Wissenschaftskreis Genomik und Gentechnik e.V.

_Wochenrückblick Woche 28 - 2023

10.07.2023 – 16.07.2023

Zusammengestellt und editiert von ***BGF*** Jany

Meeting - Veranstaltungen

Zoom Austausch mit Harald Ebner: Ded-Regulierung statt Vorsorge
Die Kreisverbände Calw, Backnang und Tübingen haben für kommenden Dienstag, den 25. Juli 2023, um 19.30 Uhr ein Zoom-Gespräch organisiert. Über folgenden Link treffen wir uns:https://us02web.zoom.us/j/87810547355?pwd=UFdjNU16ZWxybTVVTkRjZGJUZ1ZrZz09

Press Releases -Media / Presse- und Medienberichte

Biowisskomm: **Irrungen und Wirrungen zum EU-Vorschlag, die „Neuen gentechnischen Methoden" zu deregulieren.**
https://www.biowisskomm.de/2023/07/irrungen-und-wirrungen-zum-eu-vorschlag-die-neuen-gentechnischen-methoden-zu-deregulieren/?fbclid=IwAR0zMxhozwaz6Js3UXXM3P7BwQUvl7lUtrnupWTuI_BkzXhdCzCt5qE-jWI

DBG: **Stellungnahme: DBG zum Regulierungsvorschlag der EU für Neue Genomische Techniken**
https://www.deutsche-botanische-gesellschaft.de/ueber-die-dbg/aktionen/stellungnahme-regulierungsvorschlag-fuer-ngt

Giersch T.: **Der Gen-Weizen kommt doch! EU schwingt Ernährungs-Hammer**
https://www.focus.de/politik/eu-gesetz-der-gen-weizen-kommt-doch-eu-vollzieht-epochenwechsel-in-der-ernaehrungspolitik_id_198899867.html

Swaton C. und Dahm J.: **Österreich und Deutschland – die Front gegen die EU-Gentechnikpläne?**
https://www.euractiv.de/section/landwirtschaft-und-ernahrung/news/oesterreich-und-deutschland-die-front-gegen-die-eu-gentechnikplaene/

Germany, Austria in united front against Brussels' gene-editing plans
https://www.euractiv.com/section/agriculture-food/news/germany-austria-a-united-front-against-brussels-gene-editting-plans/

Struna H.: **Gene edited food: Greens bemoan Commission's empty promises**
https://www.euractiv.com/section/agriculture-food/news/gene-edited-food-greens-bemoan-commissions-empty-promises/

Bundesministerium für Umwelt, Naturschutz, nukleare Sicherheit und Verbraucherschutz: **BMUV-Informationspapier Neue Gentechnik**
https://www.bmuv.de/download/informationspapier-neue-gentechnik

ENSSER: **Analysis statement by ENSSER on the EU Commission's new GM proposal. Here for Annex 1 on NGT "equivalence criteria"**
https://ensser.org/press_release/analysis-statement-by-ensser-on-the-eu-commissions-new-gm-proposal-here-for-annex-1-on-ngt-equivalence-criteria/

The analysis: https://ensser.org/wp-content/uploads/2023/07/ENSSER-Critique-of-Annex-I-of-COM-proposal-July-2023.pdf

Testbiotech: **EU Commission draft proposal for criteria concerning the equivalence of NGT plants to conventional plants**
https://www.testbiotech.org/sites/default/files/Testbiotech%20backgrounder%20on%20Category%201%20of%20NGT%20plants.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 28

Publications – Publikationen

Castañeda-Barba, S., Top, E.M. & Stalder, T. (2023): **Plasmids, a molecular cornerstone of antimicrobial resistance in the One Health era.** Nat Rev Microbiol | https://doi.org/10.1038/s41579-023-00926-x

Antimicrobial resistance (AMR) poses a substantial threat to human health. The widespread prevalence of AMR is, in part, due to the horizontal transfer of antibiotic resistance genes (ARGs), typically mediated by plasmids. Many of the plasmid-mediated resistance genes in pathogens originate from environmental, animal or human habitats. Despite evidence that plasmids mobilize ARGs between these habitats, we have a limited understanding of the ecological and evolutionary trajectories that facilitate the emergence of multidrug resistance (MDR) plasmids in clinical pathogens. One Health, a holistic framework, enables exploration of these knowledge gaps. In this Review, we provide an overview of how plasmids drive local and global AMR spread and link different habitats. We explore some of the emerging studies integrating an eco-evolutionary perspective, opening up a discussion about the factors that affect the ecology and evolution of plasmids in complex microbial communities. Specifically, we discuss how the emergence and persistence of MDR plasmids can be affected by varying selective conditions, spatial structure, environmental heterogeneity, temporal variation and coexistence with other members of the microbiome. These factors, along with others yet to be investigated, collectively determine the emergence and transfer of plasmid-mediated AMR within and between habitats at the local and global scale.
https://www.nature.com/articles/s41579-023-00926-x

Banerjee, S., Mukherjee, A. & Kundu, A. (2023): **The current scenario and future perspectives of transgenic oilseed mustard by CRISPR-Cas9.** Mol Biol Rep | https://doi.org/10.1007/s11033-023-08660-6

Purpose: Production of a designer crop having added attributes is the primary goal of all plant biotechnologists. Specifically, development of a crop with a simple biotechnological approach and at a rapid pace is most desirable. Genetic engineering enables us to displace genes among species. The newly incorporated foreign gene(s) in the host genome can create a new trait(s) by regulating the genotypes and/or phenotypes. The advent of the CRISPR-Cas9 tools has enabled the modification of a plant genome easily by introducing mutation or replacing genomic fragment. Oilseed mustard varieties (e.g., *Brassica juncea, Brassica nigra, Brassica napus*, and *Brassica carinata*) are one such plants, which have been transformed with different genes isolated from the wide range of species. Current reports proved that the yield and value of oilseed mustard has been tremendously improved by the introduction of stably inherited new traits such as insect and herbicide resistance. However, the genetic transformation of oilseed mustard remains incompetent due to lack of potential plant transformation systems. To solve numerous complications involved in genetically modified oilseed mustard crop varieties regeneration procedures, scientific research is being conducted to rectify the unwanted complications. Thus, this study provides a broader overview of the present status of new traits introduced in each mentioned varieties of oilseed mustard plant by different genetical engineering tools, especially CRISPR-Cas9, which will be useful to improve the transformation system of oilseed mustard crop plants.
Methods: This review presents recent improvements made in oilseed mustard genetic engineering methodologies by using CRISPR-Cas9 tools, present status of new traits introduced in oilseed mustard plant varieties.
Results: The review highlighted that the transgenic oilseed mustard production is a challenging process and the transgenic varieties of oilseed mustard provide a powerful tool for enhanced mustard yield. Over expression studies and silencing of desired genes provide functional importance of genes involved in mustard growth and development under different biotic and abiotic stress conditions. Thus, it can be expected that in near future CRISPR can contribute enormously in improving the mustard plant's architecture and develop stress resilient oilseed mustard plant species.
https://link.springer.com/article/10.1007/s11033-023-08660-6

Zeidler V.G.Z. (2023): **Genetic editing of wood for sustainability -** Trees engineered to have less lignin could make paper production less polluting. Science 381, Issue 6654, pp. 124-125 | DOI: 10.1126/science.adi8186

Lignin, a polymer formed by phenylpropanoid units, is responsible for the rigidity and resistance of the lignocellulosic cells in wood (*1*). In conventional pulp production, lignin must be cleaved and dissolved under alkaline conditions or first sulfonated to make it soluble so that fiber separation can take place. Delignification processes are reagent and energy intensive, leading to costly chemical recovery (*2*). Pulp treatment methods to remove wood extractives such as lignin have been developed, but they are not yet economically viable at an industrial scale (*3*). On page 216 of this issue, Sulis *et al*. (*4*) present a multiplex CRISPR genome editing strategy to modify lignin biosynthesis genes and reduce the lignin content of *Populus trichocarpa*, a species of poplar. This approach could provide a solution to a key operational constraint in the paper and pulp industry.
https://www.science.org/doi/10.1126/science.adi8186

Satam H., Joshi, K., Mangrolia U., Waghoo S. et al. (2023): **Next-Generation Sequencing Technology: Current Trends and Advancements. Biology** 12 (7), 997 | https://doi.org/10.3390/biology12070997
The advent of next-generation sequencing (NGS) has brought about a paradigm shift in genomics research, offering unparalleled capabilities for analyzing DNA and RNA molecules in a high-throughput and cost-effective manner. This transformative technology has swiftly propelled genomics advancements across diverse domains. NGS allows for the rapid sequencing of millions of DNA fragments simultaneously, providing comprehensive insights into genome structure, genetic variations, gene expression profiles, and epigenetic modifications. The versatility of NGS platforms has expanded the scope of genomics research, facilitating studies on rare genetic diseases, cancer genomics, microbiome analysis, infectious diseases, and population genetics. Moreover, NGS has enabled the development of targeted therapies, precision medicine approaches, and improved diagnostic methods. This review provides an insightful overview of the current trends and recent advancements in NGS technology, highlighting its potential impact on diverse areas of genomic research. Moreover, the review delves into the challenges encountered and future directions of NGS technology, including endeavors to enhance the accuracy and sensitivity of sequencing data, the development of novel algorithms for data analysis, and the pursuit of more efficient, scalable, and cost-effective solutions that lie ahead.
https://www.mdpi.com/2079-7737/12/7/997

Carlson, A.B., Mathesius, C.A., Gunderson, T.A. et al. (2023): **Protein familiarity is a fundamental but rarely operationalized concept in the safety assessment of genetically modified crops: example of phosphomannose isomerase (PMI).** Transgenic Res | https://doi.org/10.1007/s11248-023-00358-6
Fundamental to the safety assessment of genetically modified (GM) crops is the concept of negligible risk for newly expressed proteins for which there is a history of safe use. Although this simple concept has been stated in international and regional guidance for assessing the risk of newly expressed proteins in GM crops, its full implementation by regulatory authorities has been lacking. As a result, safety studies are often repeated at a significant expenditure of resources by developers, study results are repeatedly reviewed by regulators, and animals are sacrificed needlessly to complete redundant animal toxicity studies. This situation is illustrated using the example of the selectable marker phosphomannose isomerase (PMI) for which familiarity has been established. Reviewed is the history of safe use for PMI and predictable results of newly conducted safety studies including bioinformatic comparisons, resistance to digestion, and acute toxicity that were repeated to gain regulatory reapproval of PMI expressed from constructs in recently developed GM maize. As expected, the results of these newly repeated hazard-identification and characterization studies for PMI indicate negligible risk. PMI expressed in recently developed GM crops provides an opportunity to use the concept of familiarity by regulatory authorities to reduce risk-disproportionate regulation of these new events and lessen the resulting waste of both developer and regulator resources, as well as eliminate unnecessary animal testing. This would also correctly imply that familiar proteins like PMI have negligible risk. Together, such modernization of regulations would benefit society through enabling broader and faster access to needed technologies.
https://link.springer.com/article/10.1007/s11248-023-00358-6

Wenjie H. Li Z., Guo Y. et al. (2023): **Efficient precise integration of large DNA sequences with 3’-overhang dsDNA donors using CRISPR/Cas9,** PNAS 120 (22) e2221127120 | https://doi.org/10.1073/pnas.2221127120
CRISPR/Cas9 genome-editing tools have tremendously boosted our capability of manipulating the eukaryotic genomes in biomedical research and innovative biotechnologies. However, the current approaches that allow precise integration of gene-sized large DNA fragments generally suffer from low efficiency and high cost. Herein, we developed a versatile and efficient approach, termed LOCK (Long dsDNA with 3’-Overhangs mediated CRISPR Knock-in), by utilizing specially designed 3’-overhang double-stranded DNA (odsDNA) donors harboring 50-nt homology arm. The length of the 3’-overhangs of odsDNA is specified by the five consecutive phosphorothioate modifications. Compared with existing methods, LOCK allows highly efficient targeted insertion of kilobase-sized DNA fragments into the mammalian genomes with low cost and low off-target effects, yielding >fivefold higher knock-in frequencies than conventional homologous recombination-based approaches. This newly designed LOCK approach based on homology-directed repair is a powerful tool suitable for gene-sized fragment integration that is urgently needed for genetic engineering, gene therapies, and synthetic biology.
https://www.pnas.org/doi/10.1073/pnas.2221127120

Kauert, D.J., Madariaga-Marcos, J., Rutkauskas, M. et al. (2023): **The energy landscape for R-loop formation by the CRISPR–Cas Cascade complex.** Nat Struct Mol Biol | https://doi.org/10.1038/s41594-023-01019-2
Clustered regularly interspaced short palindromic repeats (CRISPR) sequences and CRISPR-associated (Cas) genes comprise CIRSPR-Cas effector complexes, which have revolutionized gene editing with their ability to target specific genomic loci using CRISPR RNA (crRNA) complementarity. Recognition of double-stranded DNA targets proceeds via DNA unwinding and base pairing between crRNA and the DNA target strand, forming an R-loop structure. Full R-loop extension is a prerequisite for subsequent DNA cleavage. However, the recognition of unintended sequences with multiple mismatches has limited therapeutic applications and is still poorly understood on a mechanistic level. Here we set up ultrafast DNA unwinding experiments on the basis of

plasmonic DNA origami nanorotors to study R-loop formation by the Cascade effector complex in real time, close to base-pair resolution. We resolve a weak global downhill bias of the forming R-loop, followed by a steep uphill bias for the final base pairs. We also show that the energy landscape is modulated by base flips and mismatches. These findings suggest that Cascade-mediated R-loop formation occurs on short timescales in submillisecond single base-pair steps, but on longer timescales in six base-pair intermediate steps, in agreement with the structural periodicity of the crRNA–DNA hybrid.
https://www.nature.com/articles/s41594-023-01019-2

Edwards, A., Njaci, I., Sarkar, A. et al. (2023): **Genomics and biochemical analyses reveal a metabolon key to β-L-ODAP biosynthesis in *Lathyrus sativus***. Nat Commun 14, 876 | https://doi.org/10.1038/s41467-023-36503-2
Grass pea (*Lathyrus sativus* L.) is a rich source of protein cultivated as an insurance crop in Ethiopia, Eritrea, India, Bangladesh, and Nepal. Its resilience to both drought and flooding makes it a promising crop for ensuring food security in a changing climate. The lack of genetic resources and the crop's association with the disease neurolathyrism have limited the cultivation of grass pea. Here, we present an annotated, long read-based assembly of the 6.5 Gbp *L. sativus* genome. Using this genome sequence, we have elucidated the biosynthetic pathway leading to the formation of the neurotoxin, β-L-oxalyl-2,3-diaminopropionic acid (β-L-ODAP). The final reaction of the pathway depends on an interaction between *L. sativus* acyl-activating enzyme 3 (LsAAE3) and a BAHD-acyltransferase (LsBOS) that form a metabolon activated by CoA to produce β-L-ODAP. This provides valuable insight into the best approaches for developing varieties which produce substantially less toxin.
https://www.nature.com/articles/s41467-023-36503-2

EFSA CEP Panel (2023): Scientific Opinion on the safety evaluation of the food enzyme cellulase from the non-genetically modified *Aspergillus niger* strain 294. *EFSA Journal* 2023; 21(7):8098, 17 pp. https://doi.org/10.2903/j.efsa.2023.8098
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8098

EFSA CEP Panel (2023): Scientific Opinion on the safety evaluation of the food enzyme endo-1,4-β-xylanase from the non-genetically modified *Aspergillus tubingensis* strain LYX. *EFSA Journal* 2023; 21(7):8085, 15 pp. https://doi.org/10.2903/j.efsa.2023.8085
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8085

EFSA CEP Panel (2023): Scientific Opinion on the safety evaluation of the food enzyme endo-1,4-β-xylanase from the genetically modified *Bacillus subtilis* strain XAN. *EFSA Journal* 2023; 21(7):8017, 15 pp. https://doi.org/10.2903/j.efsa.2023.8017
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8017

EFSA BIOHAZ Panel (2023): Update of the list of qualified presumption of safety (QPS) recommended microbiological agents intentionally added to food or feed as notified to EFSA 18: Suitability of taxonomic units notified to EFSA until March 2023. *EFSA Journal* 2023; 21(7):8092, 32 pp. https://doi.org/10.2903/j.efsa.2023.8092
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.8092

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. M*ost of *the pdf files can be downloaded directly from the links.*

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