

Sunday Evening News

Week 07 (2018-02-12 / 02-18)

Selected and edited by **BGF** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,

diese Woche gab es keine hervorzuhebenden Beiträge zur Grünen Gentechnik in deutschsprachigen Medien. Karneval, GROKO oder Neuwahlen, die Personaldebatte der SPD waren wichtiger. Daher hier - mit einer Ausnahme - nur englische Beiträge. Aber alle ausgewählten Beiträge wie immer unter: <https://www.biotech-gm-food.com/presse>

Dear all,

this week, there were no significant contributions to genetic engineering / modern plant biotechnology in German-language media. Other problems were more interesting. Therefore here - with one exception - only English contributions. But as always, all selected contributions are available: <https://www.biotech-gm-food.com/presse>

Press releases

Farming Life: The UK will no long be able to hide behind Brussels

<https://www.farminglife.com/farming-news/the-uk-will-no-long-be-able-to-hide-behind-brussels-1-8382134>

Paolo De Castro: Expected green light for gene editing in agriculture a big moment for researchers, says MEP Italy's Paolo De Castro shares his vision of agriculture's future and how cuts to the EU farm budget would endanger it

<https://sciencebusiness.net/news/expected-green-light-gene-editing-agriculture-big-moment-researchers-says-mep>

McDivitt P. – Genetic Literacy Project: **Golden Rice: The GMO crop Greenpeace hates and humanitarians love**

<https://geneticliteracyproject.org/2018/02/13/golden-rice-gmo-crop-greenpeace-hates-and-humanitarians-love/>

Holloway J.

All in the genes: Food fit for a warming world

<https://newatlas.com/climate-change-friendly-crops/53446/>

Rothamsted Research: **For the first time, researchers have isolated a natural resistance gene to Septoria**

<https://phys.org/news/2018-02-isolated-natural-resistance-gene-septoria.html#jCp>

Watters S. - University of Maryland: **Researchers find gene that may greatly increase strawberry production**

<https://phys.org/news/2018-02-gene-greatly-strawberry-production.html#jCp>

Göpfrich K. - SciViews

Biohacking: Gentechnik in der heimischen Garage

„Anstatt also das Gute zu reglementieren, gilt es vielmehr, Missbrauch wirksam einzuschränken. Dann würden Amateure, Wissenschaft und Gesellschaft gleichermaßen vom Biohacking profitieren.“

<http://www.spektrum.de/video/biohacking-gentechnik-in-der-heimischen-garage/1542241>

Scientific Issues

Iyer V., Boroviak K., Thomas M., Doe B., Ryder E., Adams D. (2018): **No unexpected CRISPR-Cas9 off-target activity revealed by trio sequencing of gene-edited mice.** bioRxiv; doi:

<http://dx.doi.org/10.1101/263129> important paper in respect to the discussion about off-target effects

Klein M, Eslami-Mossallam B.; Dylan Gonzalez Arroyo D.G., and Martin Depken M. (2018): **Hybridization Kinetics Explains CRISPR-Cas Off-Targeting Rules**. Cell Reports 22, 1413–1423; <https://doi.org/10.1016/j.celrep.2018.01.045>

Due to their specificity, efficiency, and ease of programming, CRISPR-associated nucleases are popular tools for genome editing. On the genomic scale, these nucleases still show considerable off-target activity though, posing a serious obstacle to the development of therapies. Off targeting is often minimized by choosing especially high-specificity guide sequences, based on algorithms that codify empirically determined off-targeting rules. A lack of mechanistic understanding of these rules has so far necessitated their ad hoc implementation, likely contributing to the limited precision of present algorithms. To understand the targeting rules, we kinetically model the physics of guide-target hybrid formation. Using only four parameters, our model elucidates the kinetic origin of the experimentally observed off-targeting rules, thereby rationalizing the results from both binding and cleavage assays. We favorably compare our model to published data from CRISPR-Cas9, CRISPR-Cpf1, CRISPR-Cascade, as well as the human Argonaute 2 system. [http://www.cell.com/cell-reports/pdf/S2211-1247\(18\)30077-9.pdf](http://www.cell.com/cell-reports/pdf/S2211-1247(18)30077-9.pdf)

Gartland K.M.A. and Gartland J.S. (2018): **Contributions of biotechnology to meeting future food and environmental security needs**. The EuroBiotech Journal 2(1); DOI: 10.2478/ebtj-2018-0002

Biotechnology, including genetic modifications, can play a vital role in helping to meet future food and environmental security needs for our growing population. The nature and use of biotechnology crops are described and related to aspects of food security. Biotechnological applications for food and animal feed are described, together with trends on global adoption of these crops. The benefits of biotechnology crops through increased yield, reduced pesticide use and decreased environmental damage are discussed. Examples of biotechnology crops which do not involve genetic modification are also described. Applications of biotechnology to drought and salt tolerance, and biofortification in which micronutrient content is enhanced are discussed. Emergent technologies such as RNA spraying technology, use of genome editing in agriculture and future targets for improved food and environmental security are considered

Nuccio M. L., Paul M., Bate, N.J., Cohn, J. and Cutler S.R. (2018): **Where are the drought tolerant crops? An assessment of more than two decades of plant biotechnology effort in crop improvement**. Plant Science; <https://doi.org/10.1016/j.plantsci.2018.01.020>

Since the dawn of modern biotechnology public and private enterprise have pursued the development of a new breed of drought tolerant crop products. After more than 20 years of research and investment only a few such products have reached the market. This is due to several technical and market constraints. The technical challenges include the difficulty in defining tractable single-gene trait development strategies, the logistics of moving traits from initial to commercial genetic backgrounds, and the disconnect between conditions in farmer's fields and controlled environments. Market constraints include the significant difficulty, and associated costs, in obtaining access to markets around the world. Advances in the biology of plant water management, including response to water deficit reveal new opportunities to improve crop response to water deficit and new genome-based tools promise to usher in the next era of crop improvement. As biotechnology looks to improve crop productivity under drought conditions, the environmental and food security advantages will influence public perception and shift the debate toward benefits rather than risks.

<https://www.sciencedirect.com/science/article/pii/S016894521731213X>

Pellegrino E., Bedini S., Nuti M. & Ercoli L. (2018): **Impact of genetically engineered maize on agronomic, environmental and toxicological traits: a meta-analysis of 21 years of field data**. Scientific Reports 8, Article number: 3113 (2018); doi:10.1038/s41598-018-21284-2

Despite the extensive cultivation of genetically engineered (GE) maize and considerable number of scientific reports on its agro-environmental impact, the risks and benefits of GE maize are still being debated and concerns about safety remain. This meta-analysis aimed at increasing knowledge on agronomic, environmental and toxicological traits of GE maize by analyzing the peer-reviewed literature (from 1996 to 2016) on yield, grain quality, non-target organisms (NTOs), target organisms (TOs) and soil biomass decomposition. Results provided strong evidence that GE maize performed better than its near isogenic line: grain yield was 5.6 to 24.5% higher with lower concentrations of mycotoxins (–28.8%), fumonisin (–30.6%) and thricotecens (–36.5%). The NTOs analyzed were not affected by GE maize, except for Braconidae, represented by a parasitoid of European corn borer, the target of Lepidoptera active Bt maize. Biogeochemical cycle parameters such as lignin content in stalks and leaves did not vary, whereas biomass decomposition was higher in GE maize. The results support the cultivation of GE maize, mainly due to enhanced grain quality and reduction of human exposure to mycotoxins. Furthermore, the reduction of the parasitoid of the target and the lack of consistent effects on other NTOs are confirmed.

<https://www.nature.com/articles/s41598-018-21284-2.pdf>

Gao, M., Wang, X., Yang, Y., Tabashnik, B. E. and Wu, Y. (2018): **Epistasis confers resistance to Bt toxin Cry1Ac in the cotton bollworm**. *Evolutionary Applications*.

<http://dx.doi.org/10.1111/eva.12598>

Evolution of resistance by insect pests reduces the benefits of extensively cultivated transgenic crops that produce insecticidal proteins from *Bacillus thuringiensis* (Bt). Previous work showed that resistance to Bt toxin Cry1Ac, which is produced by transgenic cotton, can be conferred by mutations disrupting a cadherin protein that binds this Bt toxin in the larval midgut. However, the potential for epistatic interactions between the cadherin gene and other genes has received little attention. Here, we report evidence of epistasis conferring resistance to Cry1Ac in the cotton bollworm, *Helicoverpa armigera*, one of the world's most devastating crop pests. Resistance to Cry1Ac in strain LF256 originated from a field-captured male and was autosomal, recessive, and 220-fold relative to susceptible strain SCD. We conducted complementation tests for allelism by crossing LF256 with a strain in which resistance to Cry1Ac is conferred by a recessive allele at the cadherin locus *HaCad*. The resulting F₁ offspring were resistant, suggesting that resistance to Cry1Ac in LF256 is also conferred by resistance alleles at this locus. However, the *HaCad* amino acid sequence in LF256 lacked insertions and deletions, and did not differ consistently between LF256 and a susceptible strain. In addition, most of the cadherin alleles in LF256 were not derived from the field-captured male. Moreover, Cry1Ac resistance was not genetically linked with the *HaCad* locus in LF256. Furthermore, LF256 and the susceptible strain were similar in levels of *HaCad* transcript, cadherin protein, and binding of Cry1Ac to cadherin. Overall, the results imply that epistasis between *HaCad* and an unknown second locus in LF256 yielded the observed resistance in the F₁ progeny from the complementation test. The observed epistasis has important implications for interpreting results of the F₁ screen used widely to monitor and analyze resistance, as well as the potential to accelerate evolution of resistance.

<http://onlinelibrary.wiley.com/doi/10.1111/eva.12598/epdf>

<http://www.ask-force.org/web/Bt1/Gao-Epistasis-confers-resistance-to-Bt-toxin-Cry1Ac-cotton-bollworm-2017.pdf>

von Wettberg E.J.B. et al. (2018): **Ecology and genomics of an important crop wild relative as a prelude to agricultural innovation**. *Nature Communications* 9. Article number 649 (2018). DOI: [10.1038/s41467-018-02867-z](https://doi.org/10.1038/s41467-018-02867-z)

Domesticated species are impacted in unintended ways during domestication and breeding. Changes in the nature and intensity of selection impart genetic drift, reduce diversity, and increase the frequency of deleterious alleles. Such outcomes constrain our ability to expand the cultivation of crops into environments that differ from those under which domestication occurred. We address this need in chickpea, an important pulse legume, by harnessing the diversity of wild crop relatives. We document an extreme domestication-related genetic bottleneck and decipher the genetic history of wild populations. We provide evidence of ancestral adaptations for seed coat color crypsis, estimate the impact of environment on genetic structure and trait values, and demonstrate variation between wild and cultivated accessions for agronomic properties. A resource of genotyped, association mapping progeny functionally links the wild and cultivated gene pools and is an essential resource chickpea for improvement, while our methods inform collection of other wild crop progenitor species.

<https://www.nature.com/articles/s41467-018-02867-z.pdf>

and Brown J.E. - University of Vermont

Genetic limits threaten chickpeas, a globally critical food

<https://phys.org/news/2018-02-genetic-limits-threaten-chickpeas-globally.html#jCp>

Letter to the Editor: Caruana J.C., Sittmann J.W., Wang W., Liu Z. (2018): **Suppressor of Runnerless Encodes a DELLA Protein that Controls Runner Formation for Asexual Reproduction in Strawberry**. *Molecular Plant*. DOI: doi.org/10.1016/j.molp.2017.11.001

Saintenac C. et al. (2018): **Wheat receptor-kinase-like protein Stb6 controls gene-for-gene resistance to fungal pathogen *Zymoseptoria tritici***, *Nature Genetics* DOI: [10.1038/s41588-018-0051-x](https://doi.org/10.1038/s41588-018-0051-x)

Deployment of fast-evolving disease-resistance genes is one of the most successful strategies used by plants to fend off pathogens. In gene-for-gene relationships, most cloned disease-resistance genes encode intracellular nucleotide-binding leucine-rich-repeat proteins (NLRs) recognizing pathogen-secreted isolate-specific avirulence (Avr) effectors delivered to the host cytoplasm. This process often triggers a localized hypersensitive response, which halts further disease development. Here we report the map-based cloning of the wheat *Stb6* gene and demonstrate that it encodes a conserved wall-associated receptor kinase (WAK)-like protein, which detects the presence of a matching apoplastic effector and confers pathogen resistance without a hypersensitive response². This report demonstrates gene-for-gene disease resistance controlled by this class of proteins in plants. Moreover, *Stb6* is, to our knowledge, the first cloned gene specifying resistance to

Zymoseptoria tritici, an important foliar fungal pathogen affecting wheat and causing economically damaging septoria tritici blotch (STB) disease.

<https://www.nature.com/articles/s41588-018-0051-x>

Koide Y. et al. (2018): "**Lineage-specific gene acquisition or loss is involved in interspecific hybrid sterility in rice,**" *PNAS* (2018). www.pnas.org/cgi/doi/10.1073/pnas.1711656115

Hybrid sterility, a major reproductive barrier between species, hinders the transfer of desirable traits from one species to another. We report a forward genetic approach for creating a "neutral" allele of the *S₁* locus, a major interspecific hybrid sterility locus in rice. This neutral allele does not induce hybrid sterility in combination with alleles from either Asian or African rice species. The allele carries a deletion in the peptidase-coding gene, *SSP*, in the *S₁* locus. This work provides mechanistic and evolutionary insights into hybrid sterility and demonstrates the feasibility of the approach that allows broader access to desirable traits in distantly related species during crop breeding.

<http://www.pnas.org/content/early/2018/02/13/1711656115>

and

Hokkaido University

Mutation in single rice gene cancels interspecific hybrid sterility

<https://phys.org/news/2018-02-mutation-rice-gene-cancels-interspecific.html#jCp>

Li X.-R., Deb J., S. Vinod Kumar S.V. and Lars Østergaard L. (2018): **Temperature modulates tissue-specification program to control fruit dehiscence in Brassicaceae.** *Molecular Plant* (2018). DOI: <https://doi.org/10.1016/j.molp.2018.01.003>

Plants respond to diurnal and seasonal changes in temperature by reprogramming vital developmental pathways. Understanding the molecular mechanisms that define environmental modulation of plant growth and reproduction is critical in the context of climate change that threatens crop yield worldwide. Here, we report that elevated temperature accelerates fruit dehiscence in members of the Brassicaceae family including the model plant *Arabidopsis thaliana* and important crop species. *Arabidopsis* fruit development is controlled by a network of interacting regulatory genes. Among them, the *INDEHISCENT (IND)* gene is a key regulator of the valve-margin tissue that mediates fruit opening, hence facilitating fruit dehiscence. We demonstrated that the valve-margin development is accelerated at higher temperature and that *IND* is targeted for thermosensory control. Our results reveal that *IND* upregulation is facilitated via temperature-induced chromatin dynamics leading to accelerated valve-margin specification and dispersal of the seed. Specifically, we show that temperature-induced changes in *IND* expression are associated with thermosensory H2A.Z nucleosome dynamics. These findings establish a molecular framework connecting tissue identity with thermal sensing and set out directions for the production of temperature-resilient crops.

[http://www.cell.com/molecular-plant/fulltext/S1674-2052\(18\)30023-6](http://www.cell.com/molecular-plant/fulltext/S1674-2052(18)30023-6)

Dickinson P.J. et al. (2018): **Chloroplast Signaling Gates Thermotolerance in Arabidopsis.** *Cell Reports*, 2018; 22 (7): 1657 DOI: [10.1016/j.celrep.2018.01.054](https://doi.org/10.1016/j.celrep.2018.01.054)

Temperature is a key environmental variable influencing plant growth and survival. Protection against high temperature stress in eukaryotes is coordinated by heat shock factors (HSFs), transcription factors that activate the expression of protective chaperones such as HEAT SHOCK PROTEIN 70 (HSP70); however, the pathway by which temperature is sensed and integrated with other environmental signals into adaptive responses is not well understood. Plants are exposed to considerable diurnal variation in temperature, and we have found that there is diurnal variation in thermotolerance in *Arabidopsis thaliana*, with maximal thermotolerance coinciding with higher HSP70 expression during the day. In a forward genetic screen, we identified a key role for the chloroplast in controlling this response, suggesting that light-induced chloroplast signaling plays a key role. Consistent with this, we are able to globally activate binding of HSFA1a to its targets by altering redox status in planta independently of a heat shock.

[http://www.cell.com/cell-reports/pdf/S2211-1247\(18\)30103-7.pdf](http://www.cell.com/cell-reports/pdf/S2211-1247(18)30103-7.pdf)

Hepworth J. et al. (2018) **Absence of warmth permits epigenetic memory of winter in Arabidopsis.** *Nature Communications* (2018). DOI: [10.1038/s41467-018-03065-7](https://doi.org/10.1038/s41467-018-03065-7)

Plants integrate widely fluctuating temperatures to monitor seasonal progression. Here, we investigate the temperature signals in field conditions that result in vernalisation, the mechanism by which flowering is aligned with spring. We find that multiple, distinct aspects of the temperature profile contribute to vernalisation. In autumn, transient cold temperatures promote transcriptional shutdown of *Arabidopsis FLOWERING LOCUS C (FLC)*, independently of factors conferring epigenetic memory. As winter continues, expression of *VERNALIZATION INSENSITIVE3 (VIN3)*, a factor needed for epigenetic silencing, is upregulated by at least two independent thermosensory processes. One integrates long-term cold temperatures, while the other requires the absence of daily temperatures above 15 °C. The lack of spikes of high temperature, not just prolonged cold, is thus the major driver for vernalisation. Monitoring of peak daily temperature is an effective mechanism to judge seasonal progression, but is likely to have deleterious consequences for vernalisation as the climate becomes more variable.

<https://www.nature.com/articles/s41467-018-03065-7.pdf>

and Adrian Galvin A. - John Innes Centre

Absence of warm temperature spikes revealed as driver for vernalisation

<https://phys.org/news/2018-02-absence-temperature-spikes-revealed-driver.html#jCp>

Bigelow P.J., Loescher W., Hancock J.F., Grumet R. (2018): **Influence of inter-genotypic competition on multi-generational persistence of abiotic stress resistance transgenes in populations of *Arabidopsis thaliana*.** *Evol. Appl.* DOI: [10.1111/eva.12610](https://doi.org/10.1111/eva.12610)

Reducing crop losses due to abiotic stresses is a major target of agricultural biotechnology that will increase with climate change and global population growth. Concerns, however, have been raised about potential ecological impacts if transgenes become established in wild populations and cause increased competitiveness of weedy or invasive species. Potential risks will be a function of transgene movement, population sizes, and fitness effects on the recipient population. While key components influencing gene flow have been extensively investigated, there have been few studies on factors subsequent to transgene movement that can influence persistence and competitiveness. Here we performed multi-year, multi-generational, assessment to examine fitness effects and persistence of three mechanistically different abiotic stress tolerance genes: *C-repeat binding factor 3/drought responsive element binding factor 1a (CBF3/DREB1a)*; *Salt overly sensitive 1 (SOS1)*; and *Mannose-6-phosphate reductase (M6PR)*. Transgenic *Arabidopsis thaliana* overexpressing these genes were grown in pure populations and in competition with wild type (WT) parents for six generations spanning a range of field environment conditions. Growth, development, biomass, seed production, and transgene frequency were measured at each generation. Seed planted for each generation was obtained from the previous generation as would occur during establishment of a new genotype in the environment. The three transgenes exhibited different fitness effects and followed different establishment trajectories. In comparisons of pure populations, *CBF3* lines exhibited reduced dry weight, seed yield, and viable seed yield, relative to WT background. In contrast, overexpression of *SOS1* and *M6PR* did not significantly impact productivity measures in pure populations. In competition with WT negative fitness effects were magnified. Transgene frequencies were significantly reduced for *CBF3* and *SOS1* while frequencies of *M6PR* appeared to be subject to genetic drift. These studies demonstrate the importance of fitness effects and inter-genotype competition in influencing persistence of transgenes conferring complex traits.

<http://onlinelibrary.wiley.com/doi/10.1111/eva.12610/full>

Espeland M. et al. (2018): **A Comprehensive and Dated Phylogenomic Analysis of Butterflies.** *Current Biology* (2018). DOI: [10.1016/j.cub.2018.01.061](https://doi.org/10.1016/j.cub.2018.01.061)

[http://www.cell.com/current-biology/pdf/S0960-9822\(18\)30094-0.pdf](http://www.cell.com/current-biology/pdf/S0960-9822(18)30094-0.pdf)

and

Florida Museum of Natural History

At last, butterflies get a bigger, better evolutionary tree

<https://phys.org/news/2018-02-butterflies-bigger-evolutionary-tree.html#jCp>

Genencher B. et al. (2018): **Mutations in Cytosine-5 tRNA Methyltransferases Impact Mobile Element Expression and Genome Stability at Specific DNA Repeats.** *Cell Reports*, 2018; 22 (7): 1861 DOI: [10.1016/j.celrep.2018.01.061](https://doi.org/10.1016/j.celrep.2018.01.061)

The maintenance of eukaryotic genome stability is ensured by the interplay of transcriptional as well as post-transcriptional mechanisms that control recombination of repeat regions and the expression and mobility of transposable elements. We report here that mutations in two (cytosine-5) RNA methyl-transferases, Dnmt2 and NSun2, impact the accumulation of mobile element-derived sequences and DNA repeat integrity in *Drosophila*. Loss of Dnmt2 function caused moderate effects under standard conditions, while heat shock exacerbated these effects. In contrast, NSun2 function affected mobile element expression and genome integrity in a heat shock-independent fashion. Reduced tRNA stability in both RCMT mutants indicated that tRNA-dependent processes affected mobile element expression and DNA repeat stability. Importantly, further

experiments indicated that complex formation with RNA could also contribute to the impact of RCMT function on gene expression control. These results thus uncover a link between tRNA modification enzymes, the expression of repeat DNA, and genomic integrity.

[http://www.cell.com/cell-reports/pdf/S2211-1247\(18\)30110-4.pdf](http://www.cell.com/cell-reports/pdf/S2211-1247(18)30110-4.pdf)

Jung, YJ., Nogoy, F.M., Lee, SK. et al.: **Application of ZFN for Site Directed Mutagenesis of Rice *SSIVa* Gene**: Biotechnol Bioproc E (2018). <https://doi.org/10.1007/s12257-017-0420-9>;

Many successful studies on genome editing in plants have been reported and one of the popular genome editing technology used in plants is Zinc Finger Nucleases (ZFN), which are chimeric proteins composed of synthetic zinc finger-based DNA binding domain and a DNA cleavage domain. The objective of this research was to utilize ZFNs to induce a double-stranded break in *SSIVa*, a soluble starch synthase involved in starch biosynthesis pathway, leading to the regulation of the *SSIVa* expression. The isoform *SSIVa* is not yet well studied, thus, by modifying the endogenous loci in *SSIVa*, we can explore on the specific roles of this gene in starch biosynthesis and other possible functions it might play. In this study, we used ZFN-mediated targeted gene disruption in the coding sequence of the *SSIVa* rice gene in an effort to elucidate the functional role of the gene. Generation of transgenic plants carrying premature stop codons and substitution events, revealed no *SSIVa* mRNA expression, low starch contents and dwarf phenotypes. Remarkably, based on our analysis *SSIVa* gene disruption had no effect on other starch synthesis related genes as their expression remained at wild type levels. Therefore, the engineered ZFNs can efficiently cleave and stimulate mutations at *SSIVa* locus in rice to affect plant height, grain filling and starch content.

<https://link.springer.com/article/10.1007/s12257-017-0420-9>

Tao P., Wu X. and Rao V. (2018): **Unexpected evolutionary benefit to phages imparted by bacterial CRISPR-Cas9**. Science Advances 4 (2), eaar4134; DOI: 10.1126/sciadv.aar4134

Bacteria and bacteriophages arm themselves with various defensive and counterdefensive mechanisms to protect their own genome and degrade the other's. CRISPR (clustered regularly interspaced short palindromic repeat)–Cas (CRISPR-associated) is an adaptive bacterial defense mechanism that recognizes short stretches of invading phage genome and destroys it by nuclease attack. Unexpectedly, we discovered that the CRISPR-Cas system might also accelerate phage evolution. When *Escherichia coli* bacteria containing CRISPR-Cas9 were infected with phage T4, its cytosine hydroxymethylated and glucosylated genome was cleaved poorly by Cas9 nuclease, but the continuing CRISPR-Cas9 pressure led to rapid evolution of mutants that accumulated even by the time a single plaque was formed. The mutation frequencies are, remarkably, approximately six orders of magnitude higher than the spontaneous mutation frequency in the absence of CRISPR pressure. Our findings lead to the hypothesis that the CRISPR-Cas might be a double-edged sword, providing survival advantages to both bacteria and phages, leading to their coevolution and abundance on Earth.

<http://advances.sciencemag.org/content/4/2/eaar4134.full>

Schmierer, B., Botla, S. K., Zhang, J., Turunen, M., Kivioja, T. and Taipale, J. (2017): **CRISPR/Cas9 screening using unique molecular identifiers**. Molecular Systems Biology 13 (10)

<http://msb.embopress.org/content/msb/13/10/945.full.pdf> AND <http://www.askeforce.org/web/Genomics/Schmierer-CRISPR-Cas-screening-using-unique-molecular-identifiers-2017.pdf>

Katellaris C.H. and Beggs P.J.: (2018): **Climate change: allergens and allergic diseases**. International Medical Journal; DOI: 10.1111/imj.13699

Climate change has been described as the biggest global health threat of the 21st century. The atmospheric concentrations of greenhouse gases, such as carbon dioxide, methane and nitrous oxide, have increased significantly since the start of the Industrial Era around 1750, with much of this increase occurring over just the last 50 years or so. This is resulting in warming of the climate system as well as changes in precipitation and weather and climate extremes. These changes in climate are having wide-ranging impacts on the Earth's physical, biological and human systems, including human health. It is these impacts of climate change on human health that are the focus of this paper, particularly the impacts on allergens and allergic diseases. Such impacts are particularly significant in many countries where the prevalence of such diseases is high and/or increasing. There is now compelling evidence that rising air temperatures and carbon dioxide concentrations are, in some plant species, resulting in increased pollen production and allergenicity and advancement and lengthening of the pollen season. Changes in extreme events, such as thunderstorms and tropical cyclones, will also have impacts on allergic diseases, with, for example, the flooding associated with tropical cyclones leading to proliferation of mould growth in damp homes. The article also considers a range of responses to these health threats, including greenhouse gas mitigation, and adaptation strategies, such as enhanced environmental monitoring and health surveillance and adequate planning for the future medical workforce.

<http://onlinelibrary.wiley.com/doi/10.1111/imj.13699/epdf>

Koerberl M. et al. (2018): **Lupine allergen detecting capability and cross-reactivity of related legumes by ELISA.** *Food Chemistry*; <https://doi.org/10.1016/j.foodchem.2018.02.043>

Lupine belongs to the genus *Lupinus* and includes three species commonly consumed by humans. The *Lupinus* genus is closely related to other legumes, such as peanuts, soya, chickpeas, peas, lentils and beans. However, the consumption of lupine (and related legumes) can cause severe allergenic reactions. Therefore, reliable analytical detection methods are required for the analysis of food samples. In this study three commercially available ELISA test kits were analyzed for the detection capability of three common lupine species, as well as cross-reactivity to related legumes. All three ELISA test kits could detect the lupine species, though with different sensitivities. Cross-reactivity varied for the ELISA test kits and all showed some cross-reactivity to related legume samples analyzed.

<https://www.sciencedirect.com/science/article/pii/S030881461830270X>

Hover B.M. et al. (2018): **Culture-independent discovery of the malacidins as calcium-dependent antibiotics with activity against multidrug-resistant Gram-positive pathogens.** *Nature Microbiology* DOI: [10.1038/s41564-018-0110-1](https://doi.org/10.1038/s41564-018-0110-1)

Despite the wide availability of antibiotics, infectious diseases remain a leading cause of death worldwide¹. In the absence of new therapies, mortality rates due to untreatable infections are predicted to rise more than tenfold by 2050. Natural products (NPs) made by cultured bacteria have been a major source of clinically useful antibiotics. In spite of decades of productivity, the use of bacteria in the search for new antibiotics was largely abandoned due to high rediscovery rates^{2,3}. As only a fraction of bacterial diversity is regularly cultivated in the laboratory and just a fraction of the chemistries encoded by cultured bacteria are detected in fermentation experiments, most bacterial NPs remain hidden in the global microbiome. In an effort to access these hidden NPs, we have developed a culture-independent NP discovery platform that involves sequencing, bioinformatic analysis and heterologous expression of biosynthetic gene clusters captured on DNA extracted from environmental samples. Here, we describe the application of this platform to the discovery of the malacidins, a distinctive class of antibiotics that are commonly encoded in soil microbiomes but have never been reported in culture-based NP discovery efforts. The malacidins are active against multidrug-resistant pathogens, sterilize methicillin-resistant *Staphylococcus aureus* skin infections in an animal wound model and did not select for resistance under our laboratory conditions.

<https://www.nature.com/articles/s41564-018-0110-1.pdf>

Biswal A.K., Atmodjo M.A.; Debra Mohnen D. (2018): **Sugar release and growth of biofuel crops are improved by downregulation of pectin biosynthesis.** *Nature Biotechnology*, doi:10.1038/nbt.4067

Cell walls in crops and trees have been engineered for production of biofuels and commodity chemicals, but engineered varieties often fail multi-year field trials and are not commercialized. We engineered reduced expression of a pectin biosynthesis gene (*Galacturonosyltransferase 4, GAUT4*) in switchgrass and poplar, and find that this improves biomass yields and sugar release from biomass processing. Both traits were maintained in a 3-year field trial of *GAUT4*-knockdown switchgrass, with up to sevenfold increased saccharification and ethanol production and sixfold increased biomass yield compared with control plants. We show that *GAUT4* is an α -1,4-galacturonosyltransferase that synthesizes homogalacturonan (HG). Downregulation of *GAUT4* reduces HG and rhamnogalacturonan II (RGII), reduces wall calcium and boron, and increases extractability of cell wall sugars. Decreased recalcitrance in biomass processing and increased growth are likely due to reduced HG and RGII cross-linking in the cell wall.

<https://www.nature.com/articles/nbt.4067>

Microbial Biotechnology

Upadhyay L.S.B., Dutt A. (2017) **Microbial Detoxification of Residual Organophosphate Pesticides in Agricultural Practices.** In: Patra J., Vishnuprasad C., Das G. (eds) *Microbial Biotechnology*. Springer, Singapore; DOI https://doi.org/10.1007/978-981-10-6847-8_10

P. B.S., Ramesh V. (2017) **Tools and Techniques for Genetic Engineering of Bio-Prospective Microorganisms.** In: Patra J., Vishnuprasad C., Das G. (eds) *Microbial Biotechnology*. Springer, Singapore; DOI https://doi.org/10.1007/978-981-10-6847-8_20

Huang, J., Chen, Z., Zhang, W. et al. **d-lyxose isomerase and its application for functional sugar production.** *Appl Microbiol Biotechnol* (2018). <https://doi.org/10.1007/s00253-018-8746-6>

Functional sugars have attracted attention because of their wide application prospects in the food, cosmetics, and pharmaceutical industries in recent decades. Compared with complex chemical synthesis, enzymatic methods of creating functional sugars, characterized by high specificity, moderate reaction conditions, and

sustainability, are favored. d-lyxose isomerase (d-LI, EC 5.3.1.15), an important aldose-ketose isomerase, catalyzes the reverse isomerization reaction between d-xylulose and d-lyxose, as well as d-fructose and d-mannose. d-LI has drawn researchers' attention due to its broad substrate specificity and high potential for enzymatic production of some functional sugars such as d-xylulose, d-mannose, and d-ribose. In this article, an overview of recent advances in the biochemical properties of various d-LIs is explored in detail. Structural analysis, active site identification, and catalytic mechanisms are also provided. Additionally, the applications of d-LIs for functional sugar production, including d-lyxose, d-mannose, and l-ribose, are reviewed in detail in this paper.

<https://link.springer.com/article/10.1007/s00253-018-8746-6>

Veranstaltungen - Meetings

Frontiers in Food Allergy and Allergen Risk Assessment and Management
18th-20th April 2018 – Madrid, Spain

http://ilsi.eu/wp-content/uploads/sites/3/2018/02/Food-Allergy-Sympo-Leaflet_05022018.pdf

2nd iPLANTA conference held in Poznan, February 14-16, 2018. (Abstracts)

<http://iplanta.univpm.it/sites/iplanta.univpm.it/files/POZNAN/2nd%20iPLANTA%20conference%20Poznan%202018%20Book%20of%20abstract.pdf>

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

Bitte besuchen sie auch die Webseite des Wissenschaftlerkreis Grüne Gentechnik e.V. (WGG): www.wgg-ev.de. Hier finden Sie weitere interessante Informationen.

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

This file is saved at <https://www.biotech-gm-food.com/sunday-evening-news/> as well as at <https://www.wgg-ev.de/infos/wgg-nachrichten/>

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