

Sunday Evening News No 339

2023-08-14. – 2023-08-20

Compiled and edited by **BGF** Jany



Meetings - Veranstaltungen

BMBF: **Chancen-Talk „Neue Züchtungstechniken“**

am 25. August 2023 um 10:00 Uhr

unter www.bmbf.de/livestream

https://www.bmbf.de/bmbf/shareddocs/veranstaltungen/2023/chancentalk_nzt/chancentalk-nzt.html

Press Releases -Media / Presse- und Medienberichte

biowisskomm: **Öko-Gentechnik: die amerikanische Kastanie**

https://www.biowisskomm.de/2023/08/oeko-gentechnik-die-amerikanische-kastanie/?fbclid=IwAR2Qob07ZsCtPb-iw3rPSeWpLjvErMPH532Tlp4dD7Y3U_ex5Y17vQxpLFE

Miller H.I., Altman D.W.: **Regulation of Molecular Genetic Engineering Must Be Evidence-Based**

<https://www.acsh.org/news/2023/08/17/regulation-molecular-genetic-engineering-must-be-evidence-based-17180>

Miller H.I., Wager R.: **Greenpeace's Vile War on the Poor and Vulnerable**

<https://www.europeanscientist.com/en/features/greenpeaces-vile-war-on-the-poor-and-vulnerable/>

Lights Z.: **The European Union Is Finally Coming Around to Gene-Edited Seeds**

<https://quillette.com/2023/08/14/gene-editing-saves-lives-so-why-are-western-activists-opposing-it/>

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 week 33

Publications – Publikationen

Finger, R., Möhring, N. & Kudsk, P. (2023): **Glyphosate ban will have economic impacts on European agriculture but effects are heterogenous and uncertain.** Commun Earth Environ 4, 286 | <https://doi.org/10.1038/s43247-023-00951-x>

Glyphosate is the most widely used pesticide in Europe. However, due to its potential effects on human health, its renewal is currently under discussion in European policy. Here, we synthesize the existing evidence on potential farm-level economic impacts of a potential glyphosate ban in European agriculture using a literature review. We identified 19 studies published until 2022. We find that where glyphosate is currently used (30% and 50% of the acreage with annual and perennial tree crops respectively), such a ban can have large economic impacts. However, the range of impacts reported in the literature is substantial. Economic losses arising from a glyphosate ban estimated in peer reviewed studies range from 3 Euro/hectare in silage maize to up to 553 Euro/hectare in grapevine production. While potential losses are largest, in absolute terms (in Euro/hectare), for high-value perennial crops such as fruits and grapevines losses are similar in perennial and arable crops if expressed in relative terms (i.e. in % of per hectare profits). We currently lack assessments of economic implications of a glyphosate ban for most countries and farming systems. Thus, the overall economic implications at the European level are largely unknown.

<https://www.nature.com/articles/s43247-023-00951-x>

Shahzaib, M.; Bruegmann, T.; Shakeel, M.; Khan, S.H.; Azhar, M.T.; Atif, R.M.; Fladung, M.; Rana, I.A. (2023): **Development of Climate Smart Fruit Plants via CRISPR/Cas Genome Editing Systems: A Spatiotemporal Review.** Preprints, 2023051887 |

<https://doi.org/10.20944/preprints202305.1887.v1>

Fruit production is an important part of the gross domestic product for many countries around the world especially to those who have a strong focus on agriculture. However, long-term maintenance and yield stability of fruit production may be threatened by the ongoing climate change and its consequences like extended drought periods, heavy rain events, and floodings. Genome editing, with its progressive technological developments, offers opportunities to adapt relevant fruit plant species to new climatic conditions. Among modern genome editing techniques, CRISPR/Cas, in particular, has the potential to support breeding for those fruit plant species with extended breeding cycles, e.g., perennial fruits. In this review, we discuss CRISPR/Cas and other genome editing techniques in detail and how these techniques can be applied to support the breeding of fruit plant species for adaptation to changing climates. The chronological history of CRISPR/Cas9 systems, their associated computational tools, genomic data sources, transformation methods along with their

delivery vehicles, quality improvement, environmental-stress resiliency, limitations, and future perspectives will also be discussed with respect to securing future global fruit production.

<https://www.preprints.org/manuscript/202305.1887/v1>
https://literatur.thuenen.de/digbib_extern/dn066640.pdf

Ahmed, H.I., Heuberger, M., Schoen, A. et al. (2023): **Einkorn genomics sheds light on history of the oldest domesticated wheat.** Nature | <https://doi.org/10.1038/s41586-023-06389-7>

Einkorn (*Triticum monococcum*) was the first domesticated wheat species, and was central to the birth of agriculture and the Neolithic Revolution in the Fertile Crescent around 10,000 years ago^{1,2}. Here we generate and analyse 5.2-Gb genome assemblies for wild and domesticated einkorn, including completely assembled centromeres. Einkorn centromeres are highly dynamic, showing evidence of ancient and recent centromere shifts caused by structural rearrangements. Whole-genome sequencing analysis of a diversity panel uncovered the population structure and evolutionary history of einkorn, revealing complex patterns of hybridizations and introgressions after the dispersal of domesticated einkorn from the Fertile Crescent. We also show that around 1% of the modern bread wheat (*Triticum aestivum*) A subgenome originates from einkorn. These resources and findings highlight the history of einkorn evolution and provide a basis to accelerate the genomics-assisted improvement of einkorn and bread wheat.

<https://www.nature.com/articles/s41586-023-06389-7>

Koralesky KE, Sirovica LV, Hendricks J, Mills KE, von Keyserlingk MAG, Weary DM (2023): **Social acceptance of genetic engineering technology.** PLoS ONE 18(8): e0290070.

<https://doi.org/10.1371/journal.pone.0290070>

Genetic engineering of animals has been proposed to address societal problems, but public acceptance of the use of this technology is unclear. Previous work has shown that the source of information proposing the technology (e.g. companies, universities), the term used to describe the technology (e.g. genome editing, genetic modification), and the genetic engineering application (e.g. different food products) affects technology acceptance. We conducted three mixed-method surveys and used a causal trust-acceptability model to understand social acceptance of genetic engineering (GE) by investigating 1) the source of information proposing the technology, 2) the term used to describe the technology, and 3) the GE application for farm animals proposed. Further, participants expressed their understanding of technology using a range of terms interchangeably, all describing technology used to change an organism's DNA. We used structural equation modelling and confirmed model fit for each survey. In each survey, perceptions of benefit had the greatest effect on acceptance. Following our hypothesized model, social trust had an indirect influence on acceptance through similar effects of perceived benefit and perceived risk. Additional quantitative analysis showed that the source of information and technology term had little to no effect on acceptance. Applications involving animals were perceived as less beneficial than a plant application, and an application for increased cattle muscle growth was perceived as more risky than a plant application. When assessing the acceptability of applications participants considered impacts on plants, animals, and people, trust in actors and technologies, and weighed benefits and drawbacks of GE. Future work should consider how to best measure acceptability of GE for animals, consider contextual factors and consider the use of inductive frameworks.

<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0290070>

Mérel P, Qin Z., Sexton R.J. (2023): **Policy-induced expansion of organic farmland: implications for food prices and welfare.** European Review of Agricultural Economics, jbad024 | <https://doi.org/10.1093/erae/jbad024>

Public policies increasingly support the expansion of organic agriculture as part of a menu of food and environmental initiatives. A little-studied yet crucial element of such expansion, especially in light of scientific evidence on lower yields of organic crops, is its impact on overall food production and food prices, especially for poorer households. In this paper, we first establish a positive empirical relationship between countries' propensity to produce and consume organic foods and their per-capita income. Such correlation suggests that, even if rich countries' consumers can benefit from an increase in the organic farmland share, poor countries' consumers would likely face higher conventional food prices. We then develop and calibrate a model of world food demand and supply to assess the implications of a policy-driven expansion in organic farmland. Our results for four major grains and oilseeds show that raising the organic cropland share in rich countries from 3 to 15 per cent increases food prices in poor countries by up to 6.3 per cent, with central values of 1.2–2.5 per cent, and a commensurate reduction in consumer welfare. Model parameterisations indicate that farmers in poor countries benefit from higher crop prices, while consumers in rich countries are largely unaffected and sometimes benefit. In all cases, poor countries' consumers bear most of the distortion burden. In our preferred parameterisation, a 3 per cent increase in cropland in rich countries is needed to offset the food price increase in poor countries.

<https://academic.oup.com/erae/advance-article-abstract/doi/10.1093/erae/jbad024/7235643?redirectedFrom=fulltext&login=false>

Fawcett, J.A., Takeshima, R., Kikuchi, S. et al. (2023): **Genome sequencing reveals the genetic architecture of heterostyly and domestication history of common buckwheat.** Nat. Plants 9, 1236–1251 | <https://doi.org/10.1038/s41477-023-01474-1>

Common buckwheat, *Fagopyrum esculentum*, is an orphan crop domesticated in southwest China that exhibits heterostylous self-incompatibility. Here we present chromosome-scale assemblies of a self-compatible *F. esculentum* accession and a self-compatible wild relative, *Fagopyrum homotropicum*, together with the

resequencing of 104 wild and cultivated *F. esculentum* accessions. Using these genomic data, we report the roles of transposable elements and whole-genome duplications in the evolution of *Fagopyrum*. In addition, we show that (1) the breakdown of heterostyly occurs through the disruption of a hemizygous gene jointly regulating the style length and female compatibility and (2) southeast Tibet was involved in common buckwheat domestication. Moreover, we obtained mutants conferring the waxy phenotype for the first time in buckwheat. These findings demonstrate the utility of our *F. esculentum* assembly as a reference genome and promise to accelerate buckwheat research and breeding.
<https://www.nature.com/articles/s41477-023-01474-1>

Castellari M.P., Simsek S., Ohm J.-B., Perry R. et al. (2023): **Genetic Variation and Heritability of Sensory and Artisan Bread Traits in a Set of SRW Wheat Breeding Lines.** *Foods* 12 (13), 2617 | <https://doi.org/10.3390/foods12132617>

Focus on local food production and supply chains has heightened in recent years, as evidenced and amplified by the COVID-19 pandemic. This study aimed to assess the suitability of soft red winter (SRW) wheat breeding lines for local artisan bakers interested in locally sourced, strong gluten wheat for bread. Seventy-six genotyped SRW wheat breeding lines were milled into whole wheat flour and baked into small loaves. Bread aroma, flavor, and texture were evaluated by a sensory panel, and bread quality traits, including sedimentation volume, dough extensibility, and loaf volume, were measured to estimate heritability. SE-HPLC was performed on white flour, and breeding lines were characterized for different protein fraction ratios. Heritability of loaf volume was moderately high ($h^2 = 0.68$), while heritability of sedimentation volume, a much easier trait to measure, was slightly lower ($h^2 = 0.55$). Certain protein fraction ratios strongly related to loaf volume had high heritability ($h^2 = 0.7$). Even though only a moderate heritability estimate of dough extensibility was found in our study, high positive correlations were found between this parameter and sedimentation volume ($r = 0.6$) and loaf volume ($r = 0.53$). This low-input and highly repeatable parameter could be useful to estimate dough functionality characteristics. Flavor and texture heritability estimates ranged from 0.16 to 0.37, and the heritability estimate of aroma was not significantly different from zero. However, the sensorial characteristics were significantly correlated with each other, suggesting that we might be able to select indirectly for aroma by selecting for flavor or texture characteristics. From a genome-wide association study (GWAS), we identified six SNPs (single nucleotide polymorphisms) associated with loaf volume that could be useful in breeding for this trait. Producing high-quality strong gluten flour in our high rainfall environment is a challenge, but it provides local growers and end users with a value-added opportunity.
<https://www.mdpi.com/2304-8158/12/13/2617>

Kong X., Wang F., Wang Z., Gao X. et al. (2023): **Grain yield improvement by genome editing of *TaARF12* that decoupled peduncle and rachis development trajectories via differential regulation of gibberellin signalling in wheat.** *Plant Biotechnol. J.* | <https://doi.org/10.1111/pbi.14107>

Plant breeding is constrained by trade-offs among different agronomic traits by the pleiotropic nature of many genes. Genes that contribute to two or more favourable traits with no penalty on yield are rarely reported, especially in wheat. Here, we describe the editing of a wheat auxin response factor *TaARF12* by using CRISPR/Cas9 that rendered shorter plant height with larger spikes. Changes in plant architecture enhanced grain number per spike up to 14.7% with significantly higher thousand-grain weight and up to 11.1% of yield increase under field trials. Weighted Gene Co-Expression Network Analysis (WGCNA) of spatial-temporal transcriptome profiles revealed two hub genes: *RhtL1*, a DELLA domain-free *Rht-1* paralog, which was up-regulated in peduncle, and *TaNGR5*, an organ size regulator that was up-regulated in rachis, in *taarf12* plants. The up-regulation of *RhtL1* in peduncle suggested the repression of GA signalling, whereas up-regulation of *TaNGR5* in spike may promote GA response, a working model supported by differential expression patterns of GA biogenesis genes in the two tissues. Thus, *TaARF12* complemented plant height reduction with larger spikes that gave higher grain yield. Manipulation of *TaARF12* may represent a new strategy in trait pyramiding for yield improvement in wheat.
<https://onlinelibrary.wiley.com/doi/10.1111/pbi.14107>

Djalovic I., Kundu S., Bahuguna R.N., Pareek A. et al. (2023): **Maize and heat stress: Physiological, genetic, and molecular insights.** *The Plant Genome*, 00, e20378. | <https://doi.org/10.1002/tpg2.20378>

Global mean temperature is increasing at a rapid pace due to the rapid emission of greenhouse gases majorly from anthropogenic practices and predicted to rise up to 1.5°C above the pre-industrial level by the year 2050. The warming climate is affecting global crop production by altering biochemical, physiological, and metabolic processes resulting in poor growth, development, and reduced yield. Maize is susceptible to heat stress, particularly at the reproductive and early grain filling stages. Interestingly, heat stress impact on crops is closely regulated by associated environmental covariables such as humidity, vapor pressure deficit, soil moisture content, and solar radiation. Therefore, heat stress tolerance is considered as a complex trait, which requires multiple levels of regulations in plants. Exploring genetic diversity from landraces and wild accessions of maize is a promising approach to identify novel donors, traits, quantitative trait loci (QTLs), and genes, which can be introgressed into the elite cultivars. Indeed, genome wide association studies (GWAS) for mining of potential QTL(s) and dominant gene(s) is a major route of crop improvement. Conversely, mutation breeding is being utilized for generating variation in existing populations with narrow genetic background. Besides breeding approaches, augmented production of heat shock factors (HSFs) and heat shock proteins (HSPs) have been

reported in transgenic maize to provide heat stress tolerance. Recent advancements in molecular techniques including clustered regularly interspaced short palindromic repeats (CRISPR) would expedite the process for developing thermotolerant maize genotypes.

<https://access.onlinelibrary.wiley.com/doi/full/10.1002/tpg2.20378>

Anwar, W., Amin, H., Khan, H.A.A. et al. (2023): **Chitinase of *Trichoderma longibrachiatum* for control of *Aphis gossypii* in cotton plants.** *Sci Rep* 13, 13181 |

<https://doi.org/10.1038/s41598-023-39965-y>

Chitinase-producing fungi have now engrossed attention as one of the potential agents for the control of insect pests. Entomopathogenic fungi are used in different regions of the world to control economically important insects. However, the role of fungal chitinases are not well studied in their infection mechanism to insects. In this study, Chitinase of entomopathogenic fungi *Trichoderma longibrachiatum* was evaluated to control *Aphis gossypii*. For this purpose, fungal chitinase (*Chit1*) gene from the genomic DNA of *T. longibrachiatum* were isolated, amplified and characterised. Genomic analysis of the amplified *Chit1* showed that this gene has homology to family 18 of glycosyl hydrolases. Further, *Chit1* was expressed in the cotton plant for transient expression through the Geminivirus-mediated gene silencing vector derived from Cotton Leaf Crumple Virus (CLCrV). Transformed cotton plants showed greater chitinase activity than control, and they were resistant against nymphs and adults of *A. gossypii*. About 38.75% and 21.67% mortality of both nymphs and adults, respectively, were observed by using *Chit1* of *T. longibrachiatum*. It is concluded that *T. longibrachiatum* showed promising results in controlling aphids by producing fungal chitinase in cotton plants and could be used as an effective method in the future.

<https://www.nature.com/articles/s41598-023-39965-y>

Wagh K., Stavreva D.A., Jensen R.A.M., Paakinaho V. et al. (2023): **Dynamic switching of transcriptional regulators between two distinct low-mobility chromatin states.** *Science Advances* 9 (24) |

[DOI: 10.1126/sciadv.ade1122](https://doi.org/10.1126/sciadv.ade1122)

How chromatin dynamics relate to transcriptional activity remains poorly understood. Using single-molecule tracking, coupled with machine learning, we show that histone H2B and multiple chromatin-bound transcriptional regulators display two distinct low-mobility states. Ligand activation results in a marked increase in the propensity of steroid receptors to bind in the lowest-mobility state. Mutational analysis revealed that interactions with chromatin in the lowest-mobility state require an intact DNA binding domain and oligomerization domains. These states are not spatially separated as previously believed, but individual H2B and bound-TF molecules can dynamically switch between them on time scales of seconds. Single bound-TF molecules with different mobilities exhibit different dwell time distributions, suggesting that the mobility of TFs is intimately coupled with their binding dynamics. Together, our results identify two unique and distinct low-mobility states that appear to represent common pathways for transcription activation in mammalian cells.

<https://www.science.org/doi/10.1126/sciadv.ade1122>

Connolley, L., Schnabel, L., Thanbichler, M. et al. (2023): **Partition complex structure can arise from sliding and bridging of ParB dimers.** *Nat Commun* 14, 4567 (2023). <https://doi.org/10.1038/s41467-023-40320-y>

In many bacteria, chromosome segregation requires the association of ParB to the *parS*-containing centromeric region to form the partition complex. However, the structure and formation of this complex have been unclear. Recently, studies have revealed that CTP binding enables ParB dimers to slide along DNA and condense the centromeric region through the formation of DNA bridges. Using semi-flexible polymer simulations, we demonstrate that these properties can explain partition complex formation. Transient ParB bridges organize DNA into globular states or hairpins and helical structures, depending on bridge lifetime, while separate simulations show that ParB sliding reproduces the multi-peaked binding profile observed in *Caulobacter crescentus*. Combining sliding and bridging into a unified model, we find that short-lived ParB bridges do not impede sliding and can reproduce both the binding profile and condensation of the nucleoprotein complex. Overall, our model elucidates the mechanism of partition complex formation and predicts its fine structure.

<https://www.nature.com/articles/s41467-023-40320-y>

Tantoso, E., Eisenhaber, B., Sinha, S. et al. (2023): **Did the early full genome sequencing of yeast boost gene function discovery?** *Biol Direct* 18, 46 |

<https://doi.org/10.1186/s13062-023-00403-8>

Background: Although the genome of *Saccharomyces cerevisiae* (*S. cerevisiae*) was the first one of a eukaryote organism that was fully sequenced (in 1996), a complete understanding of the potential of encoded biomolecular mechanisms has not yet been achieved. Here, we wish to quantify how far the goal of a full list of *S. cerevisiae* gene functions still is.

Results: The scientific literature about *S. cerevisiae* protein-coding genes has been mapped onto the yeast genome via the mentioning of names for genomic regions in scientific publications. The match was quantified with the ratio of a given gene name's occurrences to those of any gene names in the article. We find that ~ 230 elite genes with ≥ 75 full publication equivalents (FPEs, FPE = 1 is an idealized publication referring to just a single gene) command ~ 45% of all literature. At the same time, about two thirds of the genes (each with less than 10 FPEs) are described in just 12% of the literature (in average each such gene has just ~ 1.5% of the literature of an elite gene). About 600 genes have not been mentioned in any dedicated article. Compared with other groups of genes, the literature growth rates were highest for uncharacterized or understudied genes until late nineties of the twentieth century. Yet, these growth rates deteriorated and became negative

thereafter. Thus, yeast function discovery for previously uncharacterized genes has returned to the level of ~ 1980. At the same time, literature for anyhow well-studied genes (with a threshold T10 (≥ 10 FPEs) and higher) remains steadily growing.

Conclusions: Did the early full genome sequencing of yeast boost gene function discovery? The data proves that the moment of publishing the full genome in reality coincides with the onset of decline of gene function discovery for previously uncharacterized genes. If the current status of literature about yeast molecular mechanisms can be extrapolated into the future, it will take about another ~ 50 years to complete the yeast gene function list. We found that a small group of scientific journals contributed extraordinarily to publishing early reports relevant to yeast gene function discoveries

<https://biologydirect.biomedcentral.com/articles/10.1186/s13062-023-00403-8>

Burgaya J., Marin J., Royer G., Condamine B., Gachet B., Clermont O. et al. (2023): **The bacterial genetic determinants of Escherichia coli capacity to cause bloodstream infections in humans.** PLoS Genet 19(8): e1010842. <https://doi.org/10.1371/journal.pgen.101084>

Escherichia coli is both a highly prevalent commensal and a major opportunistic pathogen causing bloodstream infections (BSI). A systematic analysis characterizing the genomic determinants of extra-intestinal pathogenic vs. commensal isolates in human populations, which could inform mechanisms of pathogenesis, diagnostic, prevention and treatment is still lacking. We used a collection of 912 BSI and 370 commensal *E. coli* isolates collected in France over a 17-year period (2000–2017). We compared their pangenomes, genetic backgrounds (phylogroups, STs, O groups), presence of virulence-associated genes (VAGs) and antimicrobial resistance genes, finding significant differences in all comparisons between commensal and BSI isolates. A machine learning linear model trained on all the genetic variants derived from the pangenome and controlling for population structure reveals similar differences in VAGs, discovers new variants associated with pathogenicity (capacity to cause BSI), and accurately classifies BSI vs. commensal strains. Pathogenicity is a highly heritable trait, with up to 69% of the variance explained by bacterial genetic variants. Lastly, complementing our commensal collection with an older collection from 1980, we predict that pathogenicity continuously increased through 1980, 2000, to 2010. Together our findings imply that *E. coli* exhibit substantial genetic variation contributing to the transition between commensalism and pathogenicity and that this species evolved towards higher pathogenicity.

<https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1010842>

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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