

Sunday Evening News

Week 14 (2018-04-02 / 04-08)

Selected and edited by **BGF** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,
es war eine ruhige Woche. Es gab in den deutschsprachigen Medien nichts Aufregendes in Sachen Gentechnik.

Dear all,

It was a calm week. There was nothing exciting about gene engineering in the German-speaking media.

The official **retraction of the Schaefer et al. 2017** paper in Nature Methods
Nature: **CRISPR off-targets: a reassessment**. *Nature Methods* **15**, 229–230 (2018):
doi:10.1038/nmeth.4664

There was insufficient data to support the claim of unexpected off-target effects due to CRISPR in a paper published in *Nature Methods*. More work is needed to determine whether such events occur *in vivo*. In 2017, Nature Methods published a peer-reviewed paper (Schaefer et al.) in which the authors reported that CRISPR–Cas9 caused unexpected off-target changes in mice. Since its publication, we have been contacted by many scientists challenging this work. Five of these critiques are now published, as peer-reviewed Correspondences, in this issue.

<https://www.nature.com/articles/nmeth.4664.pdf>

Val Giddings V. - ITIF

Gene Editing, Government Regulation, and Greening our Future

<https://itif.org/publications/2018/04/03/gene-editing-government-regulation-and-greening-our-future>

Smith W.J.

Opposing ‘Golden Rice’ Is Anti-Human

<https://www.nationalreview.com/corner/opposing-golden-rice-is-anti-human/>

Lynas M.

Anti-GMO activists convene to target Golden Rice

<https://www.frontiersin.org/articles/10.3389/fpls.2018.00233/full>

Ocampo K.R.

Golden rice’ will not address Vitamin A deficiency, hunger—anti-GMO coalition

<http://business.inquirer.net/248584/golden-rice-will-not-address-vitamin-deficiency-hunger-anti-gmo-coalition-gmo-napc-rice-hunger-food-security>

Health Canada is obligated to approve Golden Rice

The real issue with Golden Rice is that it’s a GMO, which Greenpeace and other opponents despise so much that they are willing to watch millions of people suffer and die rather than give an inch to science.

<https://www.producer.com/2018/04/health-canada-obligated-approve-golden-rice/>

UK public cautiously optimistic about genetic technologies

<https://royalsociety.org/news/2018/03/genetic-technologies/>

CFIA now says Non-GMO Project Verified doesn’t mean non-GMO

<https://www.realagriculture.com/2018/04/cfia-now-says-non-gmo-project-verified-doesnt-mean-non-gmo/>

Paul M.

Food allergy is linked to skin exposure and genetics

<https://news.northwestern.edu/stories/2018/april/food-allergy-is-linked-to-skin-exposure-and-genetics/>

Requat P.

News Analysis: Bayer takeover of Monsanto highlights tectonic shifts in global agrochemical industry

http://www.xinhuanet.com/english/2018-03/23/c_137058263.htm

Scientific Literature

Lipper L., McCarthy N., Zilberman D. Asfaw S. and Branca G. **Editors: Climate Smart Agriculture - Building Resilience to Climate Change.** Natural Resource Management and Policy. *Series Editors:* David Zilberman, Renan Goetz, Alberto Garrido

<http://www.springer.com/de/book/9783319611938>

<https://link.springer.com/book/10.1007%2F978-3-319-61194-5> open pdf-file

Meemken, E.-M., Qaim, M. (2018). **Organic agriculture, food security, and the environment.** *Annual Review of Resource Economics*, <https://doi.org/10.1146/annurev-resource-100517-023252>

Is organic farming the paradigm for sustainable agriculture and food security?

Organic agriculture is often perceived as more sustainable than conventional farming. In a new study published in the *Annual Review of Resource Economics*, Eva-Marie Meemken and Matin Qaim from the University of Goettingen review the available evidence from a global perspective. In terms of environmental and climate change effects, organic farming is less polluting than conventional farming when measured per unit of land but not when measured per unit of output. Organic farming, which currently accounts for only 1% of global agricultural land, is lower yielding on average. Due to high knowledge requirements for the proper use of organic methods, observed yield gaps might further increase if a larger number of farmers would switch to organic practices. Widespread upscaling of organic agriculture would cause additional loss of natural habitats and also entail output price increases, making food less affordable for poor consumers in developing countries. Organic farming is not the paradigm for sustainable agriculture and food security, but smart combinations of organic and conventional methods could contribute toward sustainable productivity increases in global agriculture.

Niehl A., Soininen M., Poranen M.M and Heinlein M. (2018): **Synthetic biology approach for plant protection using dsRNA.** *Plant Biotechnology Journal* <https://doi.org/10.1111/pbi.12904>

Pathogens induce severe damages on cultivated plants and represent a serious threat to global food security. Emerging strategies for crop protection involve the external treatment of plants with double-stranded (ds)RNA to trigger RNA interference. However, applying this technology in greenhouses and fields depends on dsRNA quality, stability and efficient large-scale production. Using components of the bacteriophage phi6, we engineered a stable and accurate *in vivo* dsRNA production system in *Pseudomonas syringae* bacteria. Unlike other *in vitro* or *in vivo* dsRNA production systems that rely on DNA transcription and postsynthetic alignment of single-stranded RNA molecules, the phi6 system is based on the replication of dsRNA by an RNA-dependent RNA polymerase, thus allowing production of high-quality, long dsRNA molecules. The phi6 replication complex was reprogrammed to multiply dsRNA sequences homologous to tobacco mosaic virus (TMV) by replacing the coding regions within two of the three phi6 genome segments with TMV sequences and introduction of these constructs into *P. syringae* together with the third phi6 segment, which encodes the components of the phi6 replication complex. The stable production of TMV dsRNA was achieved by combining all the three phi6 genome segments and by maintaining the natural dsRNA sizes and sequence elements required for efficient replication and packaging of the segments. The produced TMV-derived dsRNAs inhibited TMV propagation when applied to infected *Nicotiana benthamiana* plants. The established dsRNA production system enables the broad application of dsRNA molecules as an efficient, highly flexible, nontransgenic and environmentally friendly approach for protecting crops against viruses and other pathogens.

<https://onlinelibrary.wiley.com/doi/epdf/10.1111/pbi.12904>

Carrière Y., Williams J.L., Crowder D. W. and Tabashnik B. E. (2018): **Genotype-specific fitness cost of resistance to Bt toxin Cry1Ac in pink bollworm.** *Pest Management Science*, <https://doi.org/10.1002/ps.4928>

BACKGROUND: To improve resistance management strategies for *Bacillus thuringiensis* (Bt) crops, a better understanding of the relative fitness of pest genotypes with resistance alleles in the absence of Bt toxins is needed. Here we evaluated the impact of costs of resistance to Bt toxin Cry1Ac on relative fitness of specific pink bollworm (*Pectinophora gossypiella*) genotypes. We created two heterogeneous strains with an intermediate frequency of mutant cadherin alleles linked with resistance to Cry1Ac, reared the strains on diet without Bt and tracked the decline in frequency of resistant genotypes for 15-30 generations using PCR amplification. We used a population genetics model and sensitivity analyses to estimate the relative fitness of resistant genotypes.

RESULTS: Costs were completely recessive in one strain and almost completely recessive in the other strain. Estimates of the decline in relative fitness of the resistant homozygotes on diet without Bt were 14 to 22% in one strain and 21 to 36% in the other strain.

CONCLUSION: Our genotype-specific cost estimates and results of studies discussed herein indicate that costs associated with resistance to Bt are often large enough to significantly delay the evolution of resistance to pyramided Bt crops in pests with recessive inheritance of resistance.

<https://onlinelibrary.wiley.com/doi/pdf/10.1002/ps.4928> pdf-file available

Fang J., Nan P., Gu Z., Ge X., Feng Y-Q. and Lu B.-R. (2018): **Overexpressing Exogenous 5-Enolpyruvylshikimate-3-Phosphate Synthase (EPSPS) Genes Increases Fecundity and Auxin Content of Transgenic Arabidopsis Plants.** *Front. Plant Sci.*,

<https://doi.org/10.3389/fpls.2018.00233>

Transgenic glyphosate-tolerant plants overproducing EPSPS (5-enolpyruvylshikimate-3-phosphate synthase) may exhibit enhanced fitness in glyphosate-free environments. If so, introgression of transgenes overexpressing *EPSPS* into wild relative species may lead to increased competitiveness of crop-wild hybrids, resulting in unpredicted environmental impact. Assessing fitness effects of transgenes overexpressing *EPSPS* in a model plant species can help address this question, while elucidating how overproducing EPSPS affects the fitness-related traits of plants. We produced segregating T₂ and T₃ *Arabidopsis thaliana* lineages with or without a transgene overexpressing *EPSPS* isolated from rice or *Agrobacterium* (CP4). For each of the three transgenes, we compared glyphosate tolerance, some fitness-related traits, and auxin (indole-3-acetic acid) content in transgene-present, transgene-absent, empty vector (EV), and parental lineages in a common-garden experiment. We detected substantially increased glyphosate tolerance in T₂ plants of transgene-present lineages that overproduced EPSPS. We also documented significant increases in fecundity, which was associated with increased auxin content in T₃ transgene-present lineages containing rice *EPSPS* genes, compared with their segregating transgene-absent lineages, EV, and parental controls. Our results from *Arabidopsis* with nine transgenic events provide a strong support to the hypothesis that transgenic plants overproducing EPSPS can benefit from a fecundity advantage in glyphosate-free environments. Stimulated biosynthesis of auxin, an important plant growth hormone, by overproducing EPSPS may play a role in enhanced fecundity of the transgenic *Arabidopsis* plants. The obtained knowledge is useful for assessing environmental impact caused by introgression of transgenes overproducing EPSPS from any GE crop into populations of its wild relatives.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.00233/full>

Teramoto H. et al. (2018): **Genetic Code Expansion of the Silkworm *Bombyx mori* to Functionalize Silk Fiber,** *ACS Synthetic Biology* (2018). DOI: [10.1021/acssynbio.7b00437](https://doi.org/10.1021/acssynbio.7b00437)

The genetic code in bacteria and animal cells has been expanded to incorporate novel amino acids into proteins. Recent efforts have enabled genetic code expansion in nematodes, flies, and mice, whereas such engineering is rare with industrially useful animals. In the present study, we engineered the silkworm *Bombyx mori* to synthesize silk fiber functionalized with azidophenylalanine. For this purpose, we developed a bacterial system to screen for *B. mori* phenylalanyl-tRNA synthetases with altered amino-acid specificity. We created four transgenic *B. mori* lines expressing the selected synthetase variants in silk glands, and found that two of them supported the efficient *in vivo* incorporation of azidophenylalanine into silk fiber. The obtained silk was bio-orthogonally reactive with fluorescent molecules. The results showed that genetic code expansion in an industrial animal can be facilitated by prior bacterial selection, to accelerate the development of silk fiber with novel properties.

<https://pubs.acs.org/doi/10.1021/acssynbio.7b00437>

and

Bob Yirka, Phys.org

Altering silkworm genes to cause addition of useful protein into silk production

<https://phys.org/news/2018-04-silkworm-genes-addition-protein-silk.html#jCp>

Virag Sharma V., Hecker N., Roscito J.G., Foerster L., Langer B.E. & Michael Hiller M. (2018): **A genomics approach reveals insights into the importance of gene losses for mammalian adaptations.** *Nature Communications* 9, (1215): DOI: [10.1038/s41467-018-03667-1](https://doi.org/10.1038/s41467-018-03667-1)

Identifying the genomic changes that underlie phenotypic adaptations is a key challenge in evolutionary biology and genomics. Loss of protein-coding genes is one type of genomic change with the potential to affect phenotypic evolution. Here, we develop a genomics approach to accurately detect gene losses and investigate their importance for adaptive evolution in mammals. We discover a number of gene losses that likely contributed to morphological, physiological, and metabolic adaptations in aquatic and flying mammals. These gene losses shed light on possible molecular and cellular mechanisms that underlie these adaptive phenotypes. In addition, we show that gene loss events that occur as a consequence of relaxed selection following adaptation provide novel insights into species biology. Our results suggest that gene loss is an evolutionary mechanism for adaptation that may be more widespread than previously anticipated. Hence, investigating gene losses has great potential to reveal the genomic basis underlying macroevolutionary changes.

<https://www.nature.com/articles/s41467-018-03667-1.pdf>

and Max Planck Society

Gene loss can prove to be an advantage

<https://phys.org/news/2018-04-gene-loss-advantage.html#jCp>

Carella P., Gogleva A., Tomaselli M., Alfs C. and Schornack S. (2018): **Phytophthora palmivora establishes tissue-specific intracellular infection structures in the earliest divergent land plant lineage.** *Proceedings of the National Academy of Sciences* DOI: [10.1073/pnas.1717900115](https://doi.org/10.1073/pnas.1717900115)

The expansion of plants onto land was a formative event that brought forth profound changes to the earth's geochemistry and biota. Filamentous eukaryotic microbes developed the ability to colonize plant tissues early during the evolution of land plants, as demonstrated by intimate, symbiosis-like associations in 400 million-year-old fossils. However, the degree to which filamentous microbes establish pathogenic interactions with early divergent land plants is unclear. Here, we demonstrate that the broad host-range oomycete pathogen *Phytophthora palmivora* colonizes liverworts, the earliest divergent land plant lineage. We show that *P. palmivora* establishes a complex tissue-specific interaction with *Marchantia polymorpha*, where it completes a full infection cycle within air chambers of the dorsal photosynthetic layer. Remarkably, *P. palmivora* invaginates *M. polymorpha* cells with haustoria-like structures that accumulate host cellular trafficking machinery and the membrane syntaxin MpSYP13B, but not the related MpSYP13A. Our results indicate that the intracellular accommodation of filamentous microbes is an ancient plant trait that is successfully exploited by pathogens like *P. palmivora*.

<http://www.pnas.org/content/pnas/early/2018/03/29/1717900115.full.pdf>

and University of Cambridge

Research shows first land plants were parasitised by microbes

<https://phys.org/news/2018-04-parasitised-microbes.html#jCp>

Rahnasto-Rilla M., Tyni J., Huovinen M., Jarho E., Kulikowicz T., Ravichandran S., Bohr V.A., Ferrucci L., Lahtela-Kakkonen M. and Ruin Moaddel R- (2018): **Natural polyphenols as sirtuin 6 modulators.** *Scientific Reports*, 8 (1) DOI: [10.1038/s41598-018-22388-5](https://doi.org/10.1038/s41598-018-22388-5)

Flavonoids are polyphenolic secondary metabolites synthesized by plants and fungus with various pharmacological effects. Due to their plethora of biological activities, they have been studied extensively in drug development. They have been shown to modulate the activity of a NAD⁺-dependent histone deacetylase, SIRT6. Because SIRT6 has been implicated in longevity, metabolism, DNA-repair, and inflammatory response reduction, it is an interesting target in inflammatory and metabolic diseases as well as in cancer. Here we show, that flavonoids can alter SIRT6 activity in a structure dependent manner. Catechin derivatives with galloyl moiety displayed significant inhibition potency against SIRT6 at 10 μ M concentration. The most potent SIRT6 activator, cyanidin, belonged to anthocyanidins, and produced a 55-fold increase in SIRT6 activity compared to the 3–10 fold increase for the others. Cyanidin also significantly increased SIRT6 expression in Caco-2 cells. Results from the docking studies indicated possible binding sites for the inhibitors and activators. Inhibitors likely bind in a manner that could disturb NAD⁺ binding. The putative activator binding site was found next to a loop near the acetylated peptide substrate binding site. In some cases, the activators changed the conformation of this loop suggesting that it may play a role in SIRT6 activation.

<https://www.nature.com/articles/s41598-018-22388-5.pdf>

Víctor de Lorenzo V. et al. (2018): **The power of synthetic biology for bioproduction, remediation and pollution control.** *EMBO reports* 19: e45658

The UN's Sustainable Development Goals will inevitably require the application of molecular biology and biotechnology on a global scale

<http://embor.embopress.org/content/early/2018/03/26/embr.201745658>

Li Y., Li S., Thodey K., Trenchard I., Cravens A., Smolke C. D. (2018): **Complete biosynthesis of noscapine and halogenated alkaloids in yeast.** *Proceedings of the National Academy of Sciences*, DOI: [10.1073/pnas.1721469115](https://doi.org/10.1073/pnas.1721469115)

Microbial biosynthesis of plant natural products from simple building blocks is a promising approach toward scalable production and modification of high-value compounds. The pathway for biosynthesis of noscapine, a potential anticancer compound, from canadine was recently elucidated as a 10-gene cluster from opium poppy. Here we demonstrate the de novo production of noscapine in *Saccharomyces cerevisiae*, through the reconstruction of a biosynthetic pathway comprising over 30 enzymes from plants, bacteria, mammals, and yeast itself, including 7 plant endoplasmic reticulum (ER)-localized enzymes. Optimization directed to tuning expression of pathway enzymes, host endogenous metabolic pathways, and fermentation conditions led to an over 18,000-fold improvement from initial noscapine titers to ~2.2 mg/L. By feeding modified tyrosine derivatives to the optimized noscapine-producing strain we further demonstrated microbial production of halogenated benzyloquinoline alkaloids. This work highlights the potential for microbial biosynthetic platforms to support the synthesis of valuable and novel alkaloid compounds, which can advance alkaloid-based drug discovery and development.

<http://www.pnas.org/content/early/2018/03/27/1721469115>

Tagungen – Conferences:

Science, Food, Safety

18-21 September 2018; Parma, Italy

<https://conference.efsa.europa.eu/>

EPSO conference “[Plant Biology Europe 2018 Conference \(PBE2018\)](#)”, Copenhagen, Denmark.18 – 21 June 2018:

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. 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/>

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
zentrale@wgg-ev.de