

Sunday Evening News No 321

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Compiled and edited by **BGF** Jany



Prof. Dr. Klaus Ammann ist von uns gegangen Er verstarb am 12. April 2023. Wir haben einen hervorragenden Wissenschaftler, einen optimistischen Streiter für die Grüne Gentechnik und einen Freund verloren. Wir werden seinen wissenschaftlichen Rat und seine liebenswerte und humorvolle Art vermissen.

Prof. Dr. Klaus Ammann has passed away on April 12, 2023. We have lost an outstanding scientist, an optimistic campaigner for green genetic engineering and a friend. We will miss his scientific advice and his kind and humorous manner.

Press Releases -Media / Presse- und Medienberichte

BR: **Gen-Schere als Lösung für unsere Felder? Es gibt eine große Sorge**

https://www.focus.de/klima/report/hitze-duerre-trockenheit-unser-land-gruene-gentechnik_id_189664505.html

Swaton S.: **Österreich macht gegen EU-Pläne zu Gentechnik mobil**

<https://www.euractiv.de/section/europa-kompakt/news/oesterreich-macht-gegen-eu-plaene-zu-gentechnik-mobil/>

Austria wants food labelling transparency amid likely gene editing deregulation

https://www.euractiv.com/section/politics/news/austria-wants-food-labelling-transparency-amid-likely-gene-editing-deregulation/?_ga=2.6803186.17286851.1680792628-946518938.1680792628

Willard M.: **GMO Deregulation Delayed – Where Are We At, Where Might We Be Going?**

On March 31st, DG SANTE confirmed that the Commission’s proposal on GMO deregulation, as well as the proposal on seed marketing, will be postponed. Originally scheduled for June 7th, it will not be presented before the second half of June or later in July.

<https://www.arc2020.eu/gmo-deregulation-delayed-where-are-we-at-where-might-we-be-going/>

Testbiotech: **New GE: Risks of unintended genetic changes are ‘overlooked’**

EU Commission discussion paper leaked

<https://www.testbiotech.org/en/news/new-ge-risks-unintended-genetic-changes-are-overlooked>

Leaked paper: https://www.testbiotech.org/sites/default/files/NGT_Potential%20Criteria.pdf

infogm: **GMO: the Commission is losing supports**

<https://www.infogm.org/7720-gmo-european-commission-is-losing-supports>

Tagliabue G.M.: **“Genetically Modified Organisms”, “Contamination” and “Coexistence”**

Against the misuse of concepts and the related wrongheaded regulation in the agri-food system

<https://www.europeanscientist.com/en/features/genetically-modified-organisms-contamination-and-coexistence-against-the-misuse-of-concepts-and-the-related-wrongheaded-regulation-in-the-agri-food-system/>

With a dedication: *For Professor Klaus Ammann, who very recently passed away: committed scientist, great communicator; a man of true integrity and a dear friend.*

Carter C., Miller H.: **Viewpoint: GMO crops are key to sustainable farming—why are some scientists afraid to talk about them?**

<https://geneticliteracyproject.org/2023/04/14/viewpoint-gmo-crops-are-key-to-sustainable-farming-why-are-some-scientists-afraid-to-talk-about-them/>

Miller H.J.: **Norman Borlaug, 'Father of the Green Revolution,' Was Remarkable in Many Ways**

<https://www.acsh.org/news/2023/04/06/norman-borlaug-father-green-revolution-was-remarkable-many-ways-16974>

Celebrating Norman Borlaug: He Was Always Ahead Of His Time

<https://henrymillermd.org/26862/celebrating-norman-borlaug-he-was-always-ahead>

Informationsdienst Gentechnik: **Neue Freilandversuche mit Crispr-Pflanzen in der EU**
<https://www.keine-gentechnik.de/nachricht/34755?cHash=1f3a3a1e1ce34b037f472e972f0a2ce6>

Jaeger K.: **Trump Suggests ‘Genetically Engineered’ Marijuana May Be Causing Mass Shootings**
<https://www.marijuanamoment.net/trump-suggests-genetically-engineered-marijuana-may-be-causing-mass-shootings/>

Slisco A.: **Everything Trump Said About Mass Shootings in NRA Speech**
<https://www.newsweek.com/everything-trump-said-about-mass-shootings-nra-speech-1794538>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): April week 14 and 15

Publications – Publikationen

Callaway E. (2023): **Wheat disease’s global spread concerns researchers**
Genomic analysis reveals that the wheat blast fungus spread independently from South America to two other continents.
<https://www.nature.com/articles/d41586-023-01043-8>

Wang J., Wu X., Wang Y., Wang B. et al. (2023): **Genome-wide characterization and expression analysis of the *MLO* gene family sheds light on powdery mildew resistance in *Lagenaria siceraria***. Heliyon 9 (4), e14624 | <https://doi.org/10.1016/j.heliyon.2023.e14624>
MLO (mildew locus O) genes play a vital role in plant disease defense system, especially powdery mildew (PM). *Lagenaria siceraria* is a distinct Cucurbitaceae crop, and PM is one of the most serious diseases threatening crop production and quality. Although *MLOs* have been exploited in many Cucurbitaceae species, genome-wide mining of *MLO* gene family in bottle gourd has not been surveyed yet. Here we identified 16 *MLO* genes in our recently assembled *L. siceraria* genome. A total of 343 unique *MLO* protein sequences from 20 species were characterized and compared to deduce a generally high level of purifying selection and the occurrence of regions related to candidate susceptibility factors in the evolutionary divergence. *LsMLOs* were clustered in six clades containing seven conserved transmembrane domains and 10 clade-specific motifs along with deletion and variation. Three genes (*LsMLO3*, *LsMLO6*, and *LsMLO13*) in clade V showed high sequence identity with orthologues involved in PM susceptibility. The expression pattern of *LsMLOs* was tissue-specific but not cultivar-specific. Furthermore, it was indicated by qRT-PCR and RNA-seq that *LsMLO3* and *LsMLO13* were highly upregulated in response to PM stress. Subsequent sequence analysis revealed the structural deletion of *LsMLO13* and a single nonsynonymous substitution of *LsMLO3* in the PM-resistant genotype. Taken all together, it is speculated that *LsMLO13* is likely a major PM susceptibility factor. The results of this study provide new insights into *MLO* family genes in bottle gourd and find a potential candidate S gene for PM tolerance breeding.
<https://www.sciencedirect.com/science/article/pii/S2405844023018315>

Ceasar S.A. and Ignacimuthu S. (2023): **CRISPR/Cas genome editing in plants: Dawn of *Agrobacterium* transformation for recalcitrant and transgene-free plants for future crop breeding**. Plant Physiology and Biochemistry 196, 724-730 | <https://doi.org/10.1016/j.plaphy.2023.02.030>
Genome editing tools based on CRISPR/Cas system have been posed to solve many issues in agriculture and improve food production. Genetic engineering by *Agrobacterium*-mediated transformation has helped to impart specific traits straightaway in many crops. Many GM crops have also reached the field for commercial cultivation. Genetic engineering requires mostly a transformation protocol often mediated by *Agrobacterium* to insert a specific gene at a random locus. Genome editing with CRISPR/Cas system is a more precise technique for the targeted modification of genes/bases in the host plant genome. Unlike the conventional transformation system, wherein elimination of marker/foreign gene was possible only post-transformation, CRISPR/Cas system could generate transgene-free plants by delivering CRISPR/Cas reagents such as the Cas protein and guide RNAs gRNA(s) preassembled to form ribonucleoproteins (RNPs) into plant cells. CRISPR reagent delivery might be helpful to overcome issues with plants that are recalcitrant to *Agrobacterium* transformation and the legal hurdles due to the presence of the foreign gene. More recently, the grafting of wild-type shoots to transgenic donor rootstocks developed by the CRISPR/Cas system has reported transgene-free genome editing. CRISPR/Cas system also requires only a small piece of gRNA besides Cas9 or other effectors to target a specific region in the genome. So this system has been projected to be a key contributor to future crop breeding. In this article, we recap the main events of plant transformation, compare the difference between genetic transformation and CRISPR/Cas-mediated genome editing, and draw insights into the future application of the CRISPR/Cas system.
<https://www.sciencedirect.com/science/article/abs/pii/S0981942823001055>

Calabrese, C., Albarracín, D. (2023): **Bypassing misinformation without confrontation improves policy support as much as correcting it.** *Sci Rep* 13, 6005 |

<https://doi.org/10.1038/s41598-023-33299-5>

Curbing the negative impact of misinformation is typically assumed to require correcting misconceptions. Conceivably, however, bypassing the misinformation through alternate beliefs of opposite implications may reduce the attitudinal impact of the misinformation. Three experiments, one preregistered with a sample representative of the United States population, examined the impact of (a) directly correcting prior misinformation offered in support of restricting Genetically Modified (GM) foods (i.e., the correction strategy) and (b) discussing information in support of GM foods (i.e., the bypassing strategy), compared to a misinformation-only control condition. Findings consistently revealed that bolstering beliefs with opposite implications is just as effective at reducing opposition to GM foods as is correcting misinformation about GM foods. Thus, bypassing should be added to our arsenal of methods to curb the impact of misinformation.

<https://www.nature.com/articles/s41598-023-33299-5>

Akbari M., Ardekani Z.F. Pino G., Valizadeh N., Karbasioun M., Padash H. (2023): **Consumer Attitude towards Genetically Modified Foods in Iran: Application of Three-Dimensional Model of Corporate Social Responsibility.** *Foods* 12(7), 1553 |

<https://doi.org/10.3390/foods12071553>

Although GM food production is considered an important strategy to meet the growing food needs of the population around the world, a majority of the GM food consumers express doubts about purchasing and eating them. However, it can be argued that consumers have different opinions about GM foods and their influence on human health and the natural environment. GM food producer Corporate Social Responsibility (CSR) may significantly affect such opinions, but the effect of this variable has been partially neglected in previous research studies. To address this gap, the present study investigates Iranian consumers' concerns about GM foods, trust in these products, and perception of GM food producer CSR as determinants of attitudes towards GM food. Data were collected from Iranian consumers. A cross-sectional survey research with a multi-stage random sampling approach was employed to capture the responses of 372 Iranian consumers. The results showed that consumers have both negative and positive attitudes towards GM foods. Perceived social equity, trust, and health concerns were the most important determinants of attitude towards GM foods. According to the results, these variables could account for 52.9% (Cox and Snell R^2) and up to 70.6% (Nagelkerke R^2) of the variance of the dependent variable. Furthermore, results revealed statistically significant differences among the consumers with different educational levels in terms of perceived social equity, perceived environmental responsibility, and environmental concern. The research contributes to the body of knowledge in GM food consumption by evolving the CSR to assess attitudes of users concerning GM foods.

<https://www.mdpi.com/2304-8158/12/7/1553>

Kawamata, M., Suzuki, H.I., Kimura, R. et al. (2023): **Optimization of Cas9 activity through the addition of cytosine extensions to single-guide RNAs.** *Nat. Biomed. Eng* |

<https://doi.org/10.1038/s41551-023-01011-7>

The precise regulation of the activity of Cas9 is crucial for safe and efficient editing. Here we show that the genome-editing activity of Cas9 can be constrained by the addition of cytosine stretches to the 5'-end of conventional single-guide RNAs (sgRNAs). Such a 'safeguard sgRNA' strategy, which is compatible with Cas12a and with systems for gene activation and interference via CRISPR (clustered regularly interspaced short palindromic repeats), leads to the length-dependent inhibition of the formation of functional Cas9 complexes. Short cytosine extensions reduced p53 activation and cytotoxicity in human pluripotent stem cells, and enhanced homology-directed repair while maintaining bi-allelic editing. Longer extensions further decreased on-target activity yet improved the specificity and precision of mono-allelic editing. By monitoring indels through a fluorescence-based allele-specific system and computational simulations, we identified optimal windows of Cas9 activity for a number of genome-editing applications, including bi-allelic and mono-allelic editing, and the generation and correction of disease-associated single-nucleotide substitutions via homology-directed repair. The safeguard-sgRNA strategy may improve the safety and applicability of genome editing.

<https://www.nature.com/articles/s41551-023-01011-7>

Catoi E.A., Phaneuf P., Monk, J., and Palsson B.O. (2023): **Whole-genome sequences from wild-type and laboratory-evolved strains define the alleloome and establish its hallmarks.** *PNAS* 120 (15) e2218835120 |

<https://doi.org/10.1073/pnas.2218835120>

The genomic diversity across strains of a species forms the genetic basis for differences in their behavior. A large-scale assessment of sequence variation has been made possible by the growing availability of strain-specific whole-genome sequences (WGS) and with the advent of large-scale databases of laboratory-acquired mutations. We define the *Escherichia coli* "alleloome" through a genome-scale assessment of amino acid (AA) sequence diversity in open reading frames across 2,661 WGS from wild-type strains. We observe a highly conserved alleloome enriched in mutations unlikely to affect protein function. In contrast, 33,000 mutations acquired in laboratory evolution experiments result in more severe AA substitutions that are rarely achieved by natural selection. Large-scale assessment of the alleloome establishes a method for the quantification of bacterial allelic diversity, reveals opportunities for synthetic biology to explore novel sequence space, and offers insights into the constraints governing evolution.

<https://www.pnas.org/doi/10.1073/pnas.2218835120>

Krishna S.S., S R Chandar H. Ravi M. (2023): **Transgene-Free Genome Editing for Biotic and Abiotic Stress Resistance in Sugarcane: Prospects and Challenges.** *Agronomy* 13(4), 1000; <https://doi.org/10.3390/agronomy13041000>

Sugarcane (*Saccharum* spp.) is one of the most valuable food and industrial crops. Its production is constrained due to major biotic (fungi, bacteria, viruses and insect pests) and abiotic (drought, salt, cold/heat, water logging and heavy metals) stresses. The ever-increasing demand for sugar and biofuel and the rise of new pest and disease variants call for the use of innovative technologies to speed up the sugarcane genetic improvement process. Developing new cultivars through conventional breeding techniques requires much time and resources. The advent of CRISPR/Cas genome editing technology enables the creation of new cultivars with improved resistance/tolerance to various biotic and abiotic stresses. The presence of genome editing cassette inside the genome of genome-edited plants hinders commercial exploitation due to regulatory issues. However, this limitation can be overcome by using transgene-free genome editing techniques. Transgene-free genome editing approaches, such as delivery of the RNPs through biolistics or protoplast fusion, virus-induced genome editing (VIGE), transient expression of CRISPR/Cas reagents through *Agrobacterium*-mediated transformation and other approaches, are discussed. A well-established PCR-based assay and advanced screening systems such as visual marker system and Transgene killer CRISPR system (TKC) rapidly identify transgene-free genome edits. These advancements in CRISPR/Cas technology speed up the creation of genome-edited climate-smart cultivars that combat various biotic and abiotic stresses and produce good yields under ever-changing conditions. <https://www.mdpi.com/2073-4395/13/4/1000>

Singh P., Sean R., Patrick S., Dickinson J., Reyna-Llorens I. et al. (2023): **C₄ gene induction during de-etiolation evolved through changes in cis to allow integration with ancestral C₃ gene regulatory networks.** *Science Advances* 9, Issue 13 | DOI: [10.1126/sciadv.ade9756](https://doi.org/10.1126/sciadv.ade9756)

C₄ photosynthesis has evolved by repurposing enzymes found in C₃ plants. Compared with the ancestral C₃ state, accumulation of C₄ cycle proteins is enhanced. We used de-etiolation of C₄ *Gynandropsis gynandra* and C₃ *Arabidopsis thaliana* to understand this process. C₄ gene expression and chloroplast biogenesis in *G. gynandra* were tightly coordinated. Although C₃ and C₄ photosynthesis genes showed similar induction patterns, in *G. gynandra*, C₄ genes were more strongly induced than orthologs from *A. thaliana*. In vivo binding of TGA and homeodomain as well as light-responsive elements such as G- and I-box motifs were associated with the rapid increase in transcripts of C₄ genes. Deletion analysis confirmed that regions containing G- and I-boxes were necessary for high expression. The data support a model in which accumulation of transcripts derived from C₄ photosynthesis genes in C₄ leaves is enhanced because modifications in cis allowed integration into ancestral transcriptional networks. <https://www.science.org/doi/10.1126/sciadv.ade9756>

Sheikh A.H., Nawaz K., Tabassum, N., Almeida-Trapp M. et al. (2023): **Linker histone H1 modulates defense priming and immunity in plants.** *Nucleic Acids Research*, gkad106 DOI: [10.1093/nar/gkad106](https://doi.org/10.1093/nar/gkad106)

Linker H1 histones play an important role in animal and human pathogenesis, but their function in plant immunity is poorly understood. Here, we analyzed mutants of the three canonical variants of *Arabidopsis* H1 histones, namely H1.1, H1.2 and H1.3. We observed that double *h1.1h1.2* and triple *h1.1h1.2h1.3* (*3h1*) mutants were resistant to *Pseudomonas syringae* and *Botrytis cinerea* infections. Transcriptome analysis of *3h1* mutant plants showed H1s play a key role in regulating the expression of early and late defense genes upon pathogen challenge. Moreover, *3h1* mutant plants showed enhanced production of reactive oxygen species and activation of mitogen activated protein kinases upon pathogen-associated molecular pattern (PAMP) treatment. However, *3h1* mutant plants were insensitive to priming with flg22, a well-known bacterial PAMP which induces enhanced resistance in WT plants. The defective defense response in *3h1* upon priming was correlated with altered DNA methylation and reduced global H3K56ac levels. Our data place H1 as a molecular gatekeeper in governing dynamic changes in the chromatin landscape of defense genes during plant pathogen interaction. <https://academic.oup.com/nar/advance-article/doi/10.1093/nar/gkad106/7058184>

Kersten, S., Chang, J., Huber, Chr. D., Voichek, Y., (2023): **Standing genetic variation fuels rapid evolution of herbicide resistance in blackgrass.** *PNAS* 120 (16), e2206808120 | <https://doi.org/10.1073/pnas.2206808120>

Repeated herbicide applications in agricultural fields exert strong selection on weeds such as blackgrass (*Alopecurus myosuroides*), which is a major threat for temperate climate cereal crops. This inadvertent selection pressure provides an opportunity for investigating the underlying genetic mechanisms and evolutionary processes of rapid adaptation, which can occur both through mutations in the direct targets of herbicides and through changes in other, often metabolic, pathways, known as non-target-site resistance. How much target-site resistance (TSR) relies on de novo mutations vs. standing variation is important for developing strategies to manage herbicide resistance. We first generated a chromosome-level reference genome for *A. myosuroides* for population genomic studies of herbicide resistance and genome-wide diversity across Europe in this species. Next, through empirical data in the form of highly accurate long-read amplicons of alleles encoding acetyl-CoA carboxylase (ACCase) and acetolactate synthase (ALS) variants, we showed that most populations with resistance due to TSR mutations—23 out of 27 and six out of nine populations for ACCase and ALS, respectively—contained at least two TSR haplotypes, indicating that soft sweeps are the norm. Finally, through forward-in-time simulations, we inferred that TSR is likely to mainly result from standing genetic variation, with only a minor role for de novo mutations.

<https://www.pnas.org/doi/10.1073/pnas.2206808120>

Kersten, S., Rabanal, F.A., Herrmann, J., Hess, M., Kronenberg, Z.N., Schmid, K., Weigel, D. (2023): **Deep haplotype analyses of target-site resistance locus ACCase in blackgrass enabled by pool-based amplicon sequencing.** *Plant Biotechnol J.* <https://doi.org/10.1111/pbi.14033>

Rapid adaptation of weeds to herbicide applications in agriculture through resistance development is a widespread phenomenon. In particular, the grass *Alopecurus myosuroides* is an extremely problematic weed in cereal crops with the potential to manifest resistance in only a few generations. Target-site resistances (TSRs), with their strong phenotypic response, play an important role in this rapid adaptive response. Recently, using PacBio's long-read amplicon sequencing technology in hundreds of individuals, we were able to decipher the genomic context in which TSR mutations occur. However, sequencing individual amplicons are costly and time-consuming, thus impractical to implement for other resistance loci or applications. Alternatively, pool-based approaches overcome these limitations and provide reliable allele frequencies, although at the expense of not preserving haplotype information. In this proof-of-concept study, we sequenced with PacBio High Fidelity (HiFi) reads long-range amplicons (13.2 kb), encompassing the entire *ACCase* gene in pools of over 100 individuals, and resolved them into haplotypes using the clustering algorithm PacBio amplicon analysis (*pbaa*), a new application for pools in plants and other organisms. From these amplicon pools, we were able to recover most haplotypes from previously sequenced individuals of the same population. In addition, we analysed new pools from a Germany-wide collection of *A. myosuroides* populations and found that TSR mutations originating from soft sweeps of independent origin were common. Forward-in-time simulations indicate that TSR haplotypes will persist for decades even at relatively low frequencies and without selection, highlighting the importance of accurate measurement of TSR haplotype prevalence for weed management.

<https://onlinelibrary.wiley.com/doi/10.1111/pbi.14033>

Bruce E. Tabashnik B. , Carrière Y , Wu Y , Fabrick J.A. (2023): **Global perspectives on field-evolved resistance to transgenic Bt crops: a special collection.** *Journal of Economic Entomology*, XX(XX), 2023, 1–6 | <https://doi.org/10.1093/jee/toad054>

Crops genetically engineered to produce insect-killing proteins from *Bacillus thuringiensis* (Bt) have revolutionized management of some major pests, but their efficacy is reduced when pests evolve resistance. Practical resistance, which is field-evolved resistance that reduces the efficacy of Bt crops and has practical implications for pest management, has been reported in 26 cases in seven countries involving 11 pest species. This special collection includes six original papers that present a global perspective on field-evolved resistance to Bt crops. One is a synthetic review providing a comprehensive global summary of the status of the resistance or susceptibility to Bt crops of 24 pest species in 12 countries. Another evaluates the inheritance and fitness costs of resistance of *Diabrotica virgifera virgifera* to Gpp34/Tpp35Ab (formerly called Cry34/35Ab). Two papers describe and demonstrate advances in techniques for monitoring field-evolved resistance. One uses a modified F₂ screen for resistance to Cry1Ac and Cry2Ab in *Helicoverpa zea* in the United States. The other uses genomics to analyze nonrecessive resistance to Cry1Ac in *Helicoverpa armigera* in China. Two papers provide multi-year monitoring data for resistance to Bt corn in Spain and Canada, respectively. The monitoring data from Spain evaluate responses to Cry1Ab of the corn borers *Sesamia nonagrioides* and *Ostrinia nubilalis*, whereas the data from Canada track responses of *O. nubilalis* to Cry1Ab, Cry1Fa, Cry1A.105, and Cry2Ab. We hope the new methods, results, and conclusions reported here will spur additional research and help to enhance the sustainability of current and future transgenic insecticidal crops.

<https://academic.oup.com/jee/advance-article/doi/10.1093/jee/toad054/7109168?login=false>

Kallam K., Moreno-Giménez E., Mateos-Fernández R., Tansley C. et al. (2023): **Tunable control of insect pheromone biosynthesis in *Nicotiana benthamiana*.** *Plant Biotechnology Journal* | <https://doi.org/10.1111/pbi.14048>

Previous work has demonstrated that plants can be used as production platforms for molecules used in health, medicine, and agriculture. Production has been exemplified in both stable transgenic plants and using transient expression strategies. In particular, species of *Nicotiana* have been engineered to produce a range of useful molecules, including insect sex pheromones, which are valued for species-specific control of agricultural pests. To date, most studies have relied on strong constitutive expression of all pathway genes. However, work in microbes has demonstrated that yields can be improved by controlling and balancing gene expression. Synthetic regulatory elements that provide control over the timing and levels of gene expression are therefore useful for maximizing yields from heterologous biosynthetic pathways. In this study, we demonstrate the use of pathway engineering and synthetic genetic elements for controlling the timing and levels of production of Lepidopteran sex pheromones in *Nicotiana benthamiana*. We demonstrate that copper can be used as a low-cost molecule for tightly regulated inducible expression. Further, we show how construct architecture influences relative gene expression and, consequently, product yields in multigene constructs. We compare a number of synthetic orthogonal regulatory elements and demonstrate maximal yields from constructs in which expression is mediated by dCas9-based synthetic transcriptional activators. The approaches demonstrated here provide new insights into the heterologous reconstruction of metabolic pathways in plants.

<https://onlinelibrary.wiley.com/doi/epdf/10.1111/pbi.14048>

Singh, A., Singh, S., Kansal, S.K. et al. (2023): **Production and characterization of anthocyanin-rich beer from black wheat by an efficient isolate *Saccharomyces cerevisiae* CMS12.** *Sci Rep* 13, 5863 (2023). <https://doi.org/10.1038/s41598-023-32687-1>

Beer is the world's third most popular fermented beverage. It is typically made from malted barley. Tropical countries must import barley from temperate countries for brewing, which is an expensive process. Therefore, it is critical to investigate alternative possible substrates for beer production in order to meet the growing demand for high-nutritional-quality beer. The current study involves the creation of a fermented beverage from anthocyanin-rich black wheat with the help of yeast, *Saccharomyces cerevisiae* CMS12, isolated from fruit waste. Characterization (UV, HPLC, NMR, FTIR, and ICPMS) was then performed, as well as a comparative study with white (amber) wheat beer. Further, process parameters optimization included initial sugar concentration, inoculum size, and pH. Black wheat wort contained 568 mg GAE/L total phenolic content, 4.67 mg/L anthocyanin concentration, 6.8% (v/v) alcohol content, and a pH of 4.04. The sensory analysis revealed that black wheat beer was more acceptable than white wheat beer. The developed fermented beverage has enormous commercialization potential.

<https://www.nature.com/articles/s41598-023-32687-1>

Richter, P.K., Blázquez-Sánchez, P., Zhao, Z. et al. (2023): **Structure and function of the metagenomic plastic-degrading polyester hydrolase PHL7 bound to its product.** *Nat Commun* 14, 1905 | <https://doi.org/10.1038/s41467-023-37415-x>

The recently discovered metagenomic-derived polyester hydrolase PHL7 is able to efficiently degrade amorphous polyethylene terephthalate (PET) in post-consumer plastic waste. We present the cocrystal structure of this hydrolase with its hydrolysis product terephthalic acid and elucidate the influence of 17 single mutations on the PET-hydrolytic activity and thermal stability of PHL7. The substrate-binding mode of terephthalic acid is similar to that of the thermophilic polyester hydrolase LCC and deviates from the mesophilic *IsPETase*. The subsite I modifications L93F and Q95Y, derived from LCC, increased the thermal stability, while exchange of H185S, derived from *IsPETase*, reduced the stability of PHL7. The subsite II residue H130 is suggested to represent an adaptation for high thermal stability, whereas L210 emerged as the main contributor to the observed high PET-hydrolytic activity. Variant L210T showed significantly higher activity, achieving a degradation rate of 20 $\mu\text{m h}^{-1}$ with amorphous PET films.

<https://www.nature.com/articles/s41467-023-37415-x>

EFSA:

EFSA CEP Panel (2023): Scientific Opinion on the safety evaluation of the food enzyme asparaginase from the genetically modified *Aspergillus oryzae* strain NZYM-OA. *EFSA Journal* 2023; 21(4):7914, 16 pp. <https://doi.org/10.2903/j.efsa.2023.7914>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.7914>

Vos E., Volpato A., Bellenghi G. (2023): **Independence and transparency policies of the European Food Safety Authority (EFSA)**

This study has been commissioned by the European Parliament's Policy Department for Economic, Scientific and Quality of Life Policies, Directorate-General for Internal Policies at the request of the ENVI Committee. It analyses EFSA's independence and transparency policies and examines how legislative provisions have been implemented by EFSA and whether rules and practices adopted by EFSA can be improved.

[https://www.europarl.europa.eu/RegData/etudes/STUD/2023/740080/IPOL_STU\(2023\)740080_EN.pdf](https://www.europarl.europa.eu/RegData/etudes/STUD/2023/740080/IPOL_STU(2023)740080_EN.pdf)

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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