

2022: Sunday Evening News No 261

Week 01 (2022-12-27 – 2022-01-02)

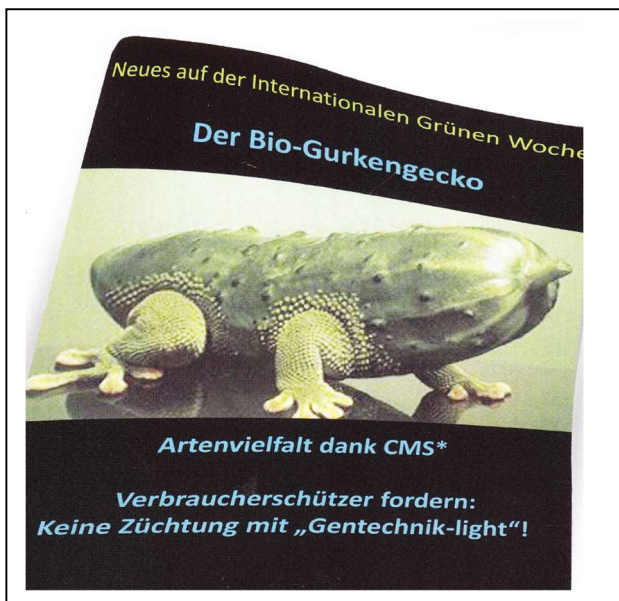
Selected and edited by **BGF** Jany

„Ein Optimist bleibt bis Mitternacht auf, um das neue Jahr zu begrüßen. Ein Pessimist bleibt wach, um sicherzustellen, dass das alte Jahr geht.“

“An optimist stays up until midnight to welcome the new year. A pessimist stays up to make sure the old year goes.”

Billy Vaughn, American musician

A Healthy New Year - and, if possible, no disabilities from Covid-19



Organic cucumber gecko

No breeding light!

► [SENews 51 - 2021](#)

► [SENews 52 – 2021](#)

► [SENews 01 – 2022](#)

Gen-Kartoffeln lassen das Gehirn schrumpfen (1998)

Am 17.12.2021 ist Dr. Arpad Pusztai im Alter von 91 Jahren verstorben. Dr. Pusztai war ein international anerkannter Wissenschaftler auf dem Gebiet der Lektinforschung. Er fühlte sich stets einer auf faktenberuhenden der Wissenschaft verpflichtet. Im August 1998 berichtete er über seine Forschungsergebnisse zu gentechnisch veränderten Kartoffeln im britischen Fernsehen und warnte vor der Gefährlichkeit gentechnisch veränderte Lebensmittel. Das Medienecho war international groß. Das erste „Erdbeben“ für Anwendungen der Gentechnik im Agrar- und Lebensmittelbereich war losgetreten. Die darauffolgende Auseinandersetzung über die Forschungsergebnisse wurde als **Pusztai-Affäre** bekannt.

► [Pusztai Affäre – Fütterungsversuche an Ratten mit Lektin-Kartoffeln](#)

Gene potatoes shrink the brain (1998)

On 17 December 17th 2021, Dr Arpad Pusztai passed away at the age of 91. Dr. Pusztai was an internationally recognised scientist in the field of lectin research. He always felt committed to a science based on facts. In August 1998, he reported on his research results on genetically modified potatoes on British television and warned of the dangers of genetically modified food. The media echo was great internationally. The first "earthquake"

for applications of genetic engineering in the agricultural and food sector was unleashed. The ensuing controversy over the research results became known as the Pusztai Affair.

► [Pusztai Affäre – Fütterungsversuche an Ratten mit Lektin-Kartoffeln](#)

EU Zulassungen 2021 von gentechnisch veränderten Pflanzen

Die EFSA hat 2021 für zehn (10) gentechnisch veränderte Pflanzen die Stellungnahmen der Sicherheitsbewertung veröffentlicht. Für vier gv-Pflanzen wurden sie bereits in das Komitologieverfahren einbezogen und das Verfahren abgeschlossen. Diese gv-Pflanzen wurde von der Kommission zugelassen ([Tabelle 1 in ► Zulassungen 2021](#))

Die [► Kommission hat 18 gentechnisch veränderte Pflanzen](#) für den Import als Lebens- und Futtermittel zugelassen. 12 gv-Pflanzen wurden erstmals zugelassen und für 6 wurde die Zulassung erneuert. Die durchschnittliche Zeitdauer für die Bearbeitung der Anträge - vom Eingang bei der EFSA bis zur Zulassung durch die Kommission - betrug für Neuzulassungen 66,3 Monate und für die Erneuerung der Zulassung 34,6 Monate.

GM plants – EU approvals -2021

In 2021 EFSA has published the safety assessment opinions for 10 GM plants. For four of them have already been included in the comitology procedure and the procedure has been completed. These GM plants have been authorised by the Commission (Table 1 in ► [Approvals 2021 Authorisations 2021](#)).

The [► Commission has approved 18 GM plants](#) for import as food and feed. 12 GM plants were authorised for the first time and for 6 the approval was renewed.

The average time taken to process applications - from receipt by EFSA to authorisation by the Commission - was 66.3 months for new authorisations and 34.6 months for authorisation renewals.

EFSA Sicherheitsbewertungen von Lebensmittelenzymen 2021

Die EFSA hat 2021 für 21 zwanzig Lebensmittelenzyme die Stellungnahmen der Sicherheitsbewertung veröffentlicht und im November 2021 noch für fünf weitere Lebensmittelenzyme die Stellungnahmen angenommen ([► Bewertung 2021](#)). Die Veröffentlichungen werden im Januar 2022 erfolgen. ► [Tabelle aller bislang sicherheitsbewerteter Lebensmittelenzyme](#).

In 2021, EFSA published the opinions of the safety assessment for 21 twenty food enzymes and in November 2021 it accepted the opinions for five further food enzymes ([► Assessment 2021](#)). The releases will probably take place in January 2022. ► [Table of all previously safety-rated food enzymes](#).

Meetings – Conferences / Tagungen - Konferenzen

Spring School 2022

Young Scientists Conference Food Biotechnology - Spring School in Geisenheim supported by DECHEMA

<https://dechema.de/Gremien+und+Netzwerke/Biotechnologie/Gremien/Lebensmittelbiotechnologie/Spring+School+2022.html>

Die Deadline zur Anmeldung ist der 15. Januar 2022.

BMEL: Global Forum for Food and Agriculture 2022

Fokus des GFFA 2022: Boden und Land

Das Global Forum for Food and Agriculture (GFFA) ist eine internationale Konferenz zu zentralen Zukunftsfragen der globalen Land- und Ernährungspolitik. Sie findet jährlich zeitgleich zur Internationalen Grünen Woche (IGW) in Berlin statt. Das GFFA wird veranstaltet vom Bundesministerium für Ernährung und Landwirtschaft (BMEL) in Kooperation mit dem Senat von Berlin, der Messe Berlin GmbH und dem GFFA Berlin e. V.

<https://www.bmel.de/SharedDocs/Termine/DE/2022-01-24-28-gffa.html>

Kaesler – Forum 2022

Antimicrobial (AMR) resistance ranks as one of the most severe health issues in the future for humans.

Moreover, livestock farming is well known as one of the significant users in the past, but what about now? How are authorities and regulations changing the use of antibiotics (AB) – and does it change the risk of resistances?

Find out more under www.kaesler.de

BVL: Programme for the 4th BVL/MRI Course on Food Safety, Food Authenticity and Risk Management

<https://www.bvl.bund.de/SharedDocs/Downloads/Events/ITS-Food/ITS-Food-2022-Programme.html?nn=16983550>

Press Releases – Media Reports / Pressemeldungen und Medienberichte

Awater-Esper S.: Veranstaltungsmarathon zur Agrarpolitik im Januar

Trotz der Absage der Internationalen Grünen Woche als Präsenzveranstaltung ist der Januar gefüllt mit digitalen Veranstaltungen zu Agrarpolitik, Landwirtschaft und Landleben.

https://www.topagrar.com/management-und-politik/news/veranstaltungsmarathon-zur-agrarpolitik-im-januar-12795708.html?utm_source=Maileon&utm_medium=email&utm_campaign=2022-01-06%20top%20agrar%20NEWS%20Donnerstag&utm_content=https://www.topagrar.com/management-und-politik/news/veranstaltungsmarathon-zur-agrarpolitik-im-januar-12795708.html

H. Bündler, M. Fehr, B. Freytag, T. Heeg, T. Neuscheler und S. Preuß: Die grüne Verwirrung

<https://www.faz.net/aktuell/wirtschaft/unternehmen/gruene-atomkraft-das-bedeutet-die-eu-neueinstufung-fuer-deutschland-17717434.html>

Tutt C.: Grüne Kompromisse: Willkommen in der Wirklichkeit

<https://www.wiwo.de/politik/deutschland/daily-punch-gruene-kompromisse-willkommen-in-der-wirklichkeit/27945546.html>

Awater-Esper S.: Özdemir fordert mehr Geld für den Umbau der Landwirtschaft

<https://www.topagrar.com/management-und-politik/news/oezdemir-fordert-mehr-geld-fuer-den-umbau-der-landwirtschaft-12792630.html>

Awater-Esper S.: Özdemir und Lemke wollen ab 2022 die Agrarpolitik umkrepeln

<https://www.topagrar.com/management-und-politik/news/oezdemir-und-lemke-wollen-ab-2022-die-agrarpolitik-umkrepeln-12787215.html>

Kockerols K.: Umweltministerin Lemke will keine Gentechnik-Reform

<https://www.topagrar.com/management-und-politik/news/umweltministerin-lemke-will-keine-gentechnik-reform-12774596.html>

Fortuna G. and Foote N.: 2022: CAP, Farm to Fork and other gifts that keep on giving

<https://www.euractiv.com/section/agriculture-food/news/2022-cap-farm-to-fork-and-other-gifts-that-keep-on-giving/>

University of Göttingen: New method to complete genetic data

<https://www.sciencedaily.com/releases/2022/01/220103121748.htm>

Hunt N.: Gene editing legislation to focus on crops - UK minister

<https://www.reuters.com/markets/commodities/gene-editing-legislation-focus-crops-uk-minister-2022-01-06/>

Dwivedi S.: Research Insights: How to Genetically Modify Rice for Less Methane Emission

<https://krishijagran.com/agriculture-world/research-insights-how-to-genetically-modify-rice-for-less-methane-emission/>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [▶ here](#): (January week 01)

December 2021

Nüsslein-Volhard C.: „Die Vernunft gebietet es, die Genschere im Ökoanbau zu nutzen“

<https://www.faz.net/aktuell/wissen/anklage-von-nobelpreistraegerin-genschere-im-oekoanbau-nutzen-17704218.html>

Max-Planck-Gesellschaft. "Radioactive radiation could damage biological tissue also via a previously unnoticed mechanism." ScienceDaily.

<http://www.sciencedaily.com/releases/2021/12/211227154333.htm>

Maxeiner D, Miersch M.: **Deutschland leidet unter gefährlicher Öko-Hysterie**

<https://www.welt.de/wirtschaft/article137324810/Deutschland-leidet-unter-gefaehrlicher-Oeko-Hysterie.html>

Publications – Publikationen

van Selm, B., Frehner, A., de Boer, I.J.M. et al. (2022): **Circularity in animal production requires a change in the EAT-Lancet diet in Europe.** *Nat Food* (2022).

<https://doi.org/10.1038/s43016-021-00425-3>

It is not known whether dietary guidelines proposing a limited intake of animal protein are compatible with the adoption of circular food systems. Using a resource-allocation model, we compared the effects of circularity on the supply of animal-source nutrients in Europe with the nutritional requirements of the EAT-Lancet reference diet. We found the two to be compatible in terms of total animal-source proteins but not specific animal-source foods; in particular, the EAT-Lancet guidelines recommend larger quantities of poultry meat over beef and pork, while a circular food system produces mainly milk, dairy-beef and pork. Compared with the EAT-Lancet reference diet, greenhouse gas emissions were reduced by up to 31% and arable land use reduced by up to 42%. Careful consideration of the feasible substitutability between animal-source foods is needed to define potential roles of animal products in circular human diets.

<https://www.nature.com/articles/s43016-021-00425-3>

<https://www.nature.com/articles/s43016-021-00425-3.pdf>

May, M., Giddings, L.V., DeLisi, C. et al. (2022): **Constructive principles for gene editing oversight.**

Nat Biotechnol | <https://doi.org/10.1038/s41587-021-01189-8>

National Academies of Sciences, Engineering, and Medicine 2021. **2021 Nobel Prize Summit:**

Our Planet, Our Future: Proceedings of a Summit. Washington, DC: The National Academies

Press. | <https://doi.org/10.17226/26310>. pdf-file: <http://nap.edu/26310>

Overcash J. and Golnar A.: (2021): **Facilitating the Conversation: Gene Drive Classification.**

Health Security 20, (1), | DOI: 10.1089/hs.2021.0109

Gene drives are an emerging technology with tremendous potential to impact public health, agriculture, and conservation. While gene drives can be described simply as selfish genetic elements (natural or engineered) that are inherited at non-Mendelian rates, upon closer inspection, engineered gene drive technology is a complex class of biotechnology that uses a diverse number of genetic features to bias rates of inheritance. As a complex technology, gene drives can be difficult to comprehend, not only for the public and stakeholders, but also to risk assessors, risk managers, and decisionmakers not familiar with gene drive literature. To address this difficulty, we describe a gene drive classification system based on 5 functional characteristics. These characteristics include a gene drive's objective, mechanism, release threshold, range, and persistence. The aggregate of the gene drive's characteristics can be described as the gene drive's architecture. Establishing a classification system to define different gene drive technologies should make them more comprehensible to the public and provide a framework to guide regulatory evaluation and decisionmaking.

<https://www.liebertpub.com/doi/abs/10.1089/hs.2021.0109?journalCode=hs> pdf-file available

Cheng Q.-Q., Ouyang Y., Tang Z.-Y., Lao C.-C., Zhang Y.-Y., Cheng C.-S., Zhou H. (2021):

Review on the Development and Applications of Medicinal Plant Genomes. *Front. Plant Sci.*

12: 791219. | doi: 10.3389/fpls.2021.791219

With the development of sequencing technology, the research on medicinal plants is no longer limited to the aspects of chemistry, pharmacology, and pharmacodynamics, but reveals them from the genetic level. As the price of next-generation sequencing technology becomes affordable, and the long-read sequencing technology is established, the medicinal plant genomes with large sizes have been sequenced and assembled more easily. Although the review of plant genomes has been reported several times, there is no review giving a systematic and comprehensive introduction about the development and application of medicinal plant genomes that have been reported until now. Here, we provide a historical perspective on the current situation of genomes in medicinal plant biology, highlight the use of the rapidly developing sequencing technologies, and conduct a comprehensive summary on how the genomes apply to solve the practical problems in medicinal plants, like genomics-assisted herb breeding, evolution history revelation, herbal synthetic biology study, and geoherb research, which are important for effective utilization, rational use and sustainable protection of medicinal plants.

<https://www.frontiersin.org/articles/10.3389/fpls.2021.791219/full>

Lentzos F., Rybicki E.P., Engelhard M., Paterson P., Sandholtz, W.A., Reeves R.G.

(2022): **Eroding norms over release of self-spreading viruses.** *Science* 375, Issue 6576, 31-33

| DOI: [10.1126/science.abj5593](https://doi.org/10.1126/science.abj5593)

An evidence-based norm collectively established and reinforced through the work of generations of virologists is that laboratory modifications of self-spreading viruses are genetically too unstable to be used safely and

predictably outside contained facilities. That norm now seems to be challenged. A range of transformational self-spreading applications have been put forward in recent years. In agriculture, for example, self-spreading viruses have been proposed as insecticides, or as vectors to modify planted crops. In health care, self-spreading viruses have been promoted as vaccines (1, 2). Yet, glossed over by these proposals is that the self-spreading dynamics of a virus repeatedly passing from host-to-host (passaging) give it substantial potential to alter its biological properties once released into the environment (see the box). We explore the consequences of this apparent norm erosion in the context of recent proposals to develop self-spreading genetically modified viruses, in wildlife management and in self-spreading vaccines.

<https://www.science.org/doi/10.1126/science.abj5593> pdf-file available

Pook T., Nemri A., Segovia R.G.G., Torres D.V., Simianer H., Schoen C.-C. (2021): **Increasing calling accuracy, coverage, and read-depth in sequence data by the use of haplotype blocks**. PLOS Genetics. 17 (12): e1009944 DOI: [10.1371/journal.pgen.1009944](https://doi.org/10.1371/journal.pgen.1009944)

High-throughput genotyping of large numbers of lines remains a key challenge in plant genetics, requiring geneticists and breeders to find a balance between data quality and the number of genotyped lines under a variety of different existing genotyping technologies when resources are limited. In this work, we are proposing a new imputation pipeline ("HBimpute") that can be used to generate high-quality genomic data from low read-depth whole-genome-sequence data. The key idea of the pipeline is the use of haplotype blocks from the software HaploBlocker to identify locally similar lines and subsequently use the reads of all locally similar lines in the variant calling for a specific line. The effectiveness of the pipeline is showcased on a dataset of 321 doubled haploid lines of a European maize landrace, which were sequenced at 0.5X read-depth. The overall imputing error rates are cut in half compared to state-of-the-art software like BEAGLE and STITCH, while the average read-depth is increased to 83X, thus enabling the calling of copy number variation. The usefulness of the obtained imputed data panel is further evaluated by comparing the performance of sequence data in common breeding applications to that of genomic data generated with a genotyping array. For both genome-wide association studies and genomic prediction, results are on par or even slightly better than results obtained with high-density array data (600k). In particular for genomic prediction, we observe slightly higher data quality for the sequence data compared to the 600k array in the form of higher prediction accuracies. This occurred specifically when reducing the data panel to the set of overlapping markers between sequence and array, indicating that sequencing data can benefit from the same marker ascertainment as used in the array process to increase the quality and usability of genomic data.

<https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1009944>

Lopez, S.C., Crawford, K.D., Lear, S.K. et al. (2021): **Precise genome editing across kingdoms of life using retron-derived DNA**. Nat Chem Biol | <https://doi.org/10.1038/s41589-021-00927-y>

Exogenous DNA can be a template to precisely edit a cell's genome. However, the delivery of in vitro-produced DNA to target cells can be inefficient, and low abundance of template DNA may underlie the low rate of precise editing. One potential tool to produce template DNA inside cells is a retron, a bacterial retroelement involved in phage defense. However, little effort has been directed at optimizing retrons to produce designed sequences. Here, we identify modifications to the retron non-coding RNA (ncRNA) that result in more abundant reverse-transcribed DNA (RT-DNA). By testing architectures of the retron operon that enable efficient reverse transcription, we find that gains in DNA production are portable from prokaryotic to eukaryotic cells and result in more efficient genome editing. Finally, we show that retron RT-DNA can be used to precisely edit cultured human cells. These experiments provide a general framework to produce DNA using retrons for genome modification.

<https://www.nature.com/articles/s41589-021-00927-y>

Piscotta F.J., Hans-Heinrich Hoffmann H.H., Choi Y.J., Small G.I. et al. (2021): **Metabolites with SARS-CoV-2 Inhibitory Activity Identified from Human Microbiome Commensals**. SM Journals / mSphere 6 (Issue 6) e00711-21 | <https://doi.org/10.1128/mSphere.00711-21>

The COVID-19 pandemic has highlighted the need to identify additional antiviral small molecules to complement existing therapies. Although increasing evidence suggests that metabolites produced by the human microbiome have diverse biological activities, their antiviral properties remain poorly explored. Using a cell-based SARS-CoV-2 infection assay, we screened culture broth extracts from a collection of phylogenetically diverse human-associated bacteria for the production of small molecules with antiviral activity. Bioassay-guided fractionation uncovered three bacterial metabolites capable of inhibiting SARS-CoV-2 infection. This included the nucleoside analogue N₆-(Δ^2 -isopentenyl)adenosine, the 5-hydroxytryptamine receptor agonist tryptamine, and the pyrazine 2,5-bis(3-indolylmethyl)pyrazine. The most potent of these, N₆-(Δ^2 -isopentenyl)adenosine, had a 50% inhibitory concentration (IC₅₀) of 2 μ M. These natural antiviral compounds exhibit structural and functional similarities to synthetic drugs that have been clinically examined for use against COVID-19. Our discovery of structurally diverse metabolites with anti-SARS-CoV-2 activity from screening a small fraction of the bacteria reported to be associated with the human microbiome suggests that continued exploration of phylogenetically diverse human-associated bacteria is likely to uncover additional small molecules that inhibit SARS-CoV-2 as well as other viral infections.

IMPORTANCE The continued prevalence of COVID-19 and the emergence of new variants has once again put the spotlight on the need for the identification of SARS-CoV-2 antivirals. The human microbiome produces an array of small molecules with bioactivities (e.g., host receptor ligands), but its ability to produce antiviral small

molecules is relatively underexplored. Here, using a cell-based screening platform, we describe the isolation of three microbiome-derived metabolites that are able to prevent SARS-CoV-2 infection *in vitro*. These molecules display structural similarities to synthetic drugs that have been explored for the treatment of COVID-19, and these results suggest that the microbiome may be a fruitful source of the discovery of small molecules with antiviral activities.

<https://journals.asm.org/doi/10.1128/mSphere.00711-21>

Gadau J. and Fewell J.H. (2022): **Supergenes, supergenomes, and complex social traits.**

PNAS 119 (2) e2118971118; | <https://doi.org/10.1073/pnas.2118971118>

In a new paper expanding the links between supergenes and complex social traits, Lagunas-Robles et al. (1) describe a supergene implicated in the control of reproductive sex allocation for two species of the ant genus *Formica*. The study identifies a supergene connected to the queen strategy of laying highly skewed or “split” sex ratios, in which colonies produce either almost all male or primarily female reproductive offspring. In doing so, the study offers a genomic insight into one of the most intriguing examples of parent–offspring conflict. Who—queens or workers—has primary control over colony allocation to reproductive sex ratios?

<https://www.sciencedirect.com/science/article/pii/S2667064X22000021>

Irwin N.A.T., Alexandros A. Pittis A. A., Richards, T.A., Patrick J. Keeling P.J. (2021):

Systematic evaluation of horizontal gene transfer between eukaryotes and viruses. Nature Microbiology | [10.1038/s41564-021-01026-3](https://doi.org/10.1038/s41564-021-01026-3)

Gene exchange between viruses and their hosts acts as a key facilitator of horizontal gene transfer and is hypothesized to be a major driver of evolutionary change. Our understanding of this process comes primarily from bacteria and phage co-evolution, but the mode and functional importance of gene transfers between eukaryotes and their viruses remain anecdotal. Here we systematically characterized viral–eukaryotic gene exchange across eukaryotic and viral diversity, identifying thousands of transfers and revealing their frequency, taxonomic distribution and projected functions. Eukaryote-derived viral genes, abundant in the *Nucleocyotiviricota*, highlighted common strategies for viral host-manipulation, including metabolic reprogramming, proteolytic degradation and extracellular modification. Furthermore, viral-derived eukaryotic genes implicate genetic exchange in the early evolution and diversification of eukaryotes, particularly through viral-derived glycosyltransferases, which have impacted structures as diverse as algal cell walls, trypanosome mitochondria and animal tissues. These findings illuminate the nature of viral–eukaryotic gene exchange and its impact on the evolution of viruses and their eukaryotic hosts.

<https://www.nature.com/articles/s41564-021-01026-3.pdf>

Lentzos F., Rybicki E.P., Engelhard, Paterson P., Sandholtz W.A., R. G. Reeves R.G. (2022):

Eroding norms over release of self-spreading viruses. Science 375, Issue 6576, 31-33, | doi/10.1126/science.abj5593

<https://www.science.org/stoken/author-tokens/ST-253/full>

del Mar Martínez-Prada M., Curti S.J. & Juan J Gutiérrez-González J.J.(2021): **Potato improvement through genetic engineering.** GM Crops & Food, 12:1, 479-496, DOI:

[10.1080/21645698.2021.1993688](https://doi.org/10.1080/21645698.2021.1993688)

Potato (*Solanum tuberosum* L.) is the third most important crop worldwide and a staple food for many people worldwide. Genetically, it poses many challenges for traditional breeding due to its autotetraploid nature and its tendency toward inbreeding depression. Breeding programs have focused on productivity, nutritional quality, and disease resistance. Some of these traits exist in wild potato relatives but their introgression into elite cultivars can take many years and, for traits such as pest resistance, their effect is often short-lasting. These problems can be addressed by genetic modification (GM) or gene editing (GE) and open a wide horizon for potato crop improvement. Current genetically modified and gene edited varieties include those with Colorado potato beetle and late blight resistance, reduction in acrylamide, and modified starch content. RNAi hairpin technology can be used to silence the haplo-alleles of multiple genes simultaneously, whereas optimization of newer gene editing technologies such as base and prime editing will facilitate the routine generation of advanced edits across the genome. These technologies will likely gain further relevance as increased target specificity and decreased off-target effects are demonstrated. In this Review, we discuss recent work related to these technologies in potato improvement

<https://www.tandfonline.com/doi/pdf/10.1080/21645698.2021.1993688?needAccess=true>

Darlington, M.; Reinders, J.D.; Sethi, A.; Lu, A.L.; et al. (2022): **RNAi for Western Corn Rootworm Management: Lessons Learned, Challenges, and Future Directions.** Insects 13, 57. |

<https://doi.org/10.3390/insects13010057>

The western corn rootworm (WCR), *Diabrotica virgifera virgifera* LeConte, is considered one of the most economically important pests of maize (*Zea mays* L.) in the United States (U.S.) Corn Belt with costs of management and yield losses exceeding USD ~1–2 billion annually. WCR management has proven challenging given the ability of this insect to evolve resistance to multiple management strategies including synthetic insecticides, cultural practices, and plant-incorporated protectants, generating a constant need to develop new management tools. One of the most recent developments is maize expressing double-stranded hairpin RNA structures targeting housekeeping genes, which triggers an RNA interference (RNAi) response and eventually

leads to insect death. Following the first description of in planta RNAi in 2007, traits targeting multiple genes have been explored. In June 2017, the U.S. Environmental Protection Agency approved the first in planta RNAi product against insects for commercial use. This product expresses a dsRNA targeting the WCR *snf7* gene in combination with Bt proteins (Cry3Bb1 and Cry34Ab1/Cry35Ab1) to improve trait durability and will be introduced for commercial use in 2022.

<https://www.mdpi.com/2075-4450/13/1/57>

Radenkovs V., Radenkova K.J., Kvišis J., Danija Lazdina D. (2021): **Lignocellulose-Degrading Enzymes: A Biotechnology Platform for Ferulic Acid Production from Agro-Industrial Side Streams.** *Foods* 10 (12), 3056; <https://doi.org/10.3390/foods10123056>

Biorefining by enzymatic hydrolysis (EH) of lignocellulosic waste material due to low costs and affordability has received enormous interest amongst scientists as a potential strategy suitable for the production of bioactive ingredients and chemicals. In this study, a sustainable and eco-friendly approach to extracting bound ferulic acid (FA) was demonstrated using single-step EH by a mixture of lignocellulose-degrading enzymes. For comparative purposes of the efficiency of EH, an online extraction and analysis technique using supercritical fluid extraction–supercritical fluid chromatography–mass spectrometry (SFE-SFC-MS) was performed. The experimental results demonstrated up to 369.3 mg 100 g⁻¹ FA release from rye bran after 48 h EH with Viscozyme L. The EH of wheat and oat bran with Viscoferm for 48 h resulted in 255.1 and 33.5 mg 100 g⁻¹ of FA, respectively. The release of FA from bran matrix using supercritical fluid extraction with carbon dioxide and ethanol as a co-solvent (SFE-CO₂-EtOH) delivered up to 464.3 mg 100 g⁻¹ of FA, though the extractability varied depending on the parameters used. The 10-fold and 30-fold scale-up experiments confirmed the applicability of EH as a bioprocessing method valid for the industrial scale. The highest yield of FA in both scale-up experiments was obtained from rye bran after 48 h of EH with Viscozyme L. In purified extracts, the absence of xylose, arabinose, and glucose as the final degradation products of lignocellulose was proven by high-performance liquid chromatography with refractive index detection (HPLC-RID). Up to 94.0% purity of FA was achieved by solid-phase extraction (SPE) using the polymeric reversed-phase Strata X column and 50% EtOH as the eluent.

https://www.mdpi.com/2304-8158/10/12/3056?type=check_update&version=2

Reimer C., Kufs J.E., Rautschek J., Regestein L., Valiante V, Hillmann F. (2022): **Engineering the amoeba *Dictyostelium discoideum* for biosynthesis of a cannabinoid precursor and other polyketides.** *Nat Biotechnol* | <https://doi.org/10.1038/s41587-021-01143-8>

Aromatic polyketides are natural polyphenolic compounds with a broad spectrum of pharmacological activities. Production of those metabolites in the model organisms *Escherichia coli* and *Saccharomyces cerevisiae* has been limited by the extensive cellular engineering needed for the coordinated biosynthesis of polyketides and their precursors. In contrast, the amoeba *Dictyostelium discoideum* is a native producer of secondary metabolites and harbors a wide, but largely unexplored, repertoire of genes for the biosynthesis of polyketides and terpenoids. Here we present *D. discoideum* as an advantageous chassis for the production of aromatic polyketides. By expressing its native and cognate plant polyketide synthase genes in *D. discoideum*, we demonstrate production of phlorocaprophenone, methyl-olivetol, resveratrol and olivetolic acid (OA), which is the central intermediate in the biosynthesis of cannabinoids. To facilitate OA synthesis, we further engineered an amoeba/plant inter-kingdom hybrid enzyme that produced OA from primary metabolites in two enzymatic steps, providing a shortcut in a synthetic cannabinoid pathway using the *D. discoideum* host system.

<https://www.nature.com/articles/s41587-021-01143-8>

Sächsischer Landtag: Thema: Gentechnik-Bakterien

Kleine Anfrage des Abgeordneten Andreas Heinz (CDU): Drs.-Nr.: 7/8239

Zusatzstoffe, Enzyme – Vorhandensein von GVO oder rDNA

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.

As always, I thank you all for hints and for publications. Most of the pdf files can be downloaded directly from the links.

Klaus-Dieter Jany
Nelkenstrasse 36
D-76351 Linkenheim-Hochstetten
jany@biotech-gm-food.com

1. Vorsitzender des WGG e.V.
Postfach 120721
D-60114 Frankfurt/Main
jany@wgg-ev.de