

# Sunday Evening News No 269

Week 11 (2022-14-03 – 2022-20-03)

Selected and edited by **BGF** Jany

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**Mr. Putin stop this war - show moral greatness and end the suffering of the population and the death of civilians**

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## Veranstaltungen:

**WGG: Genomeditierung: Neue Techniken für bessere Lebensmittelprodukte**

Anuga Food Tec 2022: Main Stage / Halle 8, Stand E80/F88: 26.04.2022 | 13:40 - 15:10 Uhr  
[https://www.anugafoodtec.de/event/genomeditierung\\_neue\\_techniken\\_fuer\\_bessere\\_lebensmittelprodukte?from=tracks](https://www.anugafoodtec.de/event/genomeditierung_neue_techniken_fuer_bessere_lebensmittelprodukte?from=tracks)

**Innoplanta Forum 2022** Berlin: 26.03.2022

Studie ZX: **Zukunftsdialog Agrar & Ernährung** - 21. Juni 2022

<https://www.studiozx.de/events/de/veranstaltungen/zeit-events/zukunftsdialog-agrar-ernaehrung-2022/>

## Press Releases – Media Reports / Pressemeldungen und Medienberichte

**Arbeiterkammer für klare Kennzeichnung bei neuer Gentechnik**

<https://fleischundco.at/info-politik/arbeiterkammer-fuer-klare-kennzeichnung-bei-neuer-gentechnik>

Informationsdienst Gentechnik: **USA erlauben Crispr-Steaks ohne Kennzeichnung**

<https://www.keine-gentechnik.de/nachricht/34573?cHash=5f14720158c2075f0a1468578d80b257>

Biobeef Blog: DNA is NOT a drug. And regulating genome edited research animals as a drug is unworkable.

<https://biobeef.faculty.ucdavis.edu/2022/03/09/dna-is-not-a-drug-and-regulating-genome-edited-research-animals-as-a-drug-is-unworkable/>

Jany Kl.-D.: **Are GM foods safe? New study of studies challenges long-established claim that GMOs pose no unique health hazards. Let's review what they found**

<https://geneticliteracyproject.org/2022/03/16/are-gm-foods-safe-new-study-of-studies-challenges-long-established-claim-that-gmos-pose-no-unique-health-hazards-lets-review-what-they-found/>

Forestry and silviculture Research, Development and Innovation, Plant production: **Brazil nut tree genome sequencing to accelerate breeding of the species**

<https://www.embrapa.br/en/busca-de-noticias/-/noticia/67848724/brazil-nut-tree-genome-sequencing-to-accelerate-breeding-of-the-species>

Airhart M.: **CRISPR critics say gene editing results in 'unknowable mistakes'. Here's how scientists are addressing that challenge**

[https://geneticliteracyproject.org/2022/03/14/crispr-critics-say-gene-editing-results-in-unknowable-mistakes-heres-how-scientists-are-addressing-that-challenge/?utm\\_source=jeeng](https://geneticliteracyproject.org/2022/03/14/crispr-critics-say-gene-editing-results-in-unknowable-mistakes-heres-how-scientists-are-addressing-that-challenge/?utm_source=jeeng) (only for reminder)

**GLP: How 'agricultural intensification' could cut global farm land use by almost 50%, increase biodiversity and help address climate change**

[https://geneticliteracyproject.org/2022/03/14/how-agricultural-intensification-could-cut-global-farm-land-use-by-almost-50-increase-biodiversity-and-help-address-climate-change/?utm\\_source=jeeng](https://geneticliteracyproject.org/2022/03/14/how-agricultural-intensification-could-cut-global-farm-land-use-by-almost-50-increase-biodiversity-and-help-address-climate-change/?utm_source=jeeng)

National Biosafety Authority Kenya (2022): **GUIDELINES FOR DETERMINING THE REGULATORY PROCESS OF GENOME EDITED ORGANISMS AND PRODUCTS IN KENYA**

<https://www.biosafetykenya.go.ke/images/GENOME-EDITING-GUIDELINES-FINAL-VERSION-25th-Feb-2022-03.pdf>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): March week 09)

## Publications – Publikationen

DECHEMA (2022): **Biotechnologie 2040 – Blick in die Zukunft einer Schlüsseltechnologie**  
<https://view.genial.ly/6019441831720d0d312eaf20>

Wessler J. (2022): **The EU's farm-to-fork strategy: An assessment from the perspective of agricultural economics.** Appl Econ Perspect Policy | <https://doi.org/10.1002/aep.13239>  
The EU Farm to Fork (F2F) strategy includes a number of policy objectives that have implications for agricultural production in the EU and beyond. This contribution discusses the possible implications from an economic perspective. We draw on economic assessments by other authors and discuss their wider implications by considering only partially quantified benefits and costs. Overall, the assessments indicate a decline in EU agricultural production in quantitative terms. The F2F strategy negatively affects aggregate consumer surplus and—depending on the assumption made—a net increase or decrease in producer surplus, thereby inducing an overall net welfare loss. Partially quantified benefits and costs include the environmental benefits and costs linked to the F2F strategy, such as implications for greenhouse gas emissions, biodiversity, or the landscape. Therefore, by launching the strategy, policy makers have implicitly concluded that the additional net benefits outweigh the losses in consumer surplus. The economic studies combined with studies on the impact of agricultural practices on biodiversity and the emission of greenhouse gases do not support this claim without further technological and institutional changes, such as supporting the application of modern biotechnology by reducing regulatory hurdles. Also, whether most consumers will share this view remains to be seen. EU policy makers have it in their hands to implement the necessary institutional changes.  
<https://onlinelibrary.wiley.com/doi/full/10.1002/aep.13239>

Medina-Lozano, I., Díaz, A. (2022): **Applications of Genomic Tools in Plant Breeding: Crop Biofortification.** Int. J. Mol. Sci. 23, 3086. | <https://doi.org/10.3390/ijms23063086>  
Crop breeding has mainly been focused on increasing productivity, either directly or by decreasing the losses caused by biotic and abiotic stresses (that is, incorporating resistance to diseases and enhancing tolerance to adverse conditions, respectively). Quite the opposite, little attention has been paid to improve the nutritional value of crops. It has not been until recently that crop biofortification has become an objective within breeding programs, through either conventional methods or genetic engineering. There are many steps along this long path, from the initial evaluation of germplasm for the content of nutrients and health-promoting compounds to the development of biofortified varieties, with the available and future genomic tools assisting scientists and breeders in reaching their objectives as well as speeding up the process. This review offers a compendium of the genomic technologies used to explore and create biodiversity, to associate the traits of interest to the genome, and to transfer the genomic regions responsible for the desirable characteristics into potential new varieties. Finally, a glimpse of future perspectives and challenges in this emerging area is offered by taking the present scenario and the slow progress of the regulatory framework as the starting point.  
<https://www.mdpi.com/1422-0067/23/6/3086>

Rodríguez A.V., Rodríguez-Oramas C., Velázquez E.S., de la Torre A.H., Armendáriz C.R., Iruzubieta C.C. (2022): **Myths and Realities about Genetically Modified Food: A Risk-Benefit Analysis,** Appl. Sci., 12 (6), 2861 | <https://doi.org/10.3390/app12062861>  
The development and consumption of genetically modified (GM) crops are surrounded by controversy. According to proponents, only molecular biology approaches and genetic engineering tools are realistic food shortage solutions for the world's ever-growing population. The main purpose of this study is to review the impact of GM products on human, animal, and environmental health. People still reject GM crops not only because of safety concerns, but also for moral reasons. Toxicity, allergies, and possible horizontal gene transfer (HGT) to the environment or to other species have been associated with the marketing of GM products. Moreover, the scarce data available about the long-term implications of using GM crops is another opponent concern. Nevertheless, science has evidenced no harm from GM crops use to date but has, instead, reported several benefits that result from their commercialization, such as economic, environmental, and health benefits for the general public. Legislation and policies about GM product labeling standards are being discussed. To overcome emerging food security challenges, considering quality scientific information is essential rather than leaving the issue and merely moving toward moral discussion. Hence, a risk–benefit analysis is necessary.  
<https://www.mdpi.com/2076-3417/12/6/2861>

Raven S.A., Payne B., Bruce M. et al. (2022): **In silico evolution of nucleic acid-binding proteins from a nonfunctional scaffold.** Nat Chem Biol | <https://doi.org/10.1038/s41589-022-00967-y>  
Directed evolution emulates the process of natural selection to produce proteins with improved or altered functions. These approaches have proven to be very powerful but are technically challenging and particularly time and resource intensive. To bypass these limitations, we constructed a system to perform the entire process of directed evolution in silico. We employed iterative computational cycles of mutation and evaluation to predict mutations that confer high-affinity binding activities for DNA and RNA to an initial de novo designed

protein with no inherent function. Beneficial mutations revealed modes of nucleic acid recognition not previously observed in natural proteins, highlighting the ability of computational directed evolution to access new molecular functions. Furthermore, the process by which new functions were obtained closely resembles natural evolution and can provide insights into the contributions of mutation rate, population size and selective pressure on functionalization of macromolecules in nature.

<https://www.nature.com/articles/s41589-022-00967-y>

Panzeri D., Guidi Nissim,W., Labra M., Grassi F. (2022): **Revisiting the Domestication Process of African Vigna Species (Fabaceae): Background, Perspectives and Challenges.**

Plants, 11, 532. | <https://doi.org/10.3390/plants11040532>

Legumes are one of the most economically important and biodiverse families in plants recognised as the basis to develop functional foods. Among these, the Vigna genus stands out as a good representative because of its relatively recent African origin as well as its outstanding potential. Africa is a great biodiversity centre in which a great number of species are spread, but only three of them, Vigna unguiculata, Vigna subterranea and Vigna vexillata, were successfully domesticated. This review aims at analysing and valorising these species by considering the perspective of human activity and what effects it exerts. For each species, we revised the origin history and gave a focus on where, when and how many times domestication occurred. We provided a brief summary of bioactive compounds naturally occurring in these species that are fundamental for human wellbeing. The great number of wild lineages is a key point to improve landraces since the domestication process caused a loss of gene diversity. Their genomes hide a precious gene pool yet mostly unexplored, and genes lost during human activity can be recovered from the wild lineages and reintroduced in cultivated forms through modern technologies. Finally, we describe how all this information is game-changing to the design of future crops by domesticating de novo.

<https://www.mdpi.com/2223-7747/11/4/532>

George J.P., Sanders T.G.M., Timmermann V. et al. (2022): **European-wide forest monitoring substantiate the necessity for a joint conservation strategy to rescue European ash species (*Fraxinus* spp.).** Sci Rep 12, 4764 | <https://doi.org/10.1038/s41598-022-08825-6>

European ash (*Fraxinus excelsior*) and narrow-leafed ash (*F. angustifolia*) are keystone forest tree species with a broad ecological amplitude and significant economic importance. Besides global warming both species are currently under significant threat by an invasive fungal pathogen that has been spreading progressively throughout the continent for almost three decades. Ash dieback caused by the ascomycete *Hymenoscyphus fraxineus* is capable of damaging ash trees of all age classes and often ultimately leads to the death of a tree after years of progressively developing crown defoliation. While studies at national and regional level already suggested rapid decline of ash populations as a result of ash dieback, a comprehensive survey at European level with harmonized crown assessment data across countries could shed more light into the population decline from a pan-European perspective and could also pave the way for a new conservation strategy beyond national borders. Here we present data from the ICP Forests Level I crown condition monitoring from 27 countries resulting in > 36,000 observations. We found a substantial increase in defoliation and mortality over time indicating that crown defoliation has almost doubled during the last three decades. Hotspots of mortality are currently situated in southern Scandinavia and north-eastern Europe. Overall survival probability after nearly 30 years of infection has already reached a critical value of 0.51, but with large differences among regions (0.20–0.86). Both a Cox proportional hazard model as well as an Aalen additive regression model strongly suggest that survival of ash is significantly lower in locations with excessive water regime and which experienced more extreme precipitation events during the last two decades. Our results underpin the necessity for fast governmental action and joint rescue efforts beyond national borders since overall mean defoliation will likely reach 50% as early as 2030 as suggested by time series forecasting.

<https://www.nature.com/articles/s41598-022-08825-6>

## Industrial Biotechnology - White gene engineering

Editor: Pradeep Verma (2022): **Industrial Microbiology and Biotechnology**

Discusses the industrial production, recovery and applications of microbial bio-active compounds such as enzymes, organic acids, vitamins, antibiotics etc.

Describes CRISPR/Cas9-Mediated genome editing technologies for industrial application

Provides details about fermentation technologies, bioreactor designs and product recovery

<https://link.springer.com/book/10.1007/978-981-16-5214-1?noAccess=true>

Banks M., Johnson R., Giver L. Bryant G., Guo M. (2022): **Industrial production of microbial protein products.** Current Opinion in Biotechnology 75, 102707 |

<https://doi.org/10.1016/j.copbio.2022.102707>

Microbial proteins provide a sustainable and nutritious alternative to traditional animal and plant-based proteins. Various strains have been demonstrated to generate biomass from a wide variety of substrates, from organic waste (e.g. banana peel) to gases (e.g. methane). Industrial production of microbial protein has proven difficult from both design (e.g. production rate) and regulatory (e.g. [allergenicity](#) of product) perspectives for both feed and food-grade products. Through use of low-cost microfluidics devices, early bioprocess design can be intensified, achieving high strain screening throughput with low titres. Integration of industrial waste streams (e.g. flue-gases, lignocellulosic residues) can reduce cost and carbon footprint of feedstock, while

bespoke reactor design (e.g. Quorn's airlift U-loop fermenter) can remediate issues of low mass-transfer and product quality.

<https://www.sciencedirect.com/science/article/abs/pii/S0958166922000349>

Matsui T., Mullis M.N., Roy K.R. et al. (2022): **The interplay of additivity, dominance, and epistasis on fitness in a diploid yeast cross.** Nat Commun 13, 1463 |

<https://doi.org/10.1038/s41467-022-29111-z>

In diploid species, genetic loci can show additive, dominance, and epistatic effects. To characterize the contributions of these different types of genetic effects to heritable traits, we use a double barcoding system to generate and phenotype a panel of ~200,000 diploid yeast strains that can be partitioned into hundreds of interrelated families. This experiment enables the detection of thousands of epistatic loci, many whose effects vary across families. Here, we show traits are largely specified by a small number of hub loci with major additive and dominance effects, and pervasive epistasis. Genetic background commonly influences both the additive and dominance effects of loci, with multiple modifiers typically involved. The most prominent dominance modifier in our data is the mating locus, which has no effect on its own. Our findings show that the interplay between additivity, dominance, and epistasis underlies a complex genotype-to-phenotype map in diploids.

<https://www.nature.com/articles/s41467-022-29111-z.pdf>

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Wie immer wird für Hinweise und der Zusendung von Publikationen und sonstigen Informationen gedankt. pdf-Dateien können meist direkt aus den links heruntergeladen werden.

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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