

# Sunday Evening News No 268

Week 07 (2022-21-02 – 2022-27-02)

Selected and edited by **BGF** Jany

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Everyone suspected it - no one wanted to imagine the inconceivable - someone turned the inconceivable into reality. The war will have lasting consequences!

Alle haben es geahnt – Keiner wollte sich das Unfassbare vorstellen - Einer hat das Unfassbare „Krieg in Europa“ in die Realität umgesetzt. Der Krieg wird nachhaltige Folgen haben!

## Press Releases – Media Reports / Pressemeldungen und Medienberichte

**AFBV: Europe Must Embrace New Genomic Technologies (NGT) to Safeguard its Food Sovereignty**

<https://european-seed.com/2022/02/europe-must-embrace-new-genomic-technologies-ngt-to-safeguard-its-food-sovereignty/>

Dietz K.-J.: **Wie stark darf sich Wissenschaft in Politik einmischen?** Biol.Unser Zeit 1/22 (52), 2-3 pdf-file available

**GeN: Hält die Ampel die Gentechnik vom Acker?**

<https://www.gen-ethisches-netzwerk.de/agrarpolitik/260/haelt-die-ampel-die-gentechnik-vom-acker>

**BW Agrar: Feldversuch-Premiere in Europa**

<https://www.bwagrar.de/Aktuelles/Feldversuch-Premiere-in-Europa,QUIEPTcwOTU1NzQmTUIEPTUxNjQ0.html>

von Eichhorn C.: **Gentechnik für das Klima**

<https://www.sueddeutsche.de/wissen/gentechnik-landwirtschaft-eu-genome-editing-1.5532138>

Popkin G.: **To fight climate change, a biotech firm has genetically engineered a very peppy poplar**

<https://www.science.org/content/article/fight-climate-change-biotech-firm-has-genetically-engineered-very-peppy-poplar>

acatech (Hrsg.): **Biotechnologie (acatech HORIZONTE)**, München 2022

<https://www.acatech.de/projekt/acatech-horizonte-biotechnologie/>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): (February week 08)

## Publications – Publikationen

Shelton A.M. (2021): **Bt Eggplant: A Personal Account of Using Biotechnology to Improve the Lives of Resource-Poor Farmers**. American Entomologist, 67 (3), 52–59 |

<https://doi.org/10.1093/ae/tmab036>

Tao Y, Chiu L.-W., Hoyle J.W., Jessica Du J. et al. (2022): **Enhanced photosynthetic efficiency for increased carbon assimilation and woody biomass production in hybrid poplar INRA 717-1B4**. Biorxiv | doi: <https://doi.org/10.1101/2022.02.16.480797>

Increasing CO<sub>2</sub> levels in the atmosphere and the resulting negative impacts on climate change have compelled global efforts to achieve carbon neutrality or negativity. Most such efforts focus on carbon sequestration through chemical or physical approaches. We aim to harness the power of synthetic biology to enhance plants' natural ability to draw down and sequester carbon, thereby positively affecting climate change. Past decades of scientific progress have shed light on strategies to overcome the intrinsic limitations of carbon drawdown and fixation through photosynthesis, particularly in row crops in hopes of improving agricultural productivity for food security. Incorporating a photorespiration bypass in C3 plants has shown promising results of increased biomass and grain yield. Despite their globally dominant role in atmospheric carbon flux, the drawdown rates of most trees are currently limited by their C3 photosynthetic metabolism, and efforts to improve the photosynthetic capacity of trees, such as by reducing energy loss in photorespiration, are currently lacking. Here, we selected a photorespiration bypass pathway and tested its effectiveness on photosynthetic enhancement in hybrid poplar INRA717-1B4. The design includes a RNAi strategy to reduce the transportation

of the photorespiration byproduct, glycolate, out of chloroplast and a shunt pathway to metabolize the retained glycolate back to CO<sub>2</sub> for fixation through the Calvin-Benson cycle. Molecular and physiological data collected from two repeated growth experiments indicates that transgenic plants expressing genes in the photorespiration bypass pathway have increased photosynthetic efficiency, leading to faster plant growth and elevated biomass production. One lead transgenic event accumulated 53% more above-ground dry biomass over a five month growth period in a controlled environment. Pilot projects with photosynthesis-enhanced trees in the field are in progress. Our results provide a proof-of-concept for engineering trees to help combat climate change.

<https://www.biorxiv.org/content/10.1101/2022.02.16.480797v1>

Goberna M.F., Whelan A.I., Godoy P. and Lewi D.M. (2022): **Genomic Editing: The Evolution in Regulatory Management Accompanying Scientific Progress**. *Front. Bioeng. Biotechnol.* 10:835378. | <https://doi.org/10.3389/fbioe.2022.835378>

Argentina currently has a regulation for genome-editing products whose criteria were updated as consultations were received to determine the regulatory status of these products. The aim of this regulation is to consider all organisms (animals, micro-organisms and plants) under the same NBT resolution independently and without being linked to commercial Genetically Modified Organism (GMO) regulations. This gives certainty to local researchers and developers (teams of local developers and researchers), which can be seen in the number of developments and consultations carried out. It should be noted that early results showed that the speed of innovation of these technologies was increasing in a short time, giving more opportunity to local developers who showed interest in generating products in different species, crops and phenotypes.

<https://www.frontiersin.org/articles/10.3389/fbioe.2022.835378/full>

Srnic W. (2022): **Gene Editing: Breakthrough Technology in Our 10,000-Year Journey of Crop Improvement**, *GEN Biotechnology*. 1 (1), 68-76 |

<http://doi.org/10.1089/genbio.2021.0009>

Humans have improved plants for their utility through selective self-pollination, crossing, and progeny selection for >10,000 years, largely based on physical characteristics. Less than 200 years ago, the genetic basis of heritability in selection was revealed, enabling breeders to accelerate genetic gain. Breakthroughs in genomics and molecular markers for the past century have enabled breeders to locate and select genomic regions affecting desirable traits, improving breeding precision. Transgenesis has enabled crop insertion of desirable exogenous genes, enabling *de novo* functionality. These technologies, along with agronomic practices, have generated more than sixfold yield improvements in crops such as corn in the past century. Gene editing, with its unique ability to precisely edit, change expression, and move genes *within* a crop's genome, has the potential to be the next breakthrough technology. For this to come to fruition, it is critical to take a holistic view considering perspectives of scientists, farmers, regulators, and consumers.

<https://www.liebertpub.com/doi/full/10.1089/genbio.2021.0009>

Paleari L., Li T., Yang Y., Wilson L.T. et al. (2022): **A trait-based model ensemble approach to design rice plant types for future climate**, *Glob Change Biol.* |

<https://doi.org/10.1111/gcb.16087>

Crop models are powerful tools to support breeding because of their capability to explore genotype × environment × management interactions that can help design promising plant types under climate change. However, relationships between plant traits and model parameters are often model specific and not necessarily direct, depending on how models formulate plant morphological and physiological features. This hinders model application in plant breeding. We developed a novel trait-based multi-model ensemble approach to improve the design of rice plant types for future climate projections. We conducted multi-model simulations targeting enhanced productivity, and aggregated results into model-ensemble sets of phenotypic traits as defined by breeders rather than by model parameters. This allowed to overcome the limitations due to ambiguities in trait-parameter mapping from single modelling approaches. Breeders' knowledge and perspective were integrated to provide clear mapping from designed plant types to breeding traits. Nine crop models from the AgMIP-Rice Project and sensitivity analysis techniques were used to explore trait responses under different climate and management scenarios at four sites. The method demonstrated the potential of yield improvement that ranged from 15.8% to 41.5% compared to the current cultivars under mid-century climate projections. These results highlight the primary role of phenological traits to improve crop adaptation to climate change, as well as traits involved with canopy development and structure. The variability of plant types derived with different models supported model ensembles to handle related uncertainty. Nevertheless, the models agreed in capturing the effect of the heterogeneity in climate conditions across sites on key traits, highlighting the need for context-specific breeding programmes to improve crop adaptation to climate change. Although further improvement is needed for crop models to fully support breeding programmes, a trait-based ensemble approach represents a major step towards the integration of crop modelling and breeding to address climate change challenges and develop adaptation options.

<https://onlinelibrary.wiley.com/doi/abs/10.1111/gcb.16087> pdf-file available

Khanale, V., Bhattacharya, A., Prashar, M. et al. (2022): **Genome editing interventions to combat rice blast disease**. *Plant Biotechnol Rep* | <https://doi.org/10.1007/s11816-022-00749-x>

Rice is the major food crop of the world. Production of rice is threatened by a number of biotic and abiotic stresses and these could result in a significant yield reduction, sometimes up to 60–100%. In addressing losses to emerging diseases, development of resistance to blast, sheath blight, and false smut is the need of the hour. The traditional approach of using resistance R genes for building sustainable resistance is not viable anymore due to continuously evolving strain of pathogens, thus causing intransigence erosion. The contemporary intervention strategy of identifying and precisely mutating susceptibility genes opens up new vistas for exploiting susceptible genes. Approaches like mutation breeding and transgenic held good promise to further yield increases in rice and provide protection against disease induced yield losses. However, all these approaches either proved inadequate over time or faced regulatory hurdles and were successful to a limited point. Recently, a new genome editing (GE) approach has offered a promising alternative to develop unique alleles in a shorter time frame without linkage drag. Thus, the present review highlights various R, non-R (S) gene choices amenable for genome editing, compared with available conventional breeding approaches, like wide-hybridisation using wild relatives, including new genetic resources. Hence, a range of breeding resources can be employed by crop breeders to assemble disease resistance against emerging diseases of rice. Many successful examples on disease resistance are collated from recently published work. It is hoped that creating new allelic series of variants would be a practical and sustainable solution to address the challenges posed to food security.

<https://link.springer.com/article/10.1007/s11816-022-00749-x>

Kashojiya ., Lu Y., Takayama M., Komatsu H. et al. (2022): **Modification of tomato breeding traits and plant hormone signaling by Target-AID, the genome-editing system inducing efficient nucleotide substitution**, Horticulture Research, 9, uhab004 |

<https://doi.org/10.1093/hr/uhab004>

Target activation-induced cytidine deaminase (Target-AID), a novel CRISPR/Cas9-based genome-editing tool, confers the base-editing capability on the Cas9 genome-editing system. It involves the fusion of cytidine deaminase (CDA), which catalyzes cytidine (C) to uridine (U) substitutions, to the mutated nickase-type nCas9 or deactivated-type dCas9. To confirm and extend the applicability of the Target-AID genome-editing system in tomatoes (*Solanum lycopersicum* L.), we transformed the model tomato cultivar “Micro-Tom” and commercial tomato cultivars using this system by targeting *SIDE*LLA, which encodes a negative regulator of the plant phytohormone gibberellic acid (GA) signaling pathway. We confirmed that the nucleotide substitutions were induced by the Target-AID system, and we isolated mutants showing high GA sensitivity in both “Micro-Tom” and the commercial cultivars. Moreover, by successfully applying this system to *ETHYLENE RECEPTOR 1* (*SIETR1*) with single sgRNA targeting, double sgRNA targeting, as well as dual-targeting of both *SIETR1* and *SIETR2* with a single sgRNA, we demonstrated that the Target-AID genome-editing system is a promising tool for molecular breeding in tomato crops. This study highlights an important aspect of the scientific and agricultural potential of the combinatorial use of the Target-AID and other base-editing systems.

<https://academic.oup.com/hr/article/doi/10.1093/hr/uhab004/6511229>

Zhao J., Sauvage C., Bitton F., Causse M. (2022): Multiple haplotype-based analyses provide genetic and evolutionary insights into tomato fruit weight and composition, Horticulture Research 9, uhab009 | <https://doi.org/10.1093/hr/uhab009>

Improving fruit quality traits such as metabolic composition remains a challenge for tomato breeders. To better understand the genetic architecture of these traits and decipher the demographic history of the loci controlling tomato quality traits, we applied an innovative approach using multiple haplotype-based analyses, aiming to test the potentials of haplotype based study in association and genomic prediction studies. We performed and compared haplotype vs SNP-based associations (hapQTL) with multi-locus mixed model (MLMM), focusing on tomato fruit weight and metabolite contents (i.e. sugars, organic acids and amino acids). Using a panel of 163 tomato accessions genotyped with 5995 SNPs, we detected a total of 784 haplotype blocks, with an average size of haplotype blocks ~58 kb. A total of 108 significant associations for 26 traits were detected thanks to Haplotype/SNP-based Bayes models. Haplotype-based Bayes model (97 associations) outperformed SNP-based Bayes model (50 associations) and MLMM (53 associations) in identifying marker-trait associations as well as in genomic prediction (especially for those traits with moderate to low heritability). To decipher the demographic history, we identified 24 positive selective sweeps using the integrated haplotype score (iHS). Most of the significant associations for tomato quality traits were located within selective sweeps (54.63% and 71.7% in hapQTL and MLMM models, respectively). Promising candidate genes were identified controlling tomato fruit weight and metabolite contents. We thus demonstrated the benefits of using haplotypes for evolutionary and genetic studies, providing novel insights into tomato quality improvement and breeding history.

<https://academic.oup.com/hr/article/doi/10.1093/hr/uhab009/6510184>

Iqbal, A., Ali, M.A., Ahmed, S. et al. (2022): **Engineered resistance and risk assessment associated with insecticidal and weeds resistant transgenic cotton using wister rat model**. Sci Rep 12, 2518 | <https://doi.org/10.1038/s41598-022-06568-y>

Stacking multiple genes into cotton crop to cop up multiple biotic stresses such as insects and weeds is a promising tool to save crop from losses. Transgenic cotton variety, VH-289, with double *Bt* and *cp4EPSPS* genes under the control of 35S promoter was used for the expression analyses and biosafety studies. The transgenic cotton plants were screened through PCR amplification of fragments, 1.7 kb for *Cry1Ac*, 582 bp for *Cry2A* and 250 bp for *cp4EPSPS*; which confirmed the presence of all genes transformed in transgenic cotton. The *Cry1Ac* + *Cry2A* and *cp4EPSPS* proteins were quantified through ELISA in transgenic cotton plants. The

Glyphosate assay performed by spraying 1900 mL per acre of glyphosate Roundup further confirmed complete survival of transgenic cotton plants as compared to the non-transgenic cotton plants and all weeds. Similarly, insect infestation data determined that almost 99% insect mortality was observed in controlled field grown transgenic cotton plants as compared to the non-transgenic control plants. Evaluation of effect of temperature and soil nutrients availability on transgene expression in cotton plants was done at two different cotton growing regions, Multan and Lahore, Pakistan and results suggested that despite of higher temperature in Multan field, an increased level of Cry and cp4EPSPS proteins was recorded due to higher soil organic matter availability compared to Lahore field. Before commercialization of any transgenic variety its biosafety study is mandatory so, a 90 days biosafety study of the transgenic cotton plants with 40% transgenic cottonseeds in standard diet showed no harmful effect on wister rat model when studied for liver function, renal function and serum electrolyte.

<https://www.nature.com/articles/s41598-022-06568-y>  
<https://www.nature.com/articles/s41598-022-06568-y.pdf>

Wright, B.W., Molloy, M.P. & Jaschke, P.R. (2022): **Overlapping genes in natural and engineered genomes.** Nat Rev Genet 23, 154–168 | <https://doi.org/10.1038/s41576-021-00417-w>

Modern genome-scale methods that identify new genes, such as proteogenomics and ribosome profiling, have revealed, to the surprise of many, that overlap in genes, open reading frames and even coding sequences is widespread and functionally integrated into prokaryotic, eukaryotic and viral genomes. In parallel, the constraints that overlapping regions place on genome sequences and their evolution can be harnessed in bioengineering to build more robust synthetic strains and constructs. With a focus on overlapping protein-coding and RNA-coding genes, this Review examines their discovery, topology and biogenesis in the context of their genome biology. We highlight exciting new uses for sequence overlap to control translation, compress synthetic genetic constructs, and protect against mutation.

<https://www.nature.com/articles/s41576-021-00417-w.pdf>

Chen Y., Romeis J., Meissle M. (2022): **No Adverse Effects of Stacked *Bacillus thuringiensis* Maize on the Midge *Chironomus riparius*,** Environmental Toxicology and Chemistry |

<https://doi.org/10.1002/etc.5293>

Material from genetically engineered maize producing insecticidal Cry proteins from *Bacillus thuringiensis* (*Bt*) may enter aquatic ecosystems and expose nontarget organisms. We investigated the effects on life table parameters of the midge *Chironomus riparius* (Diptera: Chironomidae) of SmartStax maize leaves, which contain six different Cry proteins targeting Lepidoptera and Coleoptera pests, in two plant backgrounds. For midge development and emergence, 95% confidence intervals for the means of six conventional maize lines (Rheintaler, Tasty Sweet, ES-Eurojet, Planoxx, EXP 258, and EXP 262), were used to capture the natural range of variation. For reproduction, lowest and highest means were used. The natural range of variation allows one to judge whether observed effects between *Bt* maize and the closest non-*Bt* comparator are likely to be of biological relevance. No adverse effects on *C. riparius* were observed with any *Bt* maize line compared with the respective non-*Bt* counterpart. Development time was shorter when females were fed *Bt* maize than when they were fed non-*Bt* maize, but this effect was not considered adverse. Development time, emergence ratio, sex ratio, and larvae/egg rope measured for *Bt* maize were within the natural range of variation. Fecundity for the *Bt* lines was equal to or higher than that for the conventional lines. Future risk assessment studies may consider plant background effects and the natural range of variation to judge the relevance of observed differences between particular genetically engineered and non-genetically engineered plants.

<https://setac.onlinelibrary.wiley.com/doi/full/10.1002/etc.5293>

Gyurcsó G.; Darvas B.; Baska F.; Simon L.; Takács E.; Klátyik S.; Székács A. (2022): **Herbivorous Juvenile Grass Carp (*Ctenopharyngodon idella*) Fed with Genetically Modified MON 810 and DAS-59122 Maize Varieties Containing Cry Toxins: Intestinal Histological, Developmental, and Immunological Investigations.** Toxins 14, 153 |

<https://doi.org/10.3390/toxins14020153>

Feeding experiments with juvenile grass carp (*Ctenopharyngodon idella*) fed with genetically modified maize MON 810 or DAS-59122 dried leaf biomass were carried out with 1-, 3- and 6-month exposures. Dosages of 3–7 µg/fish/day Cry1Ab or 18–55 µg/fish/day Cry34Ab1 toxin did not cause mortality. No difference occurred in body or abdominal sac weights. No differences appeared in levels of inorganic phosphate, calcium, fructosamine, bile acids, triglycerides, cholesterol, and alanine and aspartame aminotransferases. DAS-59122 did not alter blood parameters tested after 3 months of feeding. MON 810 slightly decreased serum albumin levels compared to the control, only in one group. Tapeworm (*Bothriocephalus acheilognathi*) infection changed the levels of inorganic phosphate and calcium. Cry34Ab1 toxin appeared in blood (12.6 ± 1.9 ng/mL), but not in the muscle. It was detected in *B. acheilognathi*. Cry1Ab was hardly detectable in certain samples near the limit of detection. Degradation of Cry toxins was extremely quick in the fish gastrointestinal tract. After 6 months of feeding, only mild indications in certain serum parameters were observed: MON 810 slightly increased the level of apoptotic cells in the blood and reduced the number of thrombocytes in one group; DAS-59122 mildly increased the number of granulocytes compared to the near-isogenic line.

<https://www.mdpi.com/2072-6651/14/2/153>

Debouck, D. G., Santaella, M., Santos, L. G. (2021). History and impact of a bean (*Phaseolus* spp., Leguminosae, Phaseoleae) collection. *Genetic Resources* 2 (4), 21–42. | doi: [10.46265/genresj.WJEU8358](https://doi.org/10.46265/genresj.WJEU8358).

This work explains the reasons why a bean collection was established in 1973 at the International Center of Tropical Agriculture (CIAT) near Palmira in Colombia. It shows the impact of the collection on plant breeding and in agricultural development through the distribution of germplasm to the center's bean breeding program, to successively find resistances to pests and diseases, adaptation to low phosphorus and drought, and more recently higher content of iron and zinc in seeds. The collection was also used to progress knowledge in biological sciences, as shown by a dozen of examples. A reason behind these successes was foresight and focus on diversity per se in the collection. The paper ends with a number of suggestions for the way ahead for the genetic resources conservation and management of these bean crops, and possible take-home lessons for curators in charge of other similar collections.

<https://www.genresj.org/index.php/gri/article/view/genresj.WJEU8358/92>

Liu H. and Timko M.P. (2022): **Improving Protein Quantity and Quality—The Next Level of Plant Molecular Farming**. *Int. J. Mol. Sci.* 23 (3), 1326 |

<https://doi.org/10.3390/ijms23031326>

Plants offer several unique advantages in the production of recombinant pharmaceuticals for humans and animals. Although numerous recombinant proteins have been expressed in plants, only a small fraction have been successfully put into use. The hugely distinct expression systems between plant and animal cells frequently cause insufficient yield of the recombinant proteins with poor or undesired activity. To overcome the issues that greatly constrain the development of plant-produced pharmaceuticals, great efforts have been made to improve expression systems and develop alternative strategies to increase both the quantity and quality of the recombinant proteins. Recent technological revolutions, such as targeted genome editing, deconstructed vectors, virus-like particles, and humanized glycosylation, have led to great advances in plant molecular farming to meet the industrial manufacturing and clinical application standards. In this review, we discuss the technological advances made in various plant expression platforms, with special focus on the upstream designs and milestone achievements in improving the yield and glycosylation of the plant-produced pharmaceutical proteins.

<https://www.mdpi.com/1422-0067/23/3/1326>

## Industrial Biotechnology

Liew, F.E., Nogle, R., Abdalla, T. et al. (2020'2): **Carbon-negative production of acetone and isopropanol by gas fermentation at industrial pilot scale**. *Nat Biotechnol* |

<https://doi.org/10.1038/s41587-021-01195-w>

Many industrial chemicals that are produced from fossil resources could be manufactured more sustainably through fermentation. Here we describe the development of a carbon-negative fermentation route to producing the industrially important chemicals acetone and isopropanol from abundant, low-cost waste gas feedstocks, such as industrial emissions and syngas. Using a combinatorial pathway library approach, we first mined a historical industrial strain collection for superior enzymes that we used to engineer the autotrophic acetogen *Clostridium autoethanogenum*. Next, we used omics analysis, kinetic modeling and cell-free prototyping to optimize flux. Finally, we scaled-up our optimized strains for continuous production at rates of up to ~3 g/L/h and ~90% selectivity. Life cycle analysis confirmed a negative carbon footprint for the products. Unlike traditional production processes, which result in release of greenhouse gases, our process fixes carbon. These results show that engineered acetogens enable sustainable, high-efficiency, high-selectivity chemicals production. We expect that our approach can be readily adapted to a wide range of commodity chemicals.

<https://www.nature.com/articles/s41587-021-01195-w>

<https://www.nature.com/articles/s41587-021-01195-w.pdf>

Mus F., Khokhani D., MacIntyre A.M., Rugoli E., Dixon R., Ané J.-M., Peters W. (2022): **Genetic determinants of ammonium excretion in *nifL* mutants of *Azotobacter vinelandii***. *Applied and Environmental Microbiology* | DOI: <https://doi.org/10.1128/AEM.01876-21>

The ubiquitous diazotrophic soil bacterium *Azotobacter vinelandii* has been extensively studied as a model organism for biological nitrogen fixation (BNF). In *A. vinelandii*, BNF is regulated by the NifL-NifA two-component system, where NifL acts as an anti-activator that tightly controls the activity of the nitrogen fixation specific transcriptional activator, NifA, in response to redox, nitrogen, and carbon status. While several studies reported mutations in *A. vinelandii nifL* resulted in the deregulation of nitrogenase expression and the release of large quantities of ammonium, knowledge about the specific determinants for this ammonium-excreting phenotype is lacking. In this work, we report that only specific disruptions of *nifL* lead to large quantities of ammonium accumulated in liquid culture (~12 mM). The ammonium excretion phenotype is solely associated with deletions of NifL domains combined with the insertion of a promoter sequence in the opposite orientation to *nifLA* transcription. We further demonstrated that the strength of the inserted promoter could influence the amounts of ammonium excreted by affecting *rnf1* gene expression as an additional requirement for ammonium excretion. These ammonium-excreting *nifL* mutants significantly stimulate the transfer of fixed nitrogen to rice. This work defines discrete determinants that bring about *A. vinelandii* ammonium excretion and demonstrates that strains can be generated through simple gene editing to provide promising biofertilizers capable of transferring nitrogen to crops.

<https://journals.asm.org/doi/10.1128/AEM.01876-21>

Alabdall, A.H., Aldakheel, F.A., Ababutain, I.M. et al. (2022): **Degradation of 2,6-dichlorophenol by *Trichoderma longibraciatum* Isolated from an industrial Soil Sample in Dammam, Saudi Arabia.** Sci Rep 12, 2940 | <https://doi.org/10.1038/s41598-022-07016-7>  
2,6-Dichlorophenol (2,6-DCP) is an aromatic compound with industrial importance in making insecticides, herbicides, and other organic compounds. However, it poses serious health and ecological problems. Microbial degradation of 2,6-DCP has been widely applied due to its effectiveness and eco-friendly characteristics. In this study, *Trichoderma longibraciatum* was isolated from an industrial soil sample in Dammam, Saudi Arabia using the enrichment method of mineral salt's medium (MSM) amended with 2,6-DCP. Morphological and molecular identification (using the internal transcribed spacer rRNA gene sequencing) of the 2,6-DCP tolerating fungal isolate were characterized. The fungal isolate has demonstrated a tolerance to 2,6-DCP up to 300 mg/L. Mycelial growth and fungal sporulation were reduced with increasing 2,6-DCP concentrations up to 96 h incubation period. However, after 168 h incubation period, the fungal isolate recorded maximum growth at all the tested 2,6-DCP concentrations up to 150 mg/L. Carboxy methyl cellulase production by tested fungus was decreased by increasing 2,6-DCP concentration up to 75 mg/L. The biodegradation pattern of 2,6-DCP in GM liquid medium using GC–mass analysis as well as the degradation pathway was presented. This study provides a promising fungal isolate that could be used in the bioremediation process for chlorinated phenols in soil.  
<https://www.nature.com/articles/s41598-022-07016-7.pdf>

### Red gene engineering – Rote Gentechnik

Wang, SW., Gao, C., Zheng, YM. et al. (2022): **Current applications and future perspective of CRISPR/Cas9 gene editing in cancer.** Mol Cancer 21, 57 | <https://doi.org/10.1186/s12943-022-01518-8>

Clustered regularly interspaced short palindromic repeats (CRISPR) system provides adaptive immunity against plasmids and phages in prokaryotes. This system inspires the development of a powerful genome engineering tool, the CRISPR/CRISPR-associated nuclease 9 (CRISPR/Cas9) genome editing system. Due to its high efficiency and precision, the CRISPR/Cas9 technique has been employed to explore the functions of cancer-related genes, establish tumor-bearing animal models and probe drug targets, vastly increasing our understanding of cancer genomics. Here, we review current status of CRISPR/Cas9 gene editing technology in oncological research. We first explain the basic principles of CRISPR/Cas9 gene editing and introduce several new CRISPR-based gene editing modes. We next detail the rapid progress of CRISPR screening in revealing tumorigenesis, metastasis, and drug resistance mechanisms. In addition, we introduce CRISPR/Cas9 system delivery vectors and finally demonstrate the potential of CRISPR/Cas9 engineering to enhance the effect of adoptive T cell therapy (ACT) and reduce adverse reactions.

<https://molecular-cancer.biomedcentral.com/track/pdf/10.1186/s12943-022-01518-8.pdf>

Hao K., Ermel R., Sukhavasi K., Cheng H. et al. (2022): **Integrative Prioritization of Causal Genes for Coronary Artery Disease.** Circulation: Genomic and Precision Medicine 15 (1), e003365 |

<https://doi.org/10.1161/CIRCGEN.121.003365>

<https://www.ahajournals.org/doi/epub/10.1161/CIRCGEN.121.003365>

Meghani, Z. (2022): **Regulation of genetically engineered (GE) mosquitoes as a public health tool: a public health ethics analysis.** Global Health 18, 21 |

<https://doi.org/10.1186/s12992-021-00760-x>

<https://globalizationandhealth.biomedcentral.com/track/pdf/10.1186/s12992-021-00760-x.pdf>

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Bitte besuchen sie auch die Webseite des Wissenschaftlerkreis Grüne Gentechnik e.V. (WGG): [www.wgg-ev.de](http://www.wgg-ev.de).

*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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