Sunday Evening News No 332

2023-06-26 – 2023-07-02

Compiled and edited by ***BGF*** Jany

Meetings - Lectures

Reminder: **Theodor BILLROTH' Lecture: Regulation of new genomic techniques in the EU:** Detlef Barth, BVL
Date & Time: Jul 5, 2023 03:00 PM Amsterdam, Berlin, Rome, Stockholm, Vienna

Press Releases -Media / Presse- und Medienberichte

POINT NEWSLETTER NR. 252 – JUNI 2023 - **Aktuelle Biotechnologie**

ÖAW: **Grüne Gentechnik: Offener Brief für eine wissenschaftsbasierte Beurteilung**
https://www.oeaw.ac.at/news/gruene-gentechnik-offener-brief-fuer-eine-wissenschaftsbasierte-beurteilung

Open letter for a science-based assessment of green genetic engineering
https://www.oeaw.ac.at/en/news/gruene-gentechnik-offener-brief-fuer-eine-wissenschaftsbasierte-beurteilung

Morrison & Foerster LLP : **The EU's New Proposal for Plants Developed Using New Genomic Techniques: How Does it Compare to U.S. Regulation?**
https://www.lexology.com/library/detail.aspx?g=a450007b-05ed-4612-8af1-011d4b6416e8

Schönig W.: **Commission Plans Liberalization of New Genomic Techniques (NGTs) in the EU**
https://lifesciences.mofo.com/topics/commission-plans-liberalization-of-new-genomic-techniques-ngts-in-the-eu

Euroseeds and CropLife Europe call for science-based approach in New Genomic Techniques proposal
https://euroseeds.eu/news/euroseeds-and-croplife-europe-call-for-science-based-approach-in-new-genomic-techniques-proposal/

The letter: https://euroseeds.eu/app/uploads/2023/06/23.0429.2-Letter-Euroseeds-CLE-NGTs-26-06-2023.pdf

Miller H.I.: **Regulators Should Embrace Vatican's Endorsement of Genetic Engineering**
https://www.acsh.org/news/2023/06/29/regulators-should-embrace-vatican%E2%80%99s-endorsement-genetic-engineering-17120

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

Lyu, J. (2023): **LMM gene editing.** Nat. Plants | https://doi.org/10.1038/s41477-023-01460-7

Lynas M., Adams S., Stockert K. (2023): **Gene editing achieves consistently higher favorability in social and traditional media than GMOs.** GM Crops & Food | https://doi.org/10.1080/21645698.2023.2226889
While GMOs have been the subject of negative discourse over a long time period, it is possible that newer breeding technologies like gene editing are viewed more favorably. We present data for a 5-year period between January 2018 and December 2022, showing that in content specific to agricultural biotechnology, gene editing achieves consistently higher favorability ratings than GMOs in both social and traditional English-language media. Our sentiment analysis shows that favorability is especially positive in social media, with close to 100% favorability achieved in numerous monthly values throughout our 5 years of analysis. We believe that the scientific community can therefore be cautiously optimistic based on current trends that gene editing will be accepted by the public and be able to achieve its promise of making a substantial contribution to future food security and environmental sustainability worldwide. However, there are some recent indications of more sustained downward trends, which may be a cause for concern.
https://www.tandfonline.com/doi/full/10.1080/21645698.2023.2226889

Yadav R.K., Tripathi M.K., Tiwari S., Tripathi N. et al. (2023): **Genome Editing and Improvement of Abiotic Stress Tolerance in Crop Plants.** *life*, *13* (7), 1456 | https://doi.org/10.3390/life13071456
Genome editing aims to revolutionise plant breeding and could assist in safeguarding the global food supply. The inclusion of a 12–40 bp recognition site makes mega nucleases the first tools utilized for genome editing and first generation gene-editing tools. Zinc finger nucleases (ZFNs) are the second gene-editing technique, and because they create double-stranded breaks, they are more dependable and effective. ZFNs were the original designed nuclease-based approach of genome editing. The Cys2-His2 zinc finger domain's discovery made this technique possible. Clustered regularly interspaced short palindromic repeats (CRISPR) are utilized to improve genetics, boost biomass production, increase nutrient usage efficiency, and develop disease resistance. Plant genomes can be effectively modified using genome-editing technologies to enhance characteristics without introducing foreign DNA into the genome. Next-generation plant breeding will soon be defined by these exact breeding methods. There is abroad promise that genome-edited crops will be essential in the years to come for improving the sustainability and climate-change resilience of food systems. This method also has great potential for enhancing crops' resistance to various abiotic stressors. In this review paper, we summarize the most recent findings about the mechanism of abiotic stress response in crop plants and the use of the CRISPR/Cas mediated gene-editing systems to improve tolerance to stresses including drought, salinity, cold, heat, and heavy metals.
https://www.mdpi.com/2075-1729/13/7/1456

Gouseti O, Larsen M.E., Amin A., Bakalis S. et al. (2023): **Applications of Enzyme Technology to Enhance Transition to Plant Proteins: A Review.** Foods, 12 (13), 2518 | https://doi.org/10.3390/foods12132518
As the plant-based food market grows, demand for plant protein is also increasing. Proteins are a major component in foods and are key to developing desired structures and textures. Seed storage proteins are the main plant proteins in the human diet. They are abundant in, for example, legumes or defatted oilseeds, which makes them an excellent candidate to use in the development of novel plant-based foods. However, they often have low and inflexible functionalities, as in nature they are designed to remain densely packed and inert within cell walls until they are needed during germination. Enzymes are often used by the food industry, for example, in the production of cheese or beer, to modify ingredient properties. Although they currently have limited applications in plant proteins, interest in the area is exponentially increasing. The present review first considers the current state and potential of enzyme utilization related to plant proteins, including uses in protein extraction and post-extraction modifications. Then, relevant opportunities and challenges are critically discussed. The main challenges relate to the knowledge gap, the high cost of enzymes, and the complexity of plant proteins as substrates. The overall aim of this review is to increase awareness, highlight challenges, and explore ways to address them.
https://www.mdpi.com/2304-8158/12/13/2518

Ramaraj T., Grover C.E., Mendoza A.C., Arick M.A. et al. (2023): **The Gossypium herbaceum L. Wagad genome as a resource for understanding cotton domestication.** G3 Genes|Genomes|Genetics 13 (2), jkac308 |). DOI: 10.1093/g3journal/jkac308
Gossypium herbaceum is a species of cotton native to Africa and Asia that is one of the 2 domesticated diploids. Together with its sister-species *G. arboreum*, these A-genome taxa represent models of the extinct A-genome donor of modern polyploid cotton, which provide about 95% of cotton grown worldwide. As part of a larger effort to characterize variation and improve resources among diverse diploid and polyploid cotton genomes, we sequenced and assembled the genome of *G. herbaceum* cultivar (cv.) Wagad, representing the first domesticated accession for this species. This chromosome-level genome was generated using a combination of PacBio long-read technology, HiC, and Bionano optical mapping and compared to existing genome sequences in cotton. We compare the genome of this cultivar to the existing genome of wild *G. herbaceum* subspecies *africanum* to elucidate changes in the *G. herbaceum* genome concomitant with domestication and extend these analyses to gene expression using available RNA-seq. Our results demonstrate the utility of the *G. herbaceum* cv. Wagad genome in understanding domestication in the diploid species, which could inform modern breeding programs.
https://academic.oup.com/g3journal/article/13/2/jkac308/6858943

Gann P.J.I., Dharwadker D., Cherati S.R., Vinzant K. et al. (2023): **Targeted mutagenesis of the vacuolar H^+ translocating pyrophosphatase gene reduces grain chalkiness in rice.** Plant Journal | https://doi.org/10.1111/tpj.16317
Grain chalkiness is a major concern in rice production because it impacts milling yield and cooking quality, eventually reducing market value of the rice. A gene encoding vacuolar H^+ translocating pyrophosphatase (*V-PPase*) is a major quantitative trait locus in *indica* rice, controlling grain chalkiness. Higher transcriptional activity of this gene is associated with increased chalk content. However, whether the suppression of *V-PPase* could reduce chalkiness is not clear. Furthermore, natural variation in the chalkiness of *japonica* rice has not been linked with *V-PPase*. Here, we describe promoter targeting of the *japonica V-PPase* allele that led to reduced grain chalkiness and the development of more translucent grains. Disruption of a putative GATA element by clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated protein 9 suppressed *V-PPase* activity, reduced grain chalkiness and impacted post-germination growth that could be rescued by the exogenous supply of sucrose. The mature grains of the targeted lines showed a much lower percentage of large or medium chalk. Interestingly, the targeted lines developed a significantly lower chalk

under heat stress, a major inducer of grain chalk. Metabolomic analysis showed that pathways related to starch and sugar metabolism were affected in the developing grains of the targeted lines that correlated with higher inorganic pyrophosphate and starch contents and upregulation of starch biosynthesis genes. In summary, we show a biotechnology approach of reducing grain chalkiness in rice by downregulating the transcriptional activity of *V-PPase* that presumably leads to altered metabolic rates, including starch biosynthesis, resulting in more compact packing of starch granules and formation of translucent rice grains.
https://onlinelibrary.wiley.com/doi/10.1111/tpj.16317

Yadav A.K, Butler C., Yamamoto A., +2 , and Scott M.J. (2023): **CRISPR/Cas9-based split homing gene drive targeting doublesex for population suppression of the global fruit pest Drosophila suzukii**, PNAS | DOI: 10.1073/pnas.2301525120
Genetic-based methods offer environmentally friendly species-specific approaches for control of insect pests. One method, CRISPR homing gene drive that target genes essential for development, could provide very efficient and cost-effective control. While significant progress has been made in developing homing gene drives for mosquito disease vectors, little progress has been made with agricultural insect pests. Here, we report the development and evaluation of split homing drives that target the *doublesex* (*dsx*) gene in *Drosophila suzukii*, an invasive pest of soft-skinned fruits. The drive component, consisting of *dsx* single guide RNA and DsRed genes, was introduced into the female-specific exon of *dsx*, which is essential for function in females but not males. However, in most strains, hemizygous females were sterile and produced the male *dsx* transcript. With a modified homing drive that included an optimal splice acceptor site, hemizygous females from each of the four independent lines were fertile. High transmission rates of the DsRed gene (94 to 99%) were observed with a line that expressed Cas9 with two nuclear localization sequences from the *D. suzukii nanos* promoter. Mutant alleles of *dsx* with small in-frame deletions near the Cas9 cut site were not functional and thus would not provide resistance to drive. Finally, mathematical modeling showed that the strains could be used for suppression of lab cage populations of *D. suzukii* with repeated releases at relatively low release ratios (1:4). Our results indicate that the split CRISPR homing gene drive strains could potentially provide an effective means for control of *D. suzukii* populations.
https://www.pnas.org/doi/10.1073/pnas.2301525120

Wang, X., Niu, S., Yang, J. et al. (2023): **Effects of stacking breeding on the methylome and transcriptome profile of transgenic rice with glyphosate tolerance.** Planta 258, 34 | https://doi.org/10.1007/s00425-023-04181-5
Main conclusion: Transcriptomics and methylomics were used to identify the potential effects resulting from GM rice breeding stacks, which provided scientific data for the safety assessment strategy of stacked GM crops in China.
Abstract: Gene interaction is one of the main concerns for stacked genetically modified crop safety. With the development of technology, the combination of omics and bioinformatics has become a useful tool to evaluate the unintended effects of genetically modified crops. In this study, transcriptomics and methylomics were used as molecular profiling techniques to identify the potential effects of stack through breeding. Stacked transgenic rice En-12 × Ec-26 was used as material, which was obtained through hybridization using parents En-12 and Ec-26, in which the foreign protein can form functional EPSPS protein by intein-mediated trans-splitting. Differentially methylated region (DMR) analysis showed that the effect of stacking breeding on methylation was less than that of genetic transformation at the methylome level. Differentially expressed gene (DEG) analysis showed that the DEGs between En-12 × Ec-26 and its parents were far fewer than those between transgenic rice and Zhonghua 11 (ZH11), and no unintended new genes were found in En-12 × Ec-26. Statistical analysis of gene expression and methylation involved in shikimic acid metabolism showed that there was no difference in gene expression, although there were 16 and 10 DMR genes between En-12 × Ec-26 and its parents (En and Ec) in methylation, respectively. The results indicated that the effect of stacking breeding on gene expression and DNA methylation was less than the effect of genetic transformation. This study provides scientific data supporting safety assessments of stacked GM crops in China.
https://link.springer.com/article/10.1007/s00425-023-04181-5

Ibrahim E., Rychlá A., Alquicer G., Slavíková L. et al. (2023): **Evaluation of Resistance of Oilseed Rape Genotypes to Turnip Yellows Virus.** Plants 12 (13), 2501 | https://doi.org/10.3390/plants12132501
Turnip yellows virus (TuYV), is one of the most important pathogens of oilseed rape, which has caused enormous yield losses in all growing regions of the world in recent years. Therefore, there is a need for resistant varieties for sustainable crop protection. We have investigated the resistance of known varieties and newly developed advanced-breeding lines of oilseed rape to TuYV in greenhouse and field trials. We have analysed the TuYV titre of individual genotypes inoculated with the virus using viruliferous aphids Myzus persicae. The genotypes 'DK Temptation' and 'Rescator' had the lowest and highest virus titres, respectively, and were used as resistant and susceptible models for comparative analyses with other genotypes. In the greenhouse, the best results were obtained with the genotypes 'OP-8143 DH' (2.94×10^5 copies), OP-BN-72 (3.29×10^5 copies), 'Navajo' (3.58×10^5 copies) and 'SG-C 21215' (4.09×10^5 copies), which reached virus titres about 2 times higher than the minimum virus concentration measured in 'DK Temptation' (1.80×10^5 copies). In the field trials, the genotypes 'Navajo' (3.39×10^5 copies), 'OP-8148 DH' (4.44×10^5 copies), 'SG-C 21215' (6.80×10^5 copies) and OP-8480 (7.19×10^5 copies) had the lowest virus titres and reached about 3 times the virus titre of DK Temptation (2.54×10^5 copies). Both trials showed that at least two commercial varieties (e.g., DK

Temptation, Navajo) and three advanced breeding lines (e.g., OP-8143 DH, OP-BN-72, SG-C 21215) had low titres of the virus after TuYV infection. This indicates a high level of resistance to TuYV in 'Navajo' or the newly developed breeding lines and the basis of resistance is probably different from R54 (as in 'DK Temptation'). Furthermore, the greenhouse trials together with RT -qPCR-based virus titre analysis could be a cost-effective and efficient method to assess the level of resistance of a given genotype to TuYV infection compared to the field trials. However, further research is needed to identify the underlying mechanisms causing this difference in susceptibility.
https://www.mdpi.com/2223-7747/12/13/2501

Naik B., Kumar V., Goyal S.K., Tripathi A.D. et al. (2023): **Pullulanase: unleashing the power of enzyme with a promising future in the food industry.** Front. Bioeng. Biotechnol. Volume 11 - 2023 | https://doi.org/10.3389/fbioe.2023.1139611
Pullulanases are the most important industrial group of enzymes in family 13 glycosyl hydrolases. They hydrolyze either α-1,6 and α-1,4 or both glycosidic bonds in pullulan as well as other carbohydrates to produce glucose, maltose, and maltotriose syrups, which have important uses in food and other related sectors. However, very less reports are available on pullulanase production from native strains because of low yield issues. In line with the increasing demands for pullulanase, it has become important to search for novel pullulanase-producing microorganisms with high yields. Moreover, high production costs and low yield are major limitations in the industrial production of pullulanase enzymes. The production cost of pullulanase by using the solid-state fermentation (SSF) process can be minimized by selecting agro-industrial waste. This review summarizes the types, sources, production strategies, and potential applications of pullulanase in different food and other related industries. Researchers should focus on fungal strains producing pullulanase for better yield and low production costs by using agro-waste. It will prove a better enzyme in different food processing industries and will surely reduce the cost of products.
https://www.frontiersin.org/articles/10.3389/fbioe.2023.1139611/full

EFSA

GMO panel (2023): Scientific Opinion on the assessment of genetically modified cotton COT 102 for food and feed uses, under Regulation (EC) No 1829/2003 (application EFSA-GMO-DE-2017-141). EFSA Journal 21 (6) :8031, 35 pp. | https://doi.org/10.2903/j.efsa.2023.8031
https://www.efsa.europa.eu/en/efsajournal/pub/8031

► Safety assessed food enzymes April – June 2023

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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