

Sunday Evening News No 344

2023-09-18. – 2023-09-24

Compiled and edited by **BGF** Jany



Meetings - Conferences / Veranstaltungen - Kongresse

VLOG: Vollständige Gentechnik-Kennzeichnung erhalten zum Nutzen von Verbraucher:innen und Lebensmittelwirtschaft

10.10.2023, 11:00-12:00 Uhr im Rahmen der Anuga 2023 Congress-Centrum Koelnmesse Konferenzraum 1-2 (gegenüber Pressezentrum)

<https://www.agrar-presseportal.de/landwirtschaft/veranstaltungen/vollstaendige-gentechnik-kennzeichnung-erhalten-zum-nutzen-von-verbraucher-innen-und-lebensmittelwirtschaft-37395.html>

BioWissKomm bietet ein neues, kostenloses Angebot vom 9.Okt. bis 27.Nov 2023 von Prof. Peter Westhoff seine wöchentliche online Vorlesung „**Pflanzen, Gene und Ernährungssicherheit**“ auch für die interessierte Öffentlichkeit an. Inhalte und weitere Informationen unter <https://www.biowisskomm.de/blog/> (Termine) an.

Press Releases -Media / Presse- und Medienberichte

Karl Bär und Harald Ebner zur Veröffentlichung eines Rechtsgutachtens zum Vorschlag der EU-Kommission zur Deregulierung neuer Gentechnikverfahren

<https://www.gruene-bundestag.de/presse/pressestatements/karl-baer-und-harald-ebner-zur-veroeffentlichung-eines-rechtsgutachtens-zum-vorschlag-der-eu-kommission-zur-deregulierung-neuer-gentechnikverfahren>

Stammler: Gutachten zeigt Kommissionsvorschlag zur Deregulierung der Neuen Gentechnik ist inhaltlich inkonsistent

https://www.ots.at/presseaussendung/OTS_20230922_OTS0058/stammler-gutachten-zeigt-kommissionsvorschlag-zur-deregulierung-der-neuen-gentechnik-ist-inhaltlich-inkonsistent

Das Gutachten: https://www.gruene-bundestag.de/fileadmin/media/gruenebundestag_de/themen_az/gentechnik/pdf/Gruene_im_Bundestag_Gutachten_Vereinbarkeit_des_Kommissionsvorschlags_zu_NGT_mit_dem_Vorsorgeprinzip.pdf

Greenpeace European Unit: New brand of GMOs would escape safety testing under EU Commission plan – briefing

<https://www.greenpeace.org/eu-unit/issues/nature-food/46798/new-brand-of-gmos-would-escape-safety-testing-under-eu-commission-plan-briefing/>

Arc2020: Commission Proposes 10 Year Glyphosate Renewal

<https://www.arc2020.eu/commission-proposes-10-year-glyphosate-renewal/>

Informationsdienst Gentechnik: EU-Kommission will Glyphosat bis 2033 erlauben

<https://www.keine-gentechnik.de/nachricht/34817?cHash=b88ecfa102cbaaad8f982ad2287bacfe>

Kaebnick G. E. (2023): The morally ground-shifting legacy of Ian Wilmut and Dolly the sheep

<https://www.statnews.com/2023/09/15/ian-wilmut-death-dolly-sheep-bioethics-public-engagement/>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): September week 38

Publications – Publikationen

Khaipho-Burch M., Cooper M., Crossa J., de Leon N., Holland J., Lewis R. et al. (2023): Genetic modification can improve crop yields — but stop overselling it

With a changing climate and a growing population, the world increasingly needs more-productive and resilient crops. But improving them requires a knowledge of what actually works in the field.

Nature 621, 470-473 | <https://www.nature.com/articles/d41586-023-02895-w>

Data before dogma. *Nat. Plants* **9**, 1371 (2023).

Forty years ago, Barbara McClintock — an exceptional plant scientist — was awarded the Nobel Prize for Physiology or Medicine; only the third woman to win a Nobel prize without collaborators.

<https://doi.org/10.1038/s41477-023-01534-6>

Schreiber, K. (2023). **Einleitung.** In: **Recht und Ethik der Risikoregulierung in der Grünen Gentechnik.** Springer, Wiesbaden. https://doi.org/10.1007/978-3-658-42853-2_1

Die Gentechnik als Errungenschaft des wissenschaftlichen Fortschritts stellt eine fundamentale Steigerung menschlicher Gestaltungsmacht im Hinblick auf das menschliche, tierische und pflanzliche Genom dar.

https://link.springer.com/chapter/10.1007/978-3-658-42853-2_1

Schreiber, K. (2023). **Molekularbiologische Pflanzenzüchtung als Anwendungsfeld Grüner Gentechnik.** In: **Recht und Ethik der Risikoregulierung in der Grünen Gentechnik.** Springer, Wiesbaden. https://doi.org/10.1007/978-3-658-42853-2_3

Die vorsorgebasierte Risikoregulierung von GVO ist hinsichtlich ihrer naturwissenschaftlichen Grundlagen zu betrachten, um das Spannungsfeld von Recht und Ethik vollumfänglich abzubilden. Im Jahr 2019 wurden weltweit in 29 Ländern auf 190,4 Mio ha Ackerland gentechnisch veränderte Pflanzen angebaut, was eine 112-fache Steigerung gegenüber der Anbaufläche von 1,7 Mio ha im Jahr 1996 darstellt. Vor diesem Hintergrund werden im Folgenden molekularbiologische Pflanzenzüchtungsverfahren als Anwendungsfeld Grüner Gentechnik erläutert.

https://link.springer.com/chapter/10.1007/978-3-658-42853-2_3

FSA: Literature review on analytical methods for the detection of precision bred products

DOI: <https://doi.org/10.46756/sci.fsa.ney927>

<https://www.food.gov.uk/research/novel-and-non-traditional-foods-additives-and-processes/literature-review-on-analytical-methods-for-the-detection-of-precision-bred-products>

de la Cruz V. Y., Tantriani, Cheng W., Tawarayama K. (2023): **Yield gap between organic and conventional farming systems across climate types and sub-types: A meta-analysis.**

Agricultural Systems 211, 103732 | <https://doi.org/10.1016/j.agsy.2023.103732>

Context: Organic farming is a fast-growing system considered a holistic approach that benefits the environment. However, previous studies have reported varying results on its productivity when compared to conventional farming systems. Moreover, the effect of climatic conditions on the yield gap between organic and conventional methods has not been extensively studied.

Objectives: Considering the influence of temperature and precipitation on [soil microbial activity](#) that drives the [decomposition of organic matter](#) and supports the mineralization of organic matter for plants, we hypothesized that the yield gap between organic and conventional farming systems is affected by climatic conditions; that is, it should be higher in locations with warmer climates than those in colder climates.

Methods: Yield data were collected from 105 studies that compared organic and conventional farming; 786 pairwise observations were extracted mainly from previous meta-analyses and individual studies. Using meta-analysis in R software, we examined the yield ratio between the two farming systems in different climate types (boreal, warm temperate, arid, and equatorial) and sub-types, and further investigated other influencing factors such as crop type, study location by region, and soil pH and texture.

Results and conclusions: The yield of organic farming was 18.4% ($RR = 0.83$; 95% confidence interval of 0.77 to 0.89; $p < 0.0001$) lower than that of conventional farming, regardless of climate condition, crop type, and other categorical variables. Results showed that only the warm temperate climate had a significant effect on the yield gap between organic and conventional farming systems, where organic yields were 21.18% lower than those of conventional farming ($RR = 0.79$; 95% CI 0.71 to 0.87; $p < 0.0001$; $k = 446$). However, the variability associated with temperature and precipitation was difficult to estimate using the current data. Among the categorical variables evaluated, it was found that specific crop types, regions, and soils significantly influenced the yield gap. Additional analyses revealed a confounding crop-type effect on the yield gap that requires further investigation. Nevertheless, this study suggests that when determining variations in the yields and productivity of organic and conventional farming systems, it is critical to account for interactions between variables.

Significance: The results of this study offer a preliminary understanding of how the climate type affects the yield of the two farming systems in a particular geographic location, supporting future research that will provide a quantitative context to land use development for [sustainable agriculture](#). <https://www.sciencedirect.com/science/article/abs/pii/S0308521X23001373?via%3Dihub>

Wang, L., Zhang, Z., Han, P. et al. (2023): **Association analysis of agronomic traits and construction of genetic networks by resequencing of 306 sugar beet (*Beta vulgaris* L.) lines.** *Sci Rep* 13, 15422 | <https://doi.org/10.1038/s41598-023-42182-2>

Due to the relatively brief domestication history of sugar beet (*Beta vulgaris* ssp. *vulgaris*), our understanding of the genomic diversity and functional genes in its cultivars is limited, resulting in slow breeding progress. To address this issue, a total of 306 germplasm materials of major cultivars and breeding lines from China, the USA, and Europe were selected for genome resequencing. We investigated population structure and genetic diversity and performed selective scanning of genomic regions, identifying six novel genes associated with important agronomic traits: the candidate genes DFAX2 and P5CS for skin roughness; the candidate genes FRO5, GL24, and PPR91 for root yield and sugar yield, and the pleiotropic candidate gene POLX for flourishing growth vigour, plant height, crown size, flesh coarseness, and sugar yield. In addition, we constructed a protein–protein interaction network map and a phenotype–gene network map, which provide valuable information for identifying and characterizing functional genes affecting agronomic traits in sugar beet. Overall, our study sheds light on the future improvement of sugar beet agronomic traits at the molecular level.
<https://www.nature.com/articles/s41598-023-42182-2>

Boukrouh, S., Noutfia, A., Moula, N. et al. (2023): Ecological, morpho-agronomical, and bromatological assessment of sorghum ecotypes in Northern Morocco. Sci Rep 13, 15548 (2023). <https://doi.org/10.1038/s41598-023-41565-9>

Sorghum Bicolor is a cereal used for grains as feed and food, mainly cultivated in dry areas. To study the possibilities of increasing its cultivation for feed purposes, ecological, morpho-agronomical, and bromatological characterization of some local ecotypes was conducted as the first steps toward selecting better cultivars. Indeed, twenty-one ecotypes were collected from farms in Northern Morocco in 2018. The edapho-climatic parameters of the collection sites were evaluated. The ecotypes were cultivated in 2019 in an experimental field with a randomized complete block design with three replicates. At the maturity stage, plants were evaluated for agro-morphological parameters, and grains and straw (leaves and stems) were harvested and analyzed. The results indicated significant variations between ecotypes for almost all parameters and an interesting grain yield of 3.5 T/ha with a 176% yield variation. The nutritive value of grains was interesting compared to straw, especially for mean protein contents (10.5% DM) and organic matter digestibility (81.4%). The calculated genetic parameters emphasized the possibility of selecting highly productive and nutritive cultivars. Multivariate analysis clustered the ecotypes into five groups based on agro-morphological, bromatological, and antioxidant activity parameters; the third group was characterized by high grain-yielding ecotypes, and the fifth one by high nutritive ecotypes. The E21 ecotype, belonging to this last group, was a promising selection candidate as it combines both. No significant correlation link between agro-morphological and bromatological traits of grains and geographical distances was discerned. *Sorghum bicolor* could thus be improved only according to the researched agro-morphological and bromatological traits.
<https://www.nature.com/articles/s41598-023-41565-9>

Conghao Xu et al (2023): Spontaneous movement of a retrotransposon generated genic dominant male sterility providing a useful tool for rice breeding. National Science Review 10 (9), nwad210 | <https://doi.org/10.1093/nsr/nwad210>

Male sterility in plants provides valuable breeding tools in germplasm innovation and hybrid crop production. However, genetic resources for dominant genic male sterility, which hold great promise to facilitate breeding processes, are extremely rare in natural germplasm. Here we characterized the Sanming Dominant Genic Male Sterility in rice and identified the gene *SDGMS* using a map-based cloning approach. We found that spontaneous movement of a 1978-bp long terminal repeat (LTR) retrotransposon into the promoter region of the *SDGMS* gene activates its expression in anther tapetum, which causes abnormal programmed cell death of tapetal cells resulting in dominant male sterility. *SDGMS* encodes a ribosome inactivating protein showing N-glycosidase activity. The activation of *SDGMS* triggers transcription reprogramming of genes responsive to biotic stress leading to a hypersensitive response which causes sterility. The results demonstrate that an ectopic gene activation by transposon movement can give birth to a novel trait which enriches phenotypic diversity with practical utility.
<https://academic.oup.com/nsr/article/10/9/nwad210/7237481>

Chen, R., Xiao, N., Lu, Y. et al. (2023): A de novo evolved gene contributes to rice grain shape difference between *indica* and *japonica*. Nat Commun 14, 5906 | <https://doi.org/10.1038/s41467-023-41669-w>

The role of de novo evolved genes from non-coding sequences in regulating morphological differentiation between species/subspecies remains largely unknown. Here, we show that a rice de novo gene *GSE9* contributes to grain shape difference between *indica/xian* and *japonica/geng* varieties. *GSE9* evolves from a previous non-coding region of wild rice *Oryza rufipogon* through the acquisition of start codon. This gene is inherited by most *japonica* varieties, while the original sequence (absence of start codon, *gse9*) is present in majority of *indica* varieties. Knockout of *GSE9* in *japonica* varieties leads to slender grains, whereas introgression to *indica* background results in round grains. Population evolutionary analyses reveal that *gse9* and *GSE9* are derived from wild rice Or-I and Or-III groups, respectively. Our findings uncover that the de novo *GSE9* gene contributes to the genetic and morphological divergence between *indica* and *japonica* subspecies, and provide a target for precise manipulation of rice grain shape.
<https://www.nature.com/articles/s41467-023-41669-w>

Hryhorowicz M., Lipiński D., Zeyland J. (2023): **Evolution of CRISPR/Cas Systems for Precise Genome Editing**. Int. J. Mol. Sci. 24 (18), 14233; | <https://doi.org/10.3390/ijms241814233>

The bacteria-derived CRISPR/Cas (an acronym for regularly interspaced short palindromic repeats/CRISPR-associated protein) system is currently the most widely used, versatile, and convenient tool for genome engineering. CRISPR/Cas-based technologies have been applied to disease modeling, gene therapies, transcriptional modulation, and diagnostics. Nevertheless, some challenges remain, such as the risk of immunological reactions or off-target effects. To overcome these problems, many new methods and CRISPR/Cas-based tools have been developed. In this review, we describe the current classification of CRISPR systems and new precise genome-editing technologies, summarize the latest applications of this technique in several fields of research, and, finally, discuss CRISPR/Cas system limitations, ethical issues, and challenges. <https://www.mdpi.com/1422-0067/24/18/14233>

Huang, X., Jia, H., Xu, J. et al. (2023): **Transgene-free genome editing of vegetatively propagated and perennial plant species in the T0 generation via a co-editing strategy**. Nat. Plants | <https://doi.org/10.1038/s41477-023-01520-y>

Transgene-free plant genome editing in the T0 generation is highly desirable but challenging^{1,2}. Here we achieved such a goal using a co-editing strategy via *Agrobacterium*-mediated transient expression of cytosine base editor to edit *ALS* encoding acetolactate synthase to confer herbicide chlorsulfuron resistance as a selection marker, Cas12a/CRISPR RNA for editing gene(s) of interest, and green fluorescent protein for selecting transgene-free transformants. The biallelic/homozygous transgene-free mutation rates for target genes among herbicide-resistant transformants ranged from 1.9% to 42.1% in tomato, tobacco, potato and citrus. This co-editing strategy is particularly useful for transgene-free genome editing of vegetatively propagated and perennial plant species in the T0 generation <https://www.nature.com/articles/s41477-023-01520-y>

Dewey R.E., Selote D., Griffin H.C., Dickey A.N. et al. (2023): **Cytoplasmic male sterility and abortive seed traits generated through mitochondrial genome editing coupled with allotopic expression of *atp1* in tobacco**. Front. Plant Sci., Sec. Plant Biotechnology 14 | <https://doi.org/10.3389/fpls.2023.1253640>

Allotopic expression is the term given for the deliberate relocation of gene function from an organellar genome to the nuclear genome. We hypothesized that the allotopic expression of an essential mitochondrial gene using a promoter that expressed efficiently in all cell types except those responsible for male reproduction would yield a cytoplasmic male sterility (CMS) phenotype once the endogenous mitochondrial gene was inactivated via genome editing. To test this, we repurposed the mitochondrially encoded *atp1* gene of tobacco to function in the nucleus under the transcriptional control of a CaMV 35S promoter (construct 35S:nATP1), a promoter that has been shown to be minimally expressed in early stages of anther development. The endogenous *atp1* gene was eliminated ($\Delta atp1$) from 35S:nATP1 tobacco plants using custom-designed meganucleases directed to the mitochondria. Vegetative growth of most 35S:nATP1/ $\Delta atp1$ plants appeared normal, but upon flowering produced malformed anthers that failed to shed pollen. When 35S:nATP1/ $\Delta atp1$ plants were cross-pollinated, ovary/capsule development appeared normal, but the vast majority of the resultant seeds were small, largely hollow and failed to germinate, a phenotype akin to the seedless trait known as stenospermocarpy. Characterization of the mitochondrial genomes from three independent $\Delta atp1$ events suggested that spontaneous recombination over regions of microhomology and substoichiometric shifting were the mechanisms responsible for *atp1* elimination and genome rearrangement in response to exposure to the *atp1*-targeting meganucleases. Should the results reported here in tobacco prove to be translatable to other crop species, then multiple applications of allotopic expression of an essential mitochondrial gene followed by its elimination through genome editing can be envisaged. Depending on the promoter(s) used to drive the allotopic gene, this technology may have potential application in the areas of: (1) CMS trait development for use in hybrid seed production; (2) seedless fruit production; and (3) transgene containment. <https://www.frontiersin.org/articles/10.3389/fpls.2023.1253640/full>

Soares D., Vertuan H., Bacalhau F., Jose´ M., Crivellari A., Belchior G.G. et al. (2023): **Genetically modified crops do not present variations in pollen viability and morphology when compared to their conventional counterparts**. PLoS ONE 18(5), e0285079 | <https://doi.org/10.1371/journal.pone.0285079>

Modern agricultural biotechnologies, such as those derived from genetic modification, are solutions that can enable an increase in food production, lead to more efficient use of natural resources, and promote environmental impact reduction. Crops with altered genetic materials have been extensively subjected to safety assessments to fulfill regulatory requirements prior to commercialization. The Brazilian National Technical Biosafety Commission (CTNBio) provides provisions for commercial release of transgenic crops in Brazil, including requiring information on pollen dispersion ability as part of environmental risk assessment, which includes pollen viability and morphology studies. Here we present the pollen viability and morphology of non-transgenic conventional materials, single-event genetically modified (GM) products, and stacked GM products from soybean, maize and cotton cultivated in Brazil. Microscopical observation of stained pollen grain was conducted to determine the percentage of pollen viability as well as pollen morphology, which is assessed by measuring pollen grain diameter. The pollen viability and diameter of GM soybean, maize and cotton, evaluated across a number of GM events in each crop, were similar to the conventional non-GM counterparts. Pollen

characterization data contributed to the detailed phenotypic description of GM crops, supporting the conclusion that the studied events were not fundamentally different from the conventional control.
<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0285079>

Frederic Berger F. et al (2023): **The Polycomb Repressive Complex 2 deposits H3K27me3 and represses transposable elements in a broad range of eukaryotes.** Current Biology | DOI: [10.1016/j.cub.2023.08.073](https://doi.org/10.1016/j.cub.2023.08.073)

The mobility of transposable elements (TEs) contributes to evolution of genomes. Their uncontrolled activity causes genomic instability; therefore, expression of TEs is silenced by host genomes. TEs are marked with DNA and H3K9 methylation, which are associated with silencing in flowering plants, animals, and fungi. However, in distantly related groups of eukaryotes, TEs are marked by H3K27me3 deposited by the Polycomb repressive complex 2 (PRC2), an epigenetic mark associated with gene silencing in flowering plants and animals. The direct silencing of TEs by PRC2 has so far only been shown in one species of ciliates. To test if PRC2 silences TEs in a broader range of eukaryotes, we generated mutants with reduced PRC2 activity and analyzed the role of PRC2 in extant species along the lineage of Archaeplastida and in the diatom *P. tricornutum*. In this diatom and the red alga *C. merolae*, a greater proportion of TEs than genes were repressed by PRC2, whereas a greater proportion of genes than TEs were repressed by PRC2 in bryophytes. In flowering plants, TEs contained potential *cis*-elements recognized by transcription factors and associated with neighbor genes as transcriptional units repressed by PRC2. Thus, silencing of TEs by PRC2 is observed not only in Archaeplastida but also in diatoms and ciliates, suggesting that PRC2 deposited H3K27me3 to silence TEs in the last common ancestor of eukaryotes. We hypothesize that during the evolution of Archaeplastida, TE fragments marked with H3K27me3 were selected to shape transcriptional regulation, controlling networks of genes regulated by PRC2.
[https://www.cell.com/current-biology/fulltext/S0960-9822\(23\)01153-3?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0960982223011533%3Fshowall%3Dtrue](https://www.cell.com/current-biology/fulltext/S0960-9822(23)01153-3?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0960982223011533%3Fshowall%3Dtrue)

Santinha, A.J., Klingler, E., Kuhn, M. et al. (2023): **Transcriptional linkage analysis with in vivo AAV-Perturb-seq.** Nature | <https://doi.org/10.1038/s41586-023-06570-y>

The ever-growing compendium of genetic variants associated with human pathologies demands new methods to study genotype–phenotype relationships in complex tissues in a high-throughput manner^{1,2}. Here we introduce adeno-associated virus (AAV)-mediated direct in vivo single-cell CRISPR screening, termed AAV-Perturb-seq, a tuneable and broadly applicable method for transcriptional linkage analysis as well as high-throughput and high-resolution phenotyping of genetic perturbations in vivo. We applied AAV-Perturb-seq using gene editing and transcriptional inhibition to systematically dissect the phenotypic landscape underlying 22q11.2 deletion syndrome^{3,4} genes in the adult mouse brain prefrontal cortex. We identified three 22q11.2-linked genes involved in known and previously undescribed pathways orchestrating neuronal functions in vivo that explain approximately 40% of the transcriptional changes observed in a 22q11.2-deletion mouse model. Our findings suggest that the 22q11.2-deletion syndrome transcriptional phenotype found in mature neurons may in part be due to the broad dysregulation of a class of genes associated with disease susceptibility that are important for dysfunctional RNA processing and synaptic function. Our study establishes a flexible and scalable direct in vivo method to facilitate causal understanding of biological and disease mechanisms with potential applications to identify genetic interventions and therapeutic targets for treating disease.
<https://www.nature.com/articles/s41586-023-06570-y>

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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