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2023-08-28. – 2023-09-03

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

Meetings - Veranstaltungen

Konferenz zur besseren Nutzung von Forschungsdaten erstmals in Karlsruhe
Veranstaltungsort: Audimax auf dem Campus Süd des KIT, Gebäude 30.95, Straße am Forum 1, 76131 Karlsruhe. Dienstag, 12. September 2023
https://idw-online.de/de/news819809

Press Releases -Media / Presse- und Medienberichte

dts: **Landwirtschaftsminister will Kompromiss für neue Gentechnik**
https://www.nachrichten-heute.net/1072965-landwirtschaftsminister-will-kompromiss-fuer-neue-gentechnik.html

Pehl P.: **Neue Techniken: Bundesregierung im Diskussionsprozess**
https://www.agrarzeitung.de/nachrichten/politik/gentechnik-neue-techniken-bundesregierung-im-diskussionsprozess-108634

Michel-Berger S.: **Glyphosat und Gentechnik: Das sagt Bayer-Chefin Karin Guendel-Gonzalez**
https://www.agrarheute.com/pflanze/glyphosat-gentechnik-sagt-bayer-chefin-karin-guendel-gonzalez-609615

Zachová A.: **Tschechischer Minister: Gentechnik wichtig für Ernährungs- und Klimazukunft der EU**
https://www.euractiv.de/section/europa-kompakt/news/tschechischer-minister-gentechnik-wichtig-fuer-ernaehrungs-und-klimazukunft-der-eu/

Czech minister champions gene-editing for EU's food and climate future
https://www.euractiv.com/section/politics/news/czech-minister-champions-gene-editing-for-eus-food-and-climate-future/?_ga=2.136655156.523307489.1693233385-544315556.1693233384

Testbiotech warnt vor der weitreichenden Deregulierung von Pflanzen aus Neuer Gentechnik
https://www.testbiotech.org/aktuelles/testbiotech-warnt-vor-der-weitreichenden-deregulierung-von-pflanzen-aus-neuer-gentechnik
https://www.testbiotech.org/sites/default/files/Testbiotech_Hintergrund_%20NGT_Verordnung_final.pdf

Testbiotech warns about the far-reaching deregulation of New GE plants
https://www.testbiotech.org/en/content/new-genetic-engineering-eu-commission-proposal-new-regulation-endangers-nature-environment

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ▶here: August/September week 35

Publications – Publikationen

Lokya V., Parmar S.,Pandey A.K., Sudini H.K. et al. (2023): **Prospects for developing allergen-depleted food crops.** Plant Genome | https://doi.org/10.1002/tpg2.20375
In addition to the challenge of meeting global demand for food production, there are increasing concerns about food safety and the need to protect consumer health from the negative effects of foodborne allergies. Certain bio-molecules (usually proteins) present in food can act as allergens that trigger unusual immunological reactions, with potentially life-threatening consequences. The relentless working lifestyles of the modern era often incorporate poor eating habits that include readymade prepackaged and processed foods, which contain additives such as peanuts, tree nuts, wheat, and soy-based products, rather than traditional home cooking. Of the predominant allergenic foods (soybean, wheat, fish, peanut, shellfish, tree nuts, eggs, and milk), peanuts (*Arachis hypogaea*) are the best characterized source of allergens, followed by tree nuts (*Juglans regia*, *Prunus amygdalus*, *Corylus avellana*, *Carya illinoinensis*, *Anacardium occidentale*, *Pistacia vera*, *Bertholletia excels*), wheat (*Triticum aestivum*), soybeans (*Glycine max*), and kidney beans (*Phaseolus vulgaris*). The prevalence of food allergies has risen significantly in recent years including chance of accidental

exposure to such foods. In contrast, the standards of detection, diagnosis, and cure have not kept pace and unfortunately are often suboptimal. In this review, we mainly focus on the prevalence of allergies associated with peanut, tree nuts, wheat, soybean, and kidney bean, highlighting their physiological properties and functions as well as considering research directions for tailoring allergen gene expression. In particular, we discuss how recent advances in molecular breeding, genetic engineering, and genome editing can be used to develop potential low allergen food crops that protect consumer health.
https://acsess.onlinelibrary.wiley.com/doi/full/10.1002/tpg2.20375
https://acsess.onlinelibrary.wiley.com/doi/epdf/10.1002/tpg2.20375

Schlathölter I., Broggini G.A.L., Streb S., Studer B., Patocchi A. (2023): **Field study of the fire-blight-resistant cisgenic apple line C44.4.146.** Plant Journal 113:1160-1175; | https://doi.org/10.1111/tpj.16083
Cisgenesis, the genetic modification of a plant with genes from a sexually compatible plant, was used to confer fire blight resistance to the cultivar 'Gala Galaxy' by amendment of the resistance gene *FB_MR5*, resulting in the line C44.4.146. To verify whether cisgenesis changed other tree-, flower- or fruit-related traits, a 5-year field trial was conducted with trees of C44.4.146 and multiple control genotypes, including members of the 'Gala' sports group. None of the 44 investigated tree-, flower- or fruit-related traits significantly differed between C44.4.146 and at least one of the control genotypes in all observation years. However, fruits of C44.4.146 and its wild-type 'Gala Galaxy' from tissue culture were paler in color than fruits of 'Gala Galaxy' that had not undergone tissue culture. There was no significant and consistently detected difference in the fruit flesh and peel metabolome of C44.4.146 compared with the control genotypes. Finally, the disease resistance of C44.4.146 was confirmed also when the fire blight pathogen was inoculated through the flowers. We conclude that the use of cisgenesis to confer fire blight resistance to 'Gala Galaxy' in C44.4.146 did not have unintended effects, and that the *in vitro* establishment of 'Gala Galaxy' had a greater effect on C44.4.146 properties than its generation applying cisgenesis.
https://onlinelibrary.wiley.com/doi/full/10.1111/tpj.16083

Xu L., Mo K., Ran D. Ma J. et al. (2023):**An endolysin gene from *Candidatus* Liberibacter asiaticus confers dual resistance to Huanglongbing and citrus canker.** Horticulture Research, uhad159, https://doi.org/10.1093/hr/uhad159
The most damaging citrus diseases are Huanglongbing (HLB) and citrus canker, which are *Candidatus* Liberibacter asiaticus (*Ca*Las) and *Xanthomonas citri* pv. *citri* (*Xcc*), respectively. Endolysins from bacteriophages are a possible option for disease resistance in plant breeding. Here, we report improvement of citrus resistance to HLB and citrus canker using the LasLYS1 and LasLYS2 endolysins from *Ca*Las. LasLYS2 demonstrated bactericidal efficacy against several Rhizobiaceae bacteria and *Xcc*, according to inhibition zone analyses. The two genes driven by a strong promoter 35S were integrated into Carrizo citrange via *Agrobacterium*-mediated transformation. More than two years of greenhouse testing indicated that *LasLYS2* provided substantial and long-lasting resistance to HLB, allowing transgenic plants to retain low *Ca*Las titers and no obvious symptoms while also clearing *Ca*Las from infected plants in the long term. *LasLYS2* transgenic plants with improved HLB resistance also showed resistance to *Xcc*, indicating that LasLYS2 had dual resistance to HLB and citrus canker. A microbiome study of transgenic plants revealed that the endolysins repressed Xanthomonadaceae and Rhizobiaceae populations in roots while increasing Burkholderiaceae and Rhodanobacteraceae populations, which might boost citrus defense response, according to transcriptome analysis. We also found that Lyz domain 2 is the key bactericidal motif of LasLYS1 and LasLYS2. Four endolysins with potential resistance to HLB and citrus canker were found based on the structures of LasLYS1 and LasLYS2. Overall, the work shed light on the mechanisms of resistance of *Ca*Las-derived endolysins, providing insights for designing endolysins to develop broad-spectrum disease resistance in citrus.
https://academic.oup.com/hr/advance-article/doi/10.1093/hr/uhad159/7239199

Mulaudzi P.E., Koorsen G., Mwaba I., Mahomed N.B., Allie F. (2023): **The identification of the methylation patterns of tomato curly stunt virus in resistant and susceptible tomato lines.** Frontiers in Plant Science | DOI: 10.3389/fpls.2023.1135442
Tomato curly stunt virus (ToCSV) is a monopartite begomovirus infecting tomatoes in South Africa, with sequence similarity to tomato yellow leaf curl virus (TYLCV). While there are numerous reports on the mechanism of TYLCV resistance in tomato, the underlying mechanisms in the tomato-ToCSV pathosystem is still relatively unknown. The main aim of this study was to investigate and compare the global methylation profile of ToCSV in two near-isogenic tomato lines, one with a tolerant phenotype (T, NIL396) and one with a susceptible phenotype (S, NIL395). Bisulfite conversion and PCR amplification, coupled with a next-generation sequencing approach, were used to elucidate the global pattern of methylation of ToCSV cytosine residues in T and S leave tissue at 35 days post-infection (dpi). The extent of methylation was more pronounced in tolerant plants compared to susceptible plants in all sequence (CG, CHG and CHH) contexts, however, the overall methylation levels were relatively low (<3%). Notably, a significant interaction ($p < 0.05$) was observed between the viral genomic region and susceptible vs. tolerant status for CG methylated regions where it was observed that the 3'IR CG methylation was significantly ($p < 0.05$) higher than CG methylation of other genomic regions in tolerant and susceptible plants. Additionally, statistically significant (EdgeR $p < 0.05$) differentially methylated cytosines were located primarily in the genomic regions V2/V1 and C4/C1 of ToCSV. The relative expression, using RT-qPCR, was also employed in order to quantify the expression of various key methylation-related genes, *MET1, CMT2, KYP4/SUVH4, DML2, RDM1, AGO4* and *AGO6* in T vs. S plants at 35dpi. The differential expression

between T and S was significant for *MET1, KYP4/SUVH4* and *RDM1* at p<0.05 which further supports more pronounced methylation observed in ToCSV from T plants vs. S plants. While this study provides new insights into the differences in methylation profiles of ToCSV in S vs. T tomato plants, further research is required to link tolerance and susceptibility to ToCSV.
https://www.frontiersin.org/articles/10.3389/fpls.2023.1135442/full

Daldoul S., Gargouri M., Weinert C., Jarrar A., Egert B., Mliki A., Nick P. (2023): **A Tunisian Wild Grape Leads to Metabolic Fingerprints of Salt Tolerance.** Plant Physiology 193, Issue 1, 371–388, https://doi.org/10.1093/plphys/kiad304
Soil salinity is progressively impacting agriculture, including viticulture. Identification of genetic factors rendering grapevine (*Vitis vinifera* L.) resilience that can be introgressed into commercial varieties is necessary for safeguarding viticulture against the consequences of global climate change. To gain insight into the physiological and metabolic responses enabling salt tolerance, we compared a salt-tolerant accession of *Vitis sylvestris* from Tunisia, "Tebaba", with "1103 Paulsen" rootstock widely used in the Mediterranean. Salt stress was slowly increased, simulating the situation of an irrigated vineyard. We determined that "Tebaba" does not sequester sodium in the root but can cope with salinity through robust redox homeostasis. This is linked with rechanneling of metabolic pathways toward antioxidants and compatible osmolytes, buffering photosynthesis, such that cell-wall breakdown can be avoided. We propose that salt tolerance of this wild grapevine cannot be attributed to a single genetic factor but emerges from favorable metabolic fluxes that are mutually supportive. We suggest that introgression of "Tebaba" into commercial varieties is preferred over the use of "Tebaba" as a rootstock for improving salt tolerance in grapevine.
https://academic.oup.com/plphys/article-abstract/193/1/371/7179314?redirectedFrom=fulltext&login=false

Tang Q., Wang X, Jin X., Peng J. et al. (2023): **CRISPR/Cas Technology Revolutionizes Crop Breeding.** Plants 12(17), 3119; | https://doi.org/10.3390/plants12173119
Crop breeding is an important global strategy to meet sustainable food demand. CRISPR/Cas is a most promising gene-editing technology for rapid and precise generation of novel germplasm and promoting the development of a series of new breeding techniques, which will certainly lead to the transformation of agricultural innovation. In this review, we summarize recent advances of CRISPR/Cas technology in gene function analyses and the generation of new germplasms with increased yield, improved product quality, and enhanced resistance to biotic and abiotic stress. We highlight their applications and breakthroughs in agriculture, including crop de novo domestication, decoupling the gene pleiotropy tradeoff, crop hybrid seed conventional production, hybrid rice asexual reproduction, and double haploid breeding; the continuous development and application of these technologies will undoubtedly usher in a new era for crop breeding. Moreover, the challenges and development of CRISPR/Cas technology in crops are also discussed.
https://www.mdpi.com/2223-7747/12/17/3119

Dadras, A., Fürst-Jansen, J.M.R., Darienko, T. et al. (2023): **Environmental gradients reveal stress hubs pre-dating plant terrestrialization.** Nat. Plants | https://doi.org/10.1038/s41477-023-01491-0
Plant terrestrialization brought forth the land plants (embryophytes). Embryophytes account for most of the biomass on land and evolved from streptophyte algae in a singular event. Recent advances have unravelled the first full genomes of the closest algal relatives of land plants; among the first such species was *Mesotaenium endlicherianum*. Here we used fine-combed RNA sequencing in tandem with a photophysiological assessment on *Mesotaenium* exposed to a continuous range of temperature and light cues. Our data establish a grid of 42 different conditions, resulting in 128 transcriptomes and ~1.5 Tbp (~9.9 billion reads) of data to study the combinatory effects of stress response using clustering along gradients. *Mesotaenium* shares with land plants major hubs in genetic networks underpinning stress response and acclimation. Our data suggest that lipid droplet formation and plastid and cell wall-derived signals have denominated molecular programmes since more than 600 million years of streptophyte evolution—before plants made their first steps on land.
https://www.nature.com/articles/s41477-023-01491-0

Kamble N.U., Makhamadnojov F., Fahy B., Martins C., Saalbach G., Seung D. (2023): **Initiation of B-type starch granules in wheat endosperm requires the plastidial α-glucan phosphorylase PHS1.** The Plant Cell, koad217, https://doi.org/10.1093/plcell/koad217
The plastidial α-glucan phosphorylase (PHS1) can elongate and degrade maltooligosaccharides (MOSs), but its exact physiological role in plants is poorly understood. Here, we discover a specialized role of PHS1 in establishing the unique bimodal characteristic of starch granules in wheat (*Triticum* spp.) endosperm. Wheat endosperm contains large A-type granules that initiate at early grain development, and small B-type granules that initiate in later grain development. We demonstrate that PHS1 interacts with B-GRANULE CONTENT1 (BGC1), a carbohydrate-binding protein essential for normal B-type granule initiation. Mutants of tetraploid durum wheat (*Triticum turgidum*) deficient in all homoeologs of PHS1 had normal A-type granules but fewer and larger B-type granules. Grain size and starch content were not affected by the mutations. Further, by assessing granule numbers during grain development in the *phs1* mutant and using a double mutant defective in both PHS1 and BGC1, we demonstrate that PHS1 is exclusively involved in B-type granule initiation. The total starch content and number of starch granules per chloroplast in leaves were not affected by loss of PHS1, suggesting that its role in granule initiation in wheat is limited to the endosperm. We therefore propose that

the initiation of A- and B-type granules occurs via distinct biochemical mechanisms, where PHS1 plays an exclusive role in B-type granule initiation.
https://academic.oup.com/plcell/advance-article/doi/10.1093/plcell/koad217/7246009

Bi M., Liang R., Wang J., Qu Y., Liu X. et al. (2023): **Multifaceted roles of LhWRKY44 in promoting anthocyanin accumulation in Asiatic hybrid lilies (*Lilium* spp.).** Horticulture Research, uhad167 | https://doi.org/10.1093/hr/uhad167
The Asiatic hybrid lily (*Lilium* spp.) is a horticultural crop with high commercial value and diverse anthocyanin pigmentation patterns. However, the regulatory mechanism underlying lily flower color has been largely unexplored. Here, we identified a WRKY TF from lily tepals, LhWRKY44, whose expression was closely associated with anthocyanin accumulation. Functional verification indicated that LhWRKY44 positively regulated anthocyanin accumulation. LhWRKY44 physically interacted with LhMYBSPLATTER and directly bound to the *LhMYBSPLATTER* promoter, which enhanced the effect of the LhMYBSPLATTER-LhbHLH2 MBW complex activator on anthocyanin accumulation. Moreover, EMSA and dual-luciferase assays revealed that LhWRKY44 activated and bound to the promoters of gene *LhF3H* and the intracellular anthocyanin-related glutathione S-transferase gene *LhGST*. Interestingly, our further results showed that LhWRKY44 participated in light and drought-induced anthocyanin accumulation, and improved the drought tolerance in lily via activating stress-related genes. These results generated a multifaceted regulatory mechanism for the LhWRKY44-meditaed enhancement by the environmental signal pathway of anthocyanin accumulation and expanded our understanding of the WRKY-mediated transcriptional regulatory hierarchy modulating anthocyanin accumulation in Asiatic hybrid lilies.
https://academic.oup.com/hr/advance-article/doi/10.1093/hr/uhad167/7247527?login=false

Hu, J., Sun, Y., Li, B. et al. (2023): **Strand-preferred base editing of organellar and nuclear genomes using CyDENT.** Nat Biotechnol | https://doi.org/10.1038/s41587-023-01910-9
Transcription-activator-like effector (TALE)-based tools for base editing of nuclear and organellar DNA rely on double-stranded DNA deaminases, which edit substrate bases on both strands of DNA, reducing editing precision. Here, we present CyDENT base editing, a CRISPR-free, strand-selective, modular base editor. CyDENT comprises a pair of TALEs fused with a FokI nickase, a single-strand-specific cytidine deaminase and an exonuclease to generate a single-stranded DNA substrate for deamination. We demonstrate effective base editing in nuclear, mitochondrial and chloroplast genomes. At certain mitochondrial sites, we show editing efficiencies of 14% and strand specificity of 95%. Furthermore, by exchanging the CyDENT deaminase with one that prefers editing GC motifs, we demonstrate up to 20% mitochondrial base editing at sites that are otherwise inaccessible to editing by other methods. The modular nature of CyDENT enables a suite of bespoke base editors for various applications.
https://www.nature.com/articles/s41587-023-01910-9

Guo, W.F., Guo, D.D.., Li, F. et al. (2023): **Efficient genome editing in cotton using the virus-mediated CRISPR/Cas9 and grafting system**. Plant Cell Rep |.
https://doi.org/10.1007/s00299-023-03061-2
The extensive application of CRISPR in cotton was limited due to the labor-intensive transformation process. Thus, we here established a convenient method of CRISPR in cotton by CLCrV-mediated sgRNA delivery.
https://link.springer.com/article/10.1007/s00299-023-03061-2

Tripodi P., Beretta M., Peltier P., Kalfas I. et al. (2023): **Pasquale Tripodi et al, Development and application of Single Primer Enrichment Technology (SPET) SNP assay for population genomics analysis and candidate gene discovery in lettuce.** Frontiers in Plant Science (2023). DOI: 10.3389/fpls.2023.1252777
Single primer enrichment technology (SPET) is a novel high-throughput genotyping method based on short-read sequencing of specific genomic regions harboring polymorphisms. SPET provides an efficient and reproducible method for genotyping target loci, overcoming the limits associated with other reduced representation library sequencing methods that are based on a random sampling of genomic loci. The possibility to sequence regions surrounding a target SNP allows the discovery of thousands of closely linked, novel SNPs. In this work, we report the design and application of the first SPET panel in lettuce, consisting of 41,547 probes spanning the whole genome and designed to target both coding (~96%) and intergenic (~4%) regions. A total of 81,531 SNPs were surveyed in 160 lettuce accessions originating from a total of 10 countries in Europe, America, and Asia and representing 10 horticultural types. Model ancestry population structure clearly separated the cultivated accessions (*Lactuca sativa*) from accessions of its presumed wild progenitor (*L. serriola*), revealing a total of six genetic subgroups that reflected a differentiation based on cultivar typology. Phylogenetic relationships and principal component analysis revealed a clustering of butterhead types and a general differentiation between germplasm originating from Western and Eastern Europe. To determine the potentiality of SPET for gene discovery, we performed genome-wide association analysis for main agricultural traits in *L. sativa* using six models (GLM naive, MLM, MLMM, CMLM, FarmCPU, and BLINK) to compare their strength and power for association detection. Robust associations were detected for seed color on chromosome 7 at 50 Mbp. Colocalization of association signals was found for outer leaf color and leaf anthocyanin content on chromosome 9 at 152 Mbp and on chromosome 5 at 86 Mbp. The association for bolting time was detected with the GLM, BLINK, and FarmCPU models on chromosome 7 at 164 Mbp. Associations were detected in chromosomal regions previously reported to harbor candidate genes for these traits, thus confirming the effectiveness of SPET for GWAS. Our findings illustrated the strength of SPET for discovering thousands of

variable sites toward the dissection of the genomic diversity of germplasm collections, thus allowing a better characterization of lettuce collections.
https://www.frontiersin.org/articles/10.3389/fpls.2023.1252777/full

Odom, A.R., Faits, T., Castro-Nallar, E. et al.(2023): **Metagenomic profiling pipelines improve taxonomic classification for 16S amplicon sequencing data.** Sci Rep 13, 13957 | https://doi.org/10.1038/s41598-023-40799-x
Most experiments studying bacterial microbiomes rely on the PCR amplification of all or part of the gene for the 16S rRNA subunit, which serves as a biomarker for identifying and quantifying the various taxa present in a microbiome sample. Several computational methods exist for analyzing 16S amplicon sequencing. However, the most-used bioinformatics tools cannot produce high quality genus-level or species-level taxonomic calls and may underestimate the potential accuracy of these calls. We used 16S sequencing data from mock bacterial communities to evaluate the sensitivity and specificity of several bioinformatics pipelines and genomic reference libraries used for microbiome analyses, concentrating on measuring the accuracy of species-level taxonomic assignments of 16S amplicon reads. We evaluated the tools DADA2, QIIME 2, Mothur, PathoScope 2, and Kraken 2 in conjunction with reference libraries from Greengenes, SILVA, Kraken 2, and RefSeq. Profiling tools were compared using publicly available mock community data from several sources, comprising 136 samples with varied species richness and evenness, several different amplified regions within the 16S rRNA gene, and both DNA spike-ins and cDNA from collections of plated cells. PathoScope 2 and Kraken 2, both tools designed for whole-genome metagenomics, outperformed DADA2, QIIME 2 using the DADA2 plugin, and Mothur, which are theoretically specialized for 16S analyses. Evaluations of reference libraries identified the SILVA and RefSeq/Kraken 2 Standard libraries as superior in accuracy compared to Greengenes. These findings support PathoScope and Kraken 2 as fully capable, competitive options for genus- and species-level 16S amplicon sequencing data analysis, whole genome sequencing, and metagenomics data tools.
https://www.nature.com/articles/s41598-023-40799-x

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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