

Sunday Evening News No 264

Week 04 (2022-01-24 – 2022-30-01)

Selected and edited by **BGF** Jany

Meetings – Conferences

D.B.T: Deutsche Biotechnologietage 2022

4. und 5. Mai, Hamburg

<https://www.biotechnologietage.de/de/>

AbL: Agrarpolitische Fortbildungsreihe der AbL

<https://www.abl-ev.de/initiativen/fortbildungsreihe/>

Press Releases – Media Reports / Pressemeldungen und Medienberichte

gg.sda: Nationalratskommission will Ausnahmen von Gentech-Moratorium prüfen

<http://www.bluewin.ch/de/news/schweiz/nationalratskommission-will-ausnahmen-von-gentech-moratorium-pruefen-1065253.html>

Wissen und Forschung; China erlaubt Gene Editing von Nutzpflanzen

<https://www.forschung-und-wissen.de/nachrichten/umwelt/china-erlaubt-gene-editing-von-nutzpflanzen-13375810>

Maina J.: China pushes ahead with GMO crops to safeguard food security

https://geneticliteracyproject.org/2022/01/27/china-pushes-ahead-with-gmo-crops-to-safeguard-food-security/?utm_medium=email&utm_source=jeeng

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 04)

Publications – Publikationen

Götz L., Svanidze M., Tissier, A., Alejandro D.A. (2022). Consumers' Willingness to Buy CRISPR Gene-Edited Tomatoes: Evidence from a Choice Experiment Case Study in Germany. Sustainability 14, 971. 10.3390/su14020971

The CRISPR gene-editing (GE) breeding method is used to increase the resilience of high-yielding tomato cultivars against pests and diseases, reducing crop protection requirements. This study investigated consumers' willingness to buy CRISPR GE tomatoes in a repeated discrete-choice experiment. We observed a strong positive effect of providing information on the CRISPR breeding technology, while the sensory experience of the CRISPR GE tomatoes in a visit to a greenhouse had a rather weak, predominantly negative effect on the participants' willingness to buy CRISPR GE tomatoes. We found that roughly half of the 32 participants demonstrated constant CRISPR GE tomato choices during the experiments, and these participants were mainly employed as scientists. However, the rest of the participants changed their CRISPR GE tomato choices, with the majority showing an increase in their willingness to buy CRISPR GE tomatoes; these "changers" were dominated by non-scientists. Science communication on CRISPR GE breeding technology should target people with little knowledge about the technology, and consumers of organic tomatoes seem to have more specified, stable preferences regarding the technology. Further, scientific information about the CRISPR GE methodology should preferentially be provided when new technology and information about it are not yet widespread and people have not yet formed a strong opinion about the technology

<https://www.mdpi.com/2071-1050/14/2/971>

Krink N., Löchner A.C., Cooper H., Beisel C.L. Di Ventura B. (2022): Synthetic biology landscape and community in Germany. Biotechnology Notes 3 (2022) 8–14 |

<https://doi.org/10.1016/j.biotno.2021.12.001>

Despite its start in the early 2000s, synthetic biology is still overall perceived as a young discipline. In some countries, such as the US, synthetic biology is academically and industrially established, while in others, including Germany, it is still an upcoming field of research. Issues with funding schemes, commercial translation of technologies, public perception, and regulations need to be addressed to establish synthetic biology as a key discipline of the 21st century. This perspective article reviews the German and European synthetic biology landscape and how the German Association for Synthetic Biology (GASB) is addressing the above-mentioned challenges with its events and community-building activities.

<https://www.sciencedirect.com/science/article/pii/S2665906921000179>

Rizzo G., Monzona J.P., Fatima A. Tenorio F.A., Howard R. et al. (2022): **Climate and agronomy, not genetics, underpin recent maize yield gains in favorable environments**, PNAS 119 (4) e2113629119 | <https://doi.org/10.1073/pnas.2113629119>

Quantitative understanding of factors driving yield increases of major food crops is essential for effective prioritization of research and development. Yet previous estimates had limitations in distinguishing among contributing factors such as changing climate and new agronomic and genetic technologies. Here, we distinguished the separate contribution of these factors to yield advance using an extensive database collected from the largest irrigated maize-production domain in the world located in Nebraska (United States) during the 2005-to-2018 period. We found that 48% of the yield gain was associated with a decadal climate trend, 39% with agronomic improvements, and, by difference, only 13% with improvement in genetic yield potential. The fact that these findings were so different from most previous studies, which gave much-greater weight to genetic yield potential improvement, gives urgency to the need to reevaluate contributions to yield advances for all major food crops to help guide future investments in research and development to achieve sustainable global food security. If genetic progress in yield potential is also slowing in other environments and crops, future crop-yield gains will increasingly rely on improved agronomic practices.
<https://www.pnas.org/content/pnas/119/4/e2113629119.full.pdf>

May, M., Giddings, L.V., DeLisi, C. et al. (2022): **Constructive principles for gene editing oversight**. Nat Biotechnol 40, 17–18 | <https://doi.org/10.1038/s41587-021-01189-8>
<https://www.nature.com/articles/s41587-021-01189-8.pdf>

Rull V.: (2022): **Biodiversity crisis or sixth mass extinction?**
Does the current anthropogenic biodiversity crisis really qualify as a mass extinction?
EMBO reports 23: e54193 | DOI 10.15252/embr.202154193

Mohan, C., Easterling, M. & Yau, YY. (2022): **Gene Editing Technologies for Sugarcane Improvement: Opportunities and Limitations**. Sugar Tech 24, 369–385 |
<https://doi.org/10.1007/s12355-021-01045-8>

Plant-based biofuels present a promising alternative to depleting non-renewable fuel resources. One of the benefits of biofuel is reduced environmental impact, including reduction in greenhouse gas emission which causes climate change. Sugarcane is one of the most important bioenergy crops. Sugarcane juice is used to produce table sugar and first-generation biofuel (e.g., bioethanol). Sugarcane bagasse is also a potential material for second-generation cellulosic biofuel production. Researchers worldwide are striving to improve sugarcane biomass yield and quality by a variety of means including biotechnological tools. This paper reviews the use of sugarcane as a feedstock for biofuel production, and gene manipulation tools and approaches, including RNAi and genome-editing tools, such as TALENs and CRISPR-Cas9, for improving its quality. The specific focus here is on CRISPR system because it is low cost, simple in design and versatile compared to other genome-editing tools. The advance of CRISPR-Cas9 technology has transformed plant research with its ability to precisely delete, insert or replace genes in recent years. Lignin is the primary material responsible for biomass recalcitrance in biofuel production. The use of genome editing technology to modify lignin composition and distribution in sugarcane cell wall has been realized. The current and potential applications of genome editing technology for sugarcane improvement are discussed. The advantages and limitations of utilizing RNAi and TALEN techniques in sugarcane improvement are discussed as well.
<https://link.springer.com/content/pdf/10.1007/s12355-021-01045-8.pdf>

Hüdig M., Laibach N, Hein A.-C. (2022): **Genome Editing in Crop Plant Research—Alignment of Expectations and Current Developments** Plants 11(2), 212 |
<https://doi.org/10.3390/plants11020212>

The rapid development of genome editing and other new genomic techniques (NGT) has evoked manifold expectations on purposes of the application of these techniques to crop plants. In this study, we identify and align these expectations with current scientific development. We apply a semi-quantitative text analysis approach on political, economic, and scientific opinion papers to disentangle and extract expectations towards the application of NGT-based plants. Using the sustainable development goals (SDG) of the 2030 agenda as categories, we identify contributions to food security or adaptation to climatic changes as the most frequently mentioned expectations, accompanied by the notion of sustainable agriculture and food systems. We then link SDG with relevant plant traits and review existing research and commercial field trials for genome-edited crop plants. For a detailed analysis we pick as representative traits drought tolerance and resistance against fungal pathogens. Diverse genetic setscrews for both traits have been identified, modified, and tested under laboratory conditions, although there are only a few in the field. All in all, NGT-plants that can withstand more than one stressor or different environments are not documented in advanced development states. We further conclude that developing new plants with modified traits will not be sufficient to reach food security or adaptation to climatic changes in a short time frame. Further scientific development of sustainable agricultural systems will need to play an important role to tackle SDG challenges, as well.
<https://www.mdpi.com/2223-7747/11/2/212>

Ye, C., Wang, ZW., Sheng, Y.L. et al. (2022): **GNBP1 as a potential RNAi target to enhance the virulence of *Beauveria bassiana* for aphid control.** J Pest Sci 95, 87–100 | <https://doi.org/10.1007/s10340-021-01388-x>

Gram-negative binding proteins (GNBPs) are important in the innate immune system of insects in recognition of fungi pathogen, such as *Beauveria bassiana*. However, this information in aphids is not clear, which might be exploited to develop a novel aphid control strategy based on integrating RNAi and *B. bassiana*. Here, we firstly identified two GNBPs, *ApGNBP1* and *ApGNBP2*, using the model aphid *Acyrtosiphon pisum*, and observed that two *ApGNBPs* were highly expressed in hemolymph and fat body as well as upon the injection of β -1,3-glucan and heat-killed *B. bassiana*. Intriguingly, RNAi-based silencing of *ApGNBP1* but not *ApGNBP2* decreased the activity of immune-related phenoloxidase. This led to the increased virulence of *B. bassiana* in *A. pisum* upon silencing of *ApGNBP1*, and the synergetic effects were also observed in other two aphids: *Myzus persicae* and *Aphis citricidus*. Importantly, no negative effects were detected in aphid predator *Propylaea japonica* under the co-application of the RNAi in targeting *ApGNBP1* and *B. bassiana*. Taking together, we conclude that *GNBP1* could be an optimal target in aphid control by combining RNAi, entomopathogenic fungi and ladybeetle predator.

<https://link.springer.com/article/10.1007%2Fs10340-021-01388-x>

Chu Y. et al. (2022): **Registration of three peanut allotetraploid interspecific hybrids resistant to late leaf spot disease and tomato spotted wilt,** Journal of Plant Registrations | DOI: [10.1002/plr.20146](https://doi.org/10.1002/plr.20146)

Cultivated peanut (*Arachis hypogaea* L.) has a narrow genetic base and is isolated from its wild relatives. This genetic bottleneck results in a lack of strong resistance to biotic and abiotic stress. However, high levels of genetic variation and resistance exist among the wild relatives. In order to enlarge the genetic base of cultivated peanut and introgress beneficial alleles from the wild relatives, interspecific hybrids were produced among a set of selected diploid species. Upon colchicine treatment, fertile allotetraploids were recovered from three combinations including (*A. ipaënsis* KG 30076 × *A. correntina* GKP 9530)^{4x} (Reg. no. GP-241, PI 695391), (*A. ipaënsis* KG 30076 × *A. duranensis* KGBSPSc 30060)^{4x} (Reg. no. GP-242, PI 695392), and (*A. valida* KG30011 × *A. stenosperma* V 10309)^{4x} (Reg. no. GP-243, PI 695393). All of them demonstrated high levels of resistance to leaf spot diseases in the field. Tolerance to *Tomato spotted wilt virus* was found in (*A. valida* KG 30011 × *A. stenosperma* V 10309)^{4x}. These newly created allotetraploids are cross-compatible with cultivated peanut. These genetic resources will provide peanut breeding researchers with new sources of disease resistances to improve the agronomic performance of cultivated peanut.

<https://access.onlinelibrary.wiley.com/doi/epdf/10.1002/plr.20146>

Kashojiya S., 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, uhab004, <https://doi.org/10.1093/hr/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/advance-article/doi/10.1093/hr/uhab004/6511229>

Moon S., An J.Y., Choi, Y.-J., Oh Y.-L., Ro H.-S. & Ryu H. (2021): **Construction of a CRISPR/Cas9-Mediated Genome Editing System in *Lentinula edodes*,** Mycobiology, 49:6, 599-603, DOI: [10.1080/12298093.2021.2006401](https://doi.org/10.1080/12298093.2021.2006401)

CRISPR/Cas9 genome editing systems have been established in a broad range of eukaryotic species. Herein, we report the first method for genetic engineering in pyogo (shiitake) mushrooms (*Lentinula edodes*) using CRISPR/Cas9. For *in vivo* expression of guide RNAs (gRNAs) targeting the mating-type gene *HD1* (*LeA1*), we identified an endogenous *LeU6* promoter in the *L. edodes* genome. We constructed a plasmid containing the *LeU6* and *glyceraldehyde-3-phosphate dehydrogenase* (*LeGPD*) promoters to express the Cas9 protein. Among the eight gRNAs we tested, three successfully disrupted the *LeA1* locus. Although the CRISPR-Cas9-induced alleles did not affect mating with compatible monokaryotic strains, disruption of the transcription levels of the downstream genes of *LeHD1* and *LeHD2* was detected. Based on this result, we present the first report of a simple and powerful genetic manipulation tool using the CRISPR/Cas9 toolbox for the scientifically and industrially important edible mushroom, *L. edodes*.

<https://www.tandfonline.com/doi/full/10.1080/12298093.2021.2006401>

Yao X., Lu Z., Yu Song, Y, X., Corlett R.T. (2022): **A chromosome-scale genome assembly for the holly (*Ilex polyneura*) provides insights into genomic adaptations to elevation in Southwest China**, *Horticulture Research*, Volume 9, uhab049, | <https://doi.org/10.1093/hr/uhab049>

Southwest China is a plant diversity hotspot. The near-cosmopolitan genus *Ilex* (c. 664 spp., Aquifoliaceae) reaches its maximum diversity in this region, with many narrow-range and a few widespread species. Divergent selection on widespread species leads to local adaptation, with consequences for both conservation and utilization, but is counteracted by geneflow. Many *Ilex* species are utilized as teas, medicines, ornamentals, honey plants, and timber, but variation below the species level is largely uninvestigated. We therefore studied the widespread *Ilex polyneura*, which occupies most of the elevational range available and is cultivated for its decorative leafless branches with persistent red fruits. We assembled a chromosome-scale genome using approximately 100x whole genome long-read and short-read sequencing combined with Hi-C sequencing. The genome is approximately 727.1 Mb, with a contig N50 size of 5 124 369 bp and a scaffold N50 size of 36 593 620 bp, for which the BUSCO score was 97.6%, and 98.9% of the assembly was anchored to 20 pseudochromosomes. Out of 32 838 genes predicted, 96.9% were assigned functions. Two whole genome duplication events were identified. Using this genome as a reference, we conducted a population genomics study of 112 individuals from 21 populations across the elevation range using restriction site-associated DNA sequencing (RADseq). Most populations clustered into four clades separated by distance and elevation. Selective sweep analyses identified 34 candidate genes potentially under selection at different elevations, with functions related to responses to abiotic and biotic stresses. This first high-quality genome in the Aquifoliales will facilitate the further domestication of the genus.

<https://academic.oup.com/hr/article/doi/10.1093/hr/uhab049/6497789>

Khan N.M.M., Islam K.K., Ashraf A., Barman C.N.(2022): **A review on genome editing by CRISPR-Cas9 technique for cancer treatment**. *WCRJ* 2020; 7: e1510 | DOI: 10.32113/wcrj_20203_1510

In this review, we summarize CRISPR-Cas9 system-based gene modification for the therapeutic treatment of cancer. Cancer is a group of diseases involving anomalous cell growth with the potential to invade or blow out to other parts of the body, which is considered by not only multiple genetic but also epigenetic amendments that drive malignant cell propagation and consult chemo-resistance. The ability to correct or ablating such mutations holds enormous promise for battling cancer. Recently, because of its great efficiency and truthfulness, the CRISPR-Cas9 advanced genome editing technique has been extensively used in therapeutic investigations of cancers. Several studies used CRISPR-Cas9 technique for directly pointing cancer cell genomic DNA in cellular and animal cancer models, which have shown therapeutic potential in intensifying anti-cancer protocols. Moreover, CRISPR-Cas9 can also be engaged to fight oncogenic infections, discover anticancer drugs, and engineer immune cells and oncolytic viruses for immunotherapeutic treatment of cancer. We have been discussed the challenges and enhancements in translating therapeutic methods with CRISPR-Cas9 for clinical use. Therefore, in the study we suggested the potential directions of the CRISPR-Cas9 system for future cancer therapy.

<https://www.wcrj.net/article/1510>

<https://www.wcrj.net/wp-content/uploads/sites/5/2020/03/e1510-A-review-on-genome-editing-by-crispr-cas9-technique-for-cancer-treatment.pdf>

Lee M.H., Shin J.I., Yang Y.W., Lee K.H. et al. (2022): **Genome Editing Using CRISPR-Cas9 and Autoimmune Diseases: A Comprehensive Review**. *Int. J. Mol. Sci.* 2022, 23(3), 1337; <https://doi.org/10.3390/ijms23031337>

Autoimmune diseases are disorders that destruct or disrupt the body's own tissues by its own immune system. Several studies have revealed that polymorphisms of multiple genes are involved in autoimmune diseases. Meanwhile, gene therapy has become a promising approach in autoimmune diseases, and clustered regularly interspaced palindromic repeats and CRISPR-associated protein 9 (CRISPR-Cas9) has become one of the most prominent methods. It has been shown that CRISPR-Cas9 can be applied to knock out proprotein convertase subtilisin/kexin type 9 (PCSK9) or block PCSK9, resulting in lowering low-density lipoprotein cholesterol. In other studies, it can be used to treat rare diseases such as ornithine transcarbamylase (OTC) deficiency and hereditary tyrosinemia. However, few studies on the treatment of autoimmune disease using CRISPR-Cas9 have been reported so far. In this review, we highlight the current and potential use of CRISPR-Cas9 in the management of autoimmune diseases. We summarize the potential target genes for immunomodulation using CRISPR-Cas9 in autoimmune diseases including rheumatoid arthritis (RA), inflammatory bowel diseases (IBD), systemic lupus erythematosus (SLE), multiple sclerosis (MS), type 1 diabetes mellitus (DM), psoriasis, and type 1 coeliac disease. This article will give a new perspective on understanding the use of CRISPR-Cas9 in autoimmune diseases not only through animal models but also in human models. Emerging approaches to investigate the potential target genes for CRISPR-Cas9 treatment may be promising for the tailored immunomodulation of some autoimmune diseases in the near future.

<https://www.mdpi.com/1422-0067/23/3/1337/htm>

Tan R., Krueger, R.K, Gramelspacher M.J., Zhou X. et al. (2022): **Cas11 enables genome engineering in human cells with compact CRISPR-Cas3 systems**, *Molecular Cell* | DOI: [10.1016/j.molcel.2021.12.032](https://doi.org/10.1016/j.molcel.2021.12.032)

Leading CRISPR-Cas technologies employ Cas9 and Cas12 enzymes that generate RNA-guided dsDNA breaks. Yet, the most abundant microbial adaptive immune systems, Type I CRISPRs, are under-exploited for eukaryotic applications. Here, we report the adoption of a minimal CRISPR-Cas3 from *Neisseria lactamica* (Nla) type I-C system to create targeted large deletions in the human genome. RNP delivery of its processive Cas3 nuclease and target recognition complex Cascade can confer ~95% editing efficiency. Unexpectedly, NlaCascade assembly in bacteria requires internal translation of a hidden component Cas11 from within the *cas8* gene. Furthermore, expressing a separately encoded NlaCas11 is the key to enable plasmid- and mRNA-based editing in human cells. Finally, we demonstrate that supplying *cas11* is a universal strategy to systematically implement divergent I-C, I-D, and I-B CRISPR-Cas3 editors with compact sizes, distinct PAM preferences, and guide orthogonality. These findings greatly expand our ability to engineer long-range genome edits.
<https://www.sciencedirect.com/science/article/abs/pii/S1097276521011370?via%3Dihub>

Barber, A.E., Sae-Ong, T., Kang, K. et al. (2021): ***Aspergillus fumigatus* pan-genome analysis identifies genetic variants associated with human infection.** Nat Microbiol 6, 1526–1536 | <https://doi.org/10.1038/s41564-021-00993-x>

Aspergillus fumigatus is an environmental saprobe and opportunistic human fungal pathogen. Despite an estimated annual occurrence of more than 300,000 cases of invasive disease worldwide, a comprehensive survey of the genomic diversity present in *A. fumigatus*—including the relationship between clinical and environmental isolates and how this genetic diversity contributes to virulence and antifungal drug resistance—has been lacking. In this study we define the pan-genome of *A. fumigatus* using a collection of 300 globally sampled genomes (83 clinical and 217 environmental isolates). We found that 7,563 of the 10,907 unique orthogroups (69%) are core and present in all isolates and the remaining 3,344 show presence/absence of variation, representing 16–22% of the genome of each isolate. Using this large genomic dataset of environmental and clinical samples, we found an enrichment for clinical isolates in a genetic cluster whose genomes also contain more accessory genes, including genes coding for transmembrane transporters and proteins with iron-binding activity, and genes involved in both carbohydrate and amino-acid metabolism. Finally, we leverage the power of genome-wide association studies to identify genomic variation associated with clinical isolates and triazole resistance as well as characterize genetic variation in known virulence factors. This characterization of the genomic diversity of *A. fumigatus* allows us to move away from a single reference genome that does not necessarily represent the species as a whole and better understand its pathogenic versatility, ultimately leading to better management of these infections.
<https://www.nature.com/articles/s41564-021-00993-x>

Dapa, T. et al. (2022): **Diet Leaves a Genetic Signature in a Keystone Member of the Gut Microbiota.** *Cell Host & Microbe*. doi.org/10.2139/ssrn.3907580

Dietary switch from a low-fat and high-fiber diet to a Western-style high-fat and high-sugar diet is a common cause of microbiota imbalances underlying a variety of pathological conditions (dysbiosis). Although the effects of such dietary changes on microbiota composition and functions are well documented, their putative impact in gut bacterial evolution remains unexplored. Here we followed the emergence of mutations in *Bacteroides thetaiotaomicron*, a prevalent fiber-degrading microbiota member, upon colonization of the murine gut under different dietary regimens. *B. thetaiotaomicron* evolved rapidly to the gut and Western-style diet selected for mutations that promote the degradation of mucin-derived glycans. Periodic changes in diet led to fluctuations in the frequency of such mutations and were associated with metabolic shifts, resulting in the maintenance of higher intra-species genetic diversity compared to constant dietary regimens. Finally, our results suggest that *B. thetaiotaomicron* genetic diversity can be a biomarker for dietary differences among individuals.
https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3907580

Ma, J., Wang, J., Xu, L. et al. (2022): **The beneficial effects of genetically engineered *Escherichia coli* Nissle 1917 in obese C57BL/6J mice.** Int J Obes | <https://doi.org/10.1038/s41366-022-01073-8>

Background: Genetically modified probiotics have potential for use as a novel approach to express bioactive molecules for the treatment of obesity. The objective of the present study was to investigate the beneficial effect of genetically modified *Escherichia coli* Nissle 1917 (EcN-GM) in obese C57BL/6J mice.
Methods: First, an obesity model in C57BL/6J mice was successfully established. Then, the obese mice were randomly assigned into three groups: obese mice (OB), obese mice + EcN-GM (OB + EcN-GM), and obese mice + orlistat (OB + orlistat) ($n = 10$ in each group). The three groups were gavaged with 0.3 ml of 10^{10} CFU/ml control EcN, EcN-GM (genetically engineered EcN) and 10 ml/kg orlistat. Body weight, food consumption, fat pad and organ weight, hepatic biochemistry and hepatic histopathological alterations were measured. The effects of EcN-GM on the levels of endocrine peptides and the intestinal microbiota were also analyzed.
Results: After supplementation for 8 weeks, EcN-GM was associated with decreases in body weight gain, food intake, fat pad and liver weight, and alleviation hepatocyte steatosis in obese mice. EcN-GM also increased the level of GLP-1 in serum and alleviated leptin and insulin resistance. Moreover, supplementation with EcN-GM increased the α -diversity of the intestinal microbiota but did not significantly influence the relative abundance of *Firmicutes* and *Bacteroidetes*.
Conclusions: These results indicated that EcN-GM, a genetically modified *E. coli* strain, may be a potential therapeutic approach to treat obesity. The beneficial effect of EcN-GM may be independent of the alteration of the diversity and composition of the intestinal microbiota in obese mice.
<https://www.nature.com/articles/s41366-022-01073-8>

Rubin, B.E., Diamond, S., Cress, B.F. et al. (2022): **Species- and site-specific genome editing in complex bacterial communities.** Nat Microbiol 7, 34–47 | <https://doi.org/10.1038/s41564-021-01014-7>

Understanding microbial gene functions relies on the application of experimental genetics in cultured microorganisms. However, the vast majority of bacteria and archaea remain uncultured, precluding the application of traditional genetic methods to these organisms and their interactions. Here, we characterize and validate a generalizable strategy for editing the genomes of specific organisms in microbial communities. We apply environmental transformation sequencing (ET-seq), in which nontargeted transposon insertions are mapped and quantified following delivery to a microbial community, to identify genetically tractable constituents. Next, DNA-editing all-in-one RNA-guided CRISPR–Cas transposase (DART) systems for targeted DNA insertion into organisms identified as tractable by ET-seq are used to enable organism- and locus-specific genetic manipulation in a community context. Using a combination of ET-seq and DART in soil and infant gut microbiota, we conduct species- and site-specific edits in several bacteria, measure gene fitness in a nonmodel bacterium and enrich targeted species. These tools enable editing of microbial communities for understanding and control.

<https://www.nature.com/articles/s41564-021-01014-7> pdf-file available

Gowda K., Ping S., Mani M., Kuehn S. (2022): **Genomic structure predicts metabolite dynamics in microbial communities,** Cell | DOI: 10.1016/j.cell.2021.12.036.

The metabolic activities of microbial communities play a defining role in the evolution and persistence of life on Earth, driving redox reactions that give rise to global biogeochemical cycles. Community metabolism emerges from a hierarchy of processes, including gene expression, ecological interactions, and environmental factors. In wild communities, gene content is correlated with environmental context, but predicting metabolite dynamics from genomes remains elusive. Here, we show, for the process of denitrification, that metabolite dynamics of a community are predictable from the genes each member of the community possesses. A simple linear regression reveals a sparse and generalizable mapping from gene content to metabolite dynamics for genomically diverse bacteria. A consumer-resource model correctly predicts community metabolite dynamics from single-strain phenotypes. Our results demonstrate that the conserved impacts of metabolic genes can predict community metabolite dynamics, enabling the prediction of metabolite dynamics from metagenomes, designing denitrifying communities, and discovering how genome evolution impacts metabolism.

[www.cell.com/cell/fulltext/S0092-8674\(21\)01542-7](http://www.cell.com/cell/fulltext/S0092-8674(21)01542-7)

EFSA:

GMO Panel (2022): Scientific Opinion on development needs for the allergenicity and protein safety assessment of food and feed products derived from biotechnology. EFSA Journal 2022; 20(1):7044, 38pp. <https://doi.org/10.2903/j.efsa.2022.7044>
<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2022.7044>

BIOHAZ Panel (2022): Statement on the update of the list of QPS-recommended biological agents intentionally added to food or feed as notified to EFSA 15: suitability of taxonomic units notified to EFSA until September 2021. EFSA Journal 20 (1): 7045, 40 pp.

<https://doi.org/10.2903/j.efsa.2022.7045>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2022.7045>

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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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