

Sunday Evening News No 348

2023-10-16 – 2023-10-22

Compiled and edited by **BGF** Jany



Meetings – Conferences / Tagungen - Konferenzen

Multiplex Genome Editing in Plants: Opportunities and Pitfalls

Kolloquium / Vortragsveranstaltung - Julius Kühn-Institut Quedlinburg

Über den Meeting-Link beitreten

<https://jki.webex.com/jki/j.php?MTID=mb9819918204a9c0469598a3bcb21f41c>

Mit Meeting-Kennnummer beitreten

Meeting-Kennnummer (Zugriffscod): 2744 265 5987

Meeting Passwort: KPpuSU8uc73

<https://www.julius-kuehn.de/veranstaltungen/e/event-5624?cHash=b072e025a3e4d818067e32ccbeb68347>

Press Releases -Media / Presse- und Medienberichte

► [AFBV and WGG summary comments](#) on Commission regulatory proposal on plants obtained by certain new genomic techniques and their food and feed

► [AFBV and WGG detailed comments](#) on the Commission's proposal for NGT plants

► [AFBV and WGG: Project of regulation for NGT plants - Proposal text](#)

► [AFBV and WGG: Project of regulation for NGT-plants - Annexes](#)

Committee on the Environment, Public Health and Food Safety: **DRAFT REPORT on the proposal for a regulation** of the European Parliament and of the Council on plants obtained by certain new genomic techniques and their food and feed, and amending Regulation (EU) 2017/625

https://www.europarl.europa.eu/doceo/document/ENVI-PR-754658_EN.pdf

Council: **Regulation on new genomic techniques (NGT)** – Technical paper on the rationale for the equivalence criteria in Annex I

https://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CONSIL:ST_14204_2023_INIT

Leopoldina: Für eine wissenschaftsbasierte Regulierung von mittels neuer genomischer Techniken gezüchteten Pflanzen in der EU (2023)

<https://www.leopoldina.org/publikationen/detailansicht/publication/fuer-eine-wissenschaftsbasierte-regulierung-von-mittels-neuer-genomischer-techniken-gezuechteten-pflanzen-in-der-eu-2023/>

BIO AUSTRIA: Berichterstatterin des EU-Parlaments plant Angriff auf Bio

https://www.ots.at/presseaussendung/OTS_20231020_OTS0082/bio-austria-berichterstatterin-des-eu-parlaments-plant-angriff-auf-bio

Informationsdienst Gentechnik: Bundesrat bleibt bei Kennzeichnung neuer Gentechnik vage

<https://www.keine-gentechnik.de/nachricht/34833?cHash=ff20f7cd52d6199de665bd6209f33b2a>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ► [here](#): October week 42

Publications – Publikationen

Winter G. (2023): **So nicht! Aber anders? Eine Bewertung des Kommissionsvorschlags über Pflanzen aus neuen genomischen Techniken.** AUR 2023, S. 362-367 (pdf-file vorhanden)

Williams, R. (2023): **Law and policy can support sustainable diets.** Commun Earth Environ 4, 375 | <https://doi.org/10.1038/s43247-023-01038-3>

The role of law and policy in encouraging a sustainable global diet is often underestimated. I argue that targeted laws and environmental policy are key to bring the agricultural sector on the path towards sustainability.

<https://www.nature.com/articles/s43247-023-01038-3>

Dube, S.P., Sibiyi, J. & Kutu, F. (2023): **Genetic diversity and population structure of maize inbred lines using phenotypic traits and single nucleotide polymorphism (SNP) markers.** *Sci Rep* 13, 17851 | <https://doi.org/10.1038/s41598-023-44961-3>

Understanding germplasm's genetic diversity is essential for developing new and improved cultivars with stable yields under diverse environments. The objective of this study was to determine the genetic diversity and population structure of 128 maize inbred lines sourced from the International Institute of Tropical Agriculture (IITA), the International Maize and Wheat Improvement Centre (CIMMYT), and the University of KwaZulu-Natal (UKZN) using 11,450 informative single nucleotide polymorphism (SNP) markers. The inbred lines revealed highly significant ($p < 0.001$) levels of variability for the key phenotypic traits. The SNP markers had a mean gene diversity (GD) and polymorphic information content (PIC) of 0.40 and 0.31, respectively, indicating the existence of substantial genetic variation across the germplasm panel. The model-based population structure analysis identified three subpopulations ($K = 3$) among the inbred lines. This corroborated the phylogenetic analysis using phenotypic traits and molecular markers which classified the inbred lines into three groups. The findings of this study identified considerable genetic diversity for the selection of inbred lines with favourable alleles for multiple traits and could be useful to initiate marker-assisted selection (MAS) to identify significant loci associated with agronomic performance and multiple-stress tolerance.

<https://www.nature.com/articles/s41598-023-44961-3>

Du K. et al. (2023): **Spatiotemporal miRNA and transcriptomic network dynamically regulate the developmental and senescence processes of poplar leaves.** *Horticulture Research* | [DOI: 10.1093/hr/uhad186](https://doi.org/10.1093/hr/uhad186)

Poplar is an important afforestation and urban greening species. Poplar leaf development occurs in stages, from young to mature and then from mature to senescent; these are accompanied by various phenotypic and physiological changes. However, the associated transcriptional regulatory network is relatively unexplored. We first used principal component analysis to classify poplar leaves at different leaf positions into two stages: developmental maturity the stage of maximum photosynthetic capacity, and the stage where photosynthetic capacity started to decline and gradually changed to senescence. The two stages were then further subdivided into five intervals by gene expression clustering analysis, including young leaves, the period of cell genesis and functional differentiation (L1), young leaves, the period of development and initial formation of photosynthetic capacity (L3-L7), the period of maximum photosynthetic capacity of functional leaves (L9-L13), the period of decreasing photosynthetic capacity of functional leaves (L15-L27), and the period of senescent leaves (L29). Using a weighted co-expression gene network analysis of regulatory genes, high-resolution spatiotemporal transcriptional regulatory networks were constructed to reveal the core regulators that regulate leaf development. Spatiotemporal transcriptome data of poplar leaves revealed dynamic changes in genes and miRNAs during leaf development and identified several core regulators such as GRF5, MYB5 on leaf development. This in-depth analysis of transcriptional regulation during leaf development provides a theoretical basis for exploring the biological basis of transcriptional regulation of leaf development and the molecular design of breeding for delaying leaf senescence.

<https://academic.oup.com/hr/advance-article/doi/10.1093/hr/uhad186/7283134>

Xiong, X., Liu, K., Li, Z. et al. (2023): **Split complementation of base editors to minimize off-target edits.** *Nat. Plants* | <https://doi.org/10.1038/s41477-023-01540-8>

Base editors (BEs) empower the efficient installation of beneficial or corrective point mutations in crop and human genomes. However, conventional BEs can induce unpredictable guide RNA (gRNA)-independent off-target edits in the genome and transcriptome due to spurious activities of BE-enclosing deaminases, and current improvements mostly rely on deaminase-specific mutagenesis or exogenous regulators. Here we developed a split deaminase for safe editing (SAFE) system applicable to BEs containing distinct cytidine or adenosine deaminases, with no need of external regulators. In SAFE, a BE was properly split at a deaminase domain embedded inside a Cas9 nickase, simultaneously fragmenting and deactivating both the deaminase and the Cas9 nickase. The gRNA-conditioned BE reassembly conferred robust on-target editing in plant, human and yeast cells, while minimizing both gRNA-independent and gRNA-dependent off-target DNA/RNA edits. SAFE also substantially increased product purity by eliminating indels. Altogether, SAFE provides a generalizable solution for BEs to suppress off-target editing and improve on-target performance.

<https://www.nature.com/articles/s41477-023-01540-8>

EFSA

CEP Panel (2023): **Safety evaluation of the food enzyme triacylglycerol lipase from the genetically modified *Aspergillus luchuensis* strain FL105SC.** *EFSA Journal*, 21(10), 1–12.

<https://doi.org/10.2903/j.efsa.2023.8259>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8259>

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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