9977 | <https://doi.org/10.3390/ijms24129977>

<https://www.mdpi.com/1422-0067/24/12/9977>

He, Q., Tang, S., Zhi, H. et al. (2023): A graph-based genome and pan-genome variation of the model plant *Setaria*. *Nat Genet* | <https://doi.org/10.1038/s41588-023-01423-w>  
*Setaria italica* (foxtail millet), a founder crop of East Asian agriculture, is a model plant for C4 photosynthesis and developing approaches to adaptive breeding across multiple climates. Here we established the *Setaria* pan-genome by assembling 110 representative genomes from a worldwide collection. The pan-genome is composed of 73,528 gene families, of which 23.8%, 42.9%, 29.4% and 3.9% are core, soft core, dispensable and private genes, respectively; 202,884 nonredundant structural variants were also detected. The characterization of pan-genomic variants suggests their importance during foxtail millet domestication and improvement, as exemplified by the identification of the yield gene *SiGW3*, where a 366-bp presence/absence promoter variant accompanies gene expression variation. We developed a graph-based genome and performed large-scale genetic studies for 68 traits across 13 environments, identifying potential genes for millet improvement at different geographic sites. These can be used in marker-assisted breeding, genomic selection and genome editing to accelerate crop improvement under different climatic conditions.  
<https://www.nature.com/articles/s41588-023-01423-w>

Adel S. and N. (2023): **Plant Tolerance to Drought Stress with Emphasis on Wheat.** *Plants* 12 (11), 2170 | <https://doi.org/10.3390/plants12112170>  
Environmental stresses, such as drought, have negative effects on crop yield. Drought is a stress whose impact tends to increase in some critical regions. However, the worldwide population is continuously increasing and climate change may affect its food supply in the upcoming years. Therefore, there is an ongoing effort to understand the molecular processes that may contribute to improving drought tolerance of strategic crops. These investigations should contribute to delivering drought-tolerant cultivars by selective breeding. For this reason, it is worthwhile to review regularly the literature concerning the molecular mechanisms and technologies that could facilitate gene pyramiding for drought tolerance. This review summarizes achievements obtained using QTL mapping, genomics, synteny, epigenetics, and transgenics for the selective breeding of drought-tolerant wheat cultivars. Synthetic apomixis combined with the *msh1* mutation opens the way to induce and stabilize epigenomes in crops, which offers the potential of accelerating selective breeding for drought tolerance in arid and semi-arid regions.  
<https://www.mdpi.com/2223-7747/12/11/2170>

Ryosuke I., Takeshi F., Sou T., Kayoko O. et al. (2023): **The molecular clock in long-lived tropical trees is independent of growth rate,** *eLife* (2023). DOI: 10.7554/eLife.88456.1  
The rates and patterns of somatic mutations in wild plants, as well as how they relate to longevity, are largely unknown<sup>(1)-(3)</sup>. Here, we examined the somatic mutation landscapes of slow- and fast-growing tropical species in central Borneo, Indonesia. Using newly-constructed genomes, we identified an average of 480 mutations in the slow-growing species (265-year-old, 44.1 m in height), which was five times greater than that observed in the fast-growing species (66-year-old, 43.9 m). The number of somatic mutations increased linearly with branch length. The somatic mutation rate per meter was higher in the slow-growing species, yet the rate per year remained constant across both species. The mutational spectra exhibited a dominance of spontaneous mutations, specifically cytosine-to-thymine substitutions at CpG sites. An analysis of nucleotide substitutions at both the intra- and inter-individual level revealed that somatic mutations are neutral within an individual, but those mutations transmitted to the next generation are subject to purifying selection. We developed a model to evaluate the relative contribution of cell division on mutational processes, and postulate that cell-division independent mutagenesis predominates. These findings deepen our understanding of mutational processes underlying the generation of genetic diversity in a tropical ecosystem.  
<https://elifesciences.org/reviewed-preprints/88456v1>  
<https://phys.org/news/2023-06-long-lived-tree-species-play-greater.html>

Kedisso E.G., Guenther J., Maredia K., Elagib T. et al. (2023): **Sustainable access of quality seeds of genetically engineered crops in Eastern Africa - Case study of Bt Cotton, GM Crops & Food,** 14:1, 1-23, DOI: [10.1080/21645698.2023.2210134](https://doi.org/10.1080/21645698.2023.2210134)  
The genetically engineered bollworm-resistant Bt cotton hybrid varieties offer opportunities for reducing crop losses and enhancing productivity. In Eastern Africa region, Sudan, Ethiopia, and Kenya have approved and released Bt cotton in 2012, in 2018, and in 2019, respectively. The region has potential to grow cotton in over 5 million hectares. For commercial plantings in Ethiopia, Sudan and Kenya, hybrid Bt cotton seeds have been imported from India. Due to the COVID-19 pandemic-induced supply chain disruptions, high shipment costs, bureaucratic procedures for importing seeds, and foreign exchange shortages, farmers have not been able to access Bt cotton seeds. Stakeholders are seeking local production of seeds to provide sustainable access by farmers at affordable cost. Country case studies reveal the importance of enhancing capacity for local seed production and extension advisory services. Revival of the cotton sector needs enhanced public-private partnerships to pave the way for sustainable seeds access in the region.  
<https://www.tandfonline.com/doi/full/10.1080/21645698.2023.2210134>

Melnick, R.L., Jarvis, L., Hendley, P. et al. (2023): **GENZ explorer: a tool for visualizing agroclimate to inform research and regulatory risk assessment.** *Transgenic Res* | <https://doi.org/10.1007/s11248-023-00354-w>  
Confined field trials (CFT) of genetically engineered (GE) crops are used to generate data to inform environmental risk assessments (ERA). ERAs are required by regulatory authorities before novel GE crops can be

released for cultivation. The transportability of CFT data to inform risk assessment in countries other than those where the CFT was conducted has been discussed previously in an analysis showing that the primary difference between CFT locations potentially impacting trial outcomes is the physical environment, particularly the agroclimate. This means that data from trials carried out in similar agroclimates could be considered relevant and sufficient to satisfy regulatory requirements for CFT data, irrespective of the country where the CFTs are conducted. This paper describes the development of an open-source tool to assist in determining the transportability of CFT data. This tool provides agroclimate together with overall crop production information to assist regulators and applicants in making informed choices on whether data from previous CFTs can inform an environmental risk assessment in a new country, as well as help developers determine optimal locations for planning future CFTs. The GENZ Explorer is a freely available, thoroughly documented, and open-source tool that allows users to identify the agroclimate zones that are relevant for the production of 21 major crops and crop categories or to determine the agroclimatic zone at a specific location. This tool will help provide additional scientific justification for CFT data transportability, along with spatial visualization, to help ensure regulatory transparency.

<https://link.springer.com/article/10.1007/s11248-023-00354-w>

Recio-Vega R., Facio-Campos R.-A., Hernández-González S.I. Olivas-Calderón E. (2023): **State of the Art of Genomic Technology in Toxicology: A Review**. Int. J. Mol. Sci., 24( 11), 9618 | <https://doi.org/10.3390/ijms24119618>

The rapid growth of genomics techniques has revolutionized and impacted, greatly and positively, the knowledge of toxicology, ushering it into a “new era”: the era of genomic technology (GT). This great advance permits us to analyze the whole genome, to know the gene response to toxicants and environmental stressors, and to determine the specific profiles of gene expression, among many other approaches. The aim of this work was to compile and narrate the recent research on GT during the last 2 years (2020–2022). A literature search was managed using the PubMed and Medscape interfaces on the Medline database. Relevant articles published in peer-reviewed journals were retrieved and their main results and conclusions are mentioned briefly. It is quite important to form a multidisciplinary taskforce on GT with the aim of designing and implementing a comprehensive, collaborative, and a strategic work plan, prioritizing and assessing the most relevant diseases, so as to decrease human morbimortality due to exposure to environmental chemicals and stressors.

<https://www.mdpi.com/1422-0067/24/11/9618>

Van Eenennaam, A.L., Young, A.E. (2023): **Öffentliche Wahrnehmung der Tierbiotechnologie**. In: Niemann, H., Wrenzycki, C. (eds) Biotechnologie bei Nutztieren 2. Springer, Cham.

[https://doi.org/10.1007/978-3-031-26042-1\\_13](https://doi.org/10.1007/978-3-031-26042-1_13)

Die Kommerzialisierung eines jeden Produkts hängt von der Akzeptanz der Verbraucher ab. Seit der Einführung gentechnisch veränderter Nutzpflanzen in den 1990er-Jahren hat die Gentechnik in dieser Hinsicht einen schweren Stand. Die öffentliche Wahrnehmung von gentechnisch veränderten Tieren ist im Allgemeinen negativ, wobei biomedizinische Anwendungen positiver gesehen werden als landwirtschaftliche Anwendungen. Bislang wurden die meisten gentechnisch veränderten Tiere in privaten oder universitären Labors zu Forschungszwecken entwickelt. Der Widerstand gegen gentechnisch veränderte Tiere wird oft mit dem Widerstand gegen die Verwendung von Tieren in der Forschung im Allgemeinen sowie mit dem Widerstand gegen Aspekte der intensiven Tierhaltung verbunden. Im Allgemeinen werden die Bedenken gegenüber der Tierbiotechnologie beeinflusst durch (1) Ansichten über den moralischen Status von Tieren, die Grenze zwischen „natürlich“ und „unnatürlich“ und die wahrgenommenen Risiken und Vorteile von gentechnisch veränderten Tieren für die Gesundheit und die Umwelt (persönliche und kulturelle Merkmale); (2) den Zweck der Anwendung, die angewandte(n) Methode(n) und die Motivation der Forschungsgruppe, die die genetische Veränderung vornimmt (Forschungsmerkmale); (3) die veränderte Tierart (Tiermerkmale). Daher ist es schwierig, die öffentliche Wahrnehmung von gentechnisch veränderten Tieren als eine eigenständige Kategorie zu verallgemeinern. Die erste Zulassung eines gentechnisch veränderten Lebensmitteltieres, des AquAdvantage-Lachses, im Jahr 2015 erfolgte nach jahrelanger Verzögerung durch die Behörden, die teilweise auf die negative öffentliche Wahrnehmung der Gentechnik zurückzuführen war. Es gibt eine Reihe neuer Tieranwendungen in der Entwicklung, die durch neue Methoden ermöglicht werden und speziell auf Merkmale für die Gesundheit und das Wohlbefinden der Tiere abzielen. Eine differenzierte Betrachtung dieser Anwendungen durch diejenigen, die nicht per se gegen die Technologie sind, könnte die öffentliche Wahrnehmung von gentechnisch veränderten Tieren positiv beeinflussen.

[https://link.springer.com/chapter/10.1007/978-3-031-26042-1\\_13](https://link.springer.com/chapter/10.1007/978-3-031-26042-1_13)

Petersen, B. (2023): **DNA-Nukleasen und ihre Verwendung in der Viehzucht**. In: Niemann, H., Wrenzycki, C. (eds) Biotechnologie bei Nutztieren 2. Springer, Cham.

[https://doi.org/10.1007/978-3-031-26042-1\\_7](https://doi.org/10.1007/978-3-031-26042-1_7)

DNA-Nukleasen, darunter Zink-Finger-Nukleasen (ZFN), Transkriptionsaktivator-ähnliche Endonukleasen (TALENs) und Meganukleasen, besitzen lange Erkennungsstellen und Schneidedomänen und sind daher in der Lage, DNA auf sehr spezifische Weise zu schneiden. Diese molekularen Scheren bewirken gezielte genetische Veränderungen, indem sie die DNA-Mutationsrate durch Induktion von Doppelstrangbrüchen an einer vorbestimmten genomischen Stelle erhöhen. Im Vergleich zum konventionellen Gen-Targeting auf der Basis homologer Rekombination können DNA-Nukleasen die Targeting-Rate um das bis zu 10.000-fache erhöhen, und die Genunterbrechung durch mutagene DNA-Reparatur wird mit einer ähnlichen Häufigkeit stimuliert. Die erfolgreiche Anwendung verschiedener DNA-Nukleasen wurde bei einer Vielzahl von Organismen nachgewiesen, darunter Insekten, Amphibien, Pflanzen, Fadenwürmer und Säugetiere, einschließlich Nutztiere.



Kürzlich wurde eine weitere neue Klasse von molekularen Scheren beschrieben, die kurze RNA-Sequenzen verwenden, um eine bestimmte Stelle im Genom zu verändern (Abb. 7.1). CRISPR/CAS9 geht auf einen bakteriellen Abwehrmechanismus zurück und kann so programmiert werden, dass es auf fast jede Stelle im Genom verändern kann. Die einfache und kostengünstige Möglichkeit, mit Hilfe von DNA-Nukleasen sehr spezifische genetische Veränderungen zu erzeugen, hat die Produktion von gentechnisch veränderten Nutztieren revolutioniert. Aktuelle Ergebnisse deuten darauf hin, dass DNA-Nukleasen erfolgreich in einem breiten Spektrum von Organismen eingesetzt werden können, was sie für ein besseres Verständnis komplexer physiologischer Systeme, für die Erzeugung genetisch veränderter Tiere, einschließlich der Schaffung von Großtiermodellen für menschliche Krankheiten und für die Schaffung spezifischer Zelllinien nützlich macht. Gentechnische Veränderungen könnten auch den Tierschutz verbessern, indem sie das Enthornen oder die Geschlechtsbestimmung überflüssig oder Nutztiere resistent/resistent gegen bestimmte Krankheitserreger machen. Nutztiere mit einem gewünschten Phänotyp oder Merkmal können mit bisher unbekannter Präzision und Leichtigkeit und innerhalb eines sehr kurzen Zeitraums erzeugt werden, was vor Einführung der DNA Nukleasen als unmöglich galt. Dieses Kapitel bietet einen aktuellen Überblick über DNA-Nukleasen und die ihnen zugrunde liegenden Mechanismen und konzentriert sich auf ihre Verwendung in der Tierproduktion. Dabei ist zu bedenken, dass zum Zeitpunkt der Abfassung dieses Kapitels noch keine gentechnisch veränderten Nutztiere in die Nahrungskette gelangt sind oder für die Herstellung von aus Nutztieren gewonnenen Produkten verwendet wurden.

[https://link.springer.com/chapter/10.1007/978-3-031-26042-1\\_7](https://link.springer.com/chapter/10.1007/978-3-031-26042-1_7)

Hiekel, S. (2023). **Genom-Editierung als Züchtungstechnik im Bereich der landwirtschaftlichen Nutztiere**. In: Tierwohl durch Genom-Editierung?. Techno:Phil – Aktuelle Herausforderungen der Technikphilosophie, vol 8. J.B. Metzler, Berlin, Heidelberg. [https://doi.org/10.1007/978-3-662-66943-3\\_1](https://doi.org/10.1007/978-3-662-66943-3_1)

In diesem Kapitel werden die Methode und das Verfahren der Genom-Editierung samt Risiken für betroffene Individuen im Überblick dargestellt und erläutert. Zudem werden Züchtungsvorhaben systematisch zusammengestellt, die mittels der Genom-Editierung dafür sorgen sollen, dass es Nutztieren besser geht. Einzelne solcher Vorhaben werden skizziert, damit ein Eindruck davon entsteht, was der Stand der derzeitigen Forschung ist, und welcher Art die Vorhaben sind, die den Gegenstand der folgenden ethischen Überlegungen darstellen.

[https://link.springer.com/chapter/10.1007/978-3-662-66943-3\\_1](https://link.springer.com/chapter/10.1007/978-3-662-66943-3_1)

Li, C., Wang, L., Cseke, L.J. et al. (2023): **Efficient CRISPR-Cas9 based cytosine base editors for phytopathogenic bacteria**. Commun Biol 6, 56 | <https://doi.org/10.1038/s42003-023-04451-8>

Phytopathogenic bacteria play important roles in plant productivity, and developments in gene editing have potential for enhancing the genetic tools for the identification of critical genes in the pathogenesis process. CRISPR-based genome editing variants have been developed for a wide range of applications in eukaryotes and prokaryotes. However, the unique mechanisms of different hosts restrict the wide adaptation for specific applications. Here, CRISPR-dCas9 (dead Cas9) and nCas9 (Cas9 nickase) deaminase vectors were developed for a broad range of phytopathogenic bacteria. A gene for a dCas9 or nCas9, cytosine deaminase CDA1, and glycosylase inhibitor fusion protein (cytosine base editor, or CBE) was applied to base editing under the control of different promoters. Results showed that the RecA promoter led to nearly 100% modification of the target region. When residing on the broad host range plasmid pHM1, CBE<sub>RecAp</sub> is efficient in creating base edits in strains of *Xanthomonas*, *Pseudomonas*, *Erwinia* and *Agrobacterium*. CBE based on nCas9 extended the editing window and produced a significantly higher editing rate in *Pseudomonas*. Strains with nonsynonymous mutations in test genes displayed expected phenotypes. By multiplexing guide RNA genes, the vectors can modify up to four genes in a single round of editing. Whole-genome sequencing of base-edited isolates of *Xanthomonas oryzae* pv. *oryzae* revealed guide RNA-independent off-target mutations. Further modifications of the CBE, using a CDA1 variant (CBE<sub>RecAp-A</sub>) reduced off-target effects, providing an improved editing tool for a broad group of phytopathogenic bacteria.

<https://www.nature.com/articles/s42003-023-04451-8>

EFSA GMO Panel (2023): **Scientific Opinion on the assessment of genetically modified maize Bt11 × MIR162 × MIR604 × MON 89034 × 5307 × GA21 and 30 subcombinations, for food and feed uses, under Regulation (EC) No 1829/2003 (application EFSA-GMO-DE-2018-149)**. EFSA Journal 2023; 21 ( 6):8011, 59 pp. | <https://doi.org/10.2903/j.efsa.2023.8011>  
<https://efsa.onlinelibrary.wiley.com/doi/full/10.2903/j.efsa.2023.8011>

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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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