

Sunday Evening News

Week 13 (2018-03-26 / 04-01)

Selected and edited by **BGF** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,
schöne und erholsame Ostertage

Dear all,

happy Eastern

Genome Editing

Der WGG hat die Initiative ergriffen und gemeinsam mit dem VBIO werden verschiedene aktuelle Standpunkte zur rechtlichen Einordnung von Genome Editing bei Pflanzen aus der Sicht der Wissenschaft zusammengestellt. Alle Informationen finden Sie auch gebündelt in unserem [Reader](#).

<https://www.wgg-ev.de/aktuelles/regulation-standpunkte/> only in German, an English translation will follow

Symposium des Wissenschaftlerkreis Grüne Gentechnik e.V. auf der Anuga FoodTech 2018

Genome Editing: Neue Techniken zur Herstellung verbesserter Lebensmittelprodukte

<https://www.wgg-ev.de/aktuelles/veranstaltungen/anuga-foodtech2018/>

Secretary Perdue Issues USDA Statement on Plant Breeding Innovation

U.S. Secretary of Agriculture Sonny Perdue today issued a statement providing clarification on the U.S. Department of Agriculture's (USDA) oversight of plants produced through innovative new breeding techniques which include techniques called genome editing.

<https://www.usda.gov/media/press-releases/2018/03/28/secretary-perdue-issues-usda-statement-plant-breeding-innovation>

and

USDA Has No Plans To Regulate CRISPR

USDA on Wednesday gave the market a clear signal it will not seek to regulate emerging gene editing technologies that could open a new era of plant development for agriculture. U.S. Secretary of Agriculture Sonny Perdue issued the following statement on USDA oversight of plants developed through these new techniques:

<https://www.agweb.com/article/usda-has-no-plans-to-regulate-crispr/>

Burall S. (2018): **Rethink public engagement for gene editing**. Nature 555, 438-439 (2018)

doi: 10.1038/d41586-018-03269-3

The breadth of social and moral questions raised requires a new architecture for democratic debate, insists Simon Burall.

<https://www.nature.com/articles/d41586-018-03269-3> pdf-file available

Jasanoff S. & Hurlbut J.B. (2018): A global observatory for gene editing. Nature 555, 435-437

doi: 10.1038/d41586-018-03270-w

Sheila Jasanoff and J. Benjamin Hurlbut call for an international network of scholars and organizations to support a new kind of conversation.

<https://www.nature.com/articles/d41586-018-03270-w> pdf-file available

Enserink M.: Interested in responsible gene editing? Join the (new) club

The new Association for Responsible Research and Innovation in Genome Editing isn't just for scientists, but also for patient advocates, environmental groups, industry, and funders.

<http://www.sciencemag.org/news/2018/03/interested-responsible-gene-editing-join-new-club>

G-TWYST Feeding study -reminder

Walia A. -Global Research

Ten Scientific Studies Prove that Genetically Modified Food Can Be Harmful To Human Health

<https://www.globalresearch.ca/ten-scientific-studies-proving-gmos-can-be-harmful-to-human-health/5377054>

Freistetter F. **Nachwirkungen einer unhaltbaren Studie zur Schädlichkeit von Gentechnik**

Ein 2012 veröffentlichtes Paper musste wegen schwerer Mängel wieder zurückgezogen werden. Doch es dient bis heute als Munition in einer ideologischen Schlammschlacht

<https://www.derstandard.de/story/2000076850180/nachwirkungen-einer-unhaltbaren-studie-zur-schaedlichkeit-von-gentechnik>

Sánchez M.A. and Parrott W.A. (2017): **Characterization of scientific studies usually cited as evidence of adverse effects of GM food/feed** Plant Biotechnology J. 15 (10), 1227-1234

GM crops are the most studied crops in history. Approximately 5% of the safety studies on them show adverse effects that are a cause for concern and tend to be featured in media reports. Although these reports are based on just a handful of GM events, they are used to cast doubt on all GM crops. Furthermore, they tend to come from just a few laboratories and are published in less important journals. Importantly, a close examination of these reports invariably shows methodological flaws that invalidate any conclusions of adverse effects. Twenty years after commercial cultivation of GM crops began, a bona fide report of an adverse health effect due to a commercialized modification in a crop has yet to be reported.

<https://onlinelibrary.wiley.com/doi/full/10.1111/pbi.12798>

Meine selektive Auswahl an Presse- und Medienberichten sowie an wissenschaftlicher Literatur. Wie immer alle Beiträge <https://www.biotech-gm-food.com/presse>

Here a selection of press releases, media reports and scientific literature. As always, all selected contributions are available: <https://www.biotech-gm-food.com/presse>

Press releases

Interview: Christiane Grefe und Jens Tönnesmann

Wie gefährlich ist Monsanto?

Die EU-Kommission hat Bayer grünes Licht für die Übernahme des umstrittenen Saatgutherstellers gegeben. Bedroht der Zusammenschluss die Landwirtschaft – oder erleichtert er die Ernährung der Welt? Ein Streitgespräch

<http://www.zeit.de/2018/14/saatgut-bayer-monsanto-wwf-streitgesprach-uebernahme-landwirtschaft-ernaehrung/komplettansicht>

Bioland will weniger Gentechnik

Auf der Bioland-Bundesdelegiertenversammlung in Fulda wurde von 160 Delegierten deshalb eine Resolution für den Erhalt der Gentechnikfreiheit auf Äckern und Tellern verabschiedet.

<https://www.agrarheute.com/wochenblatt/politik/bioland-will-weniger-gentechnik-543741>

Testbiotech participating in a pilot project investigating gene drive

Testbiotech beteiligt sich an Pilotprojekt zum Thema Gene Drive

<https://www.testbiotech.org/node/1903>

Polen verschiebt GVO-Verbot in der Fütterung

Polen will gentechnisch veränderte Organismen (GVO) in der Fütterung schon seit längerem verbieten, stößt dabei aber auf praktische Schwierigkeiten.

<https://www.bauernzeitung.ch/news-archiv/2018/polen-verschiebt-gvo-verbot-in-der-fuetterung>

SCoPAFF – Zuckerrübe / sugar beat H7-1

Nicht überraschend konnte im SCoPAFF am 19. März 2018 weder für eine Zulassung noch gegen eine Zulassung der Zuckerrübe H7-1 eine qualifizierte Mehrheit gefunden werden. Überraschend war jedoch, dass Deutschland für die Zulassung gestimmt hat. Dies sollte jedoch nicht als Wende im Verhalten Deutschland gegenüber der Gentechnik gewertet werden. Es war mehr ein Zeichen, dass die neuen Ministerien sich noch finden und abstimmen müssen.

Not surprisingly, on March 19, 2018 the SCoPAFF could not achieve a qualified majority, neither for approval nor for non-approval of sugar beet H7-1. However, surprising was that

Germany had voted in favor. This should not be seen as a turnaround in the behavior to gm-plants or genetic engineering. It was more a sign that the new ministries still need to organize themselves and how to handle this issue.

Publications:

Reminder: Nature Publication Schaefer?

Our previous publication suggested CRISPR-Cas9 editing at the zygotic stage might unexpectedly introduce a multitude of subtle but unintended mutations, an interpretation that not surprisingly raised numerous questions.

Schaefer K. A. et al. (2017): **Corrigendum and follow-up: Whole genome sequencing of multiple CRISPRedited mouse lines suggests no excess mutations**

Taken together, these whole-genome-sequencing-level results support the idea that in specific cases, CRISPR-Cas9 editing can precisely edit the genome at the organismal level and may not introduce numerous, unintended, off-target mutations. Although further analysis is needed, along with experiments specifically designed to include parental controls in mice undergoing CRISPR homology directed repair, use of specific gRNAs, updated Cas9 variants, and injection approach may allow for CRISPR-Cas9 gene editing without genome-wide mutations, and suggest a path towards clinically viable CRISPR-based gene editing, including studies to optimize precision and experimentally confirm genome-wide safety.

<http://dx.doi.org/10.1101/154450>

Zeng, DD., Yang, CC., Qin, R. et al.(2018): **A guanine insert in *OsBBS1* leads to early leaf senescence and salt stress sensitivity in rice (*Oryza sativa* L.)** Plant Cell Rep

<https://doi.org/10.1007/s00299-018-2280-y>

Early leaf senescence can cause negative effects on rice yield, but the underlying molecular regulation is not fully understood. *bilateral blade senescence 1 (bbs1)*, an early leaf senescence mutant with a premature senescence phenotype that occurs mainly performing at the leaf margins, was isolated from a rice mutant population generated by ethylmethane sulfonate (EMS) treatment. The mutant showed premature leaf senescence beginning at the tillering stage and exhibited severe symptoms at the late grain-filling stage. *bbs1* showed accelerated dark-induced leaf senescence. The *OsBBS1* gene was cloned by a map-based cloning strategy, and a guanine (G) insertion was found in the first exon of *LOC_Os03g24930*. This gene encodes a receptor-like cytoplasmic kinase and was named *OsRLCK109* in a previous study. Transgenic *LOC_Os03g24930* knockout plants generated by a CRISPR/Cas9 strategy exhibited similar early leaf senescence phenotypes as did the *bbs1* mutant, which confirmed that *LOC_Os03g24930* was the *OsBBS1* gene. *OsBBS1/OsRLCK109* was expressed in all detected tissues and was predominantly expressed in the main vein region of mature leaves. The expression of *OsBBS1* could be greatly induced by salt stress, and the *bbs1* mutant exhibited hypersensitivity to salt stress. In conclusion, this is the first identification of *OsRLCKs* participating in leaf senescence and playing critical roles in the salt stress response in rice (*Oryza sativa* L.).

<https://link.springer.com/article/10.1007/s00299-018-2280-y>

Wasin Sakulkoo W. et al. (2018): **A single fungal MAP kinase controls plant cell-to-cell invasion by the rice blast fungus.** *Science* 359 (6382), 1399-1403; DOI: 10.1126/science.aaq0892

Blast disease destroys up to 30% of the rice crop annually and threatens global food security. The blast fungus *Magnaporthe oryzae* invades plant tissue with hyphae that proliferate and grow from cell to cell, often through pit fields, where plasmodesmata cluster. We showed that chemical genetic inhibition of a single fungal mitogen-activated protein (MAP) kinase, Pmk1, prevents *M. oryzae* from infecting adjacent plant cells, leaving the fungus trapped within a single plant cell. Pmk1 regulates expression of secreted fungal effector proteins implicated in suppression of host immune defenses, preventing reactive oxygen species generation and excessive callose deposition at plasmodesmata. Furthermore, Pmk1 controls the hyphal constriction required for fungal growth from one rice cell to the neighboring cell, enabling host tissue colonization and blast disease.

<http://science.sciencemag.org/content/359/6382/1399>

Lüthi C, Álvarez-Alfageme F, Romeis J. **The bean α -amylase inhibitor α AI-1 in genetically modified chickpea seeds does not harm parasitoid wasps.** Pest Manag Sci. 2018 Mar 23. doi: 10.1002/ps.4919.

BACKGROUND: Legumes have been genetically engineered to express α AI-1, an α -amylase inhibitor of the common bean, in their seeds. Whereas the genetically modified (GM) seeds are immune to multiple bruchid pest species, the cosmopolitan bruchid *Acanthoscelides obtectus* is tolerant to α AI-1 and their larvae develop normally inside the seeds. Hymenopteran bruchid parasitoids, the most important natural enemies of bruchids, might be exposed to α AI-1 when attacking *A. obtectus* larvae developing inside GM seeds. Exposure might reduce parasitoid fitness, resulting in a decline of the natural control of *A. obtectus* and thus promote its spread. We investigated the impact of the presence of α AI-1 in legume seeds on parasitoid fitness in tritrophic experiments with α AI-1 GM or non-GM chickpea seeds, *A. obtectus*, and three parasitoid species. Additionally, we investigated the exposure of parasitoids to α AI-1 using a fourth, highly sensitive parasitoid species.

RESULTS: We show that parasitoid fitness is not affected when using *A. obtectus* in GM chickpea seeds as hosts and that this lack of effects is likely due to the fact that exposure of the parasitoids to α AI-1 is negligible.

CONCLUSION: We conclude that the release of GM chickpeas containing α AI-1 should not harm this important group of non-target insects.

<https://www.ncbi.nlm.nih.gov/pubmed/29569394> pdf-file available

The ***Solanum lycopersicoides* Genome Consortium**: *Solanum lycopersicoides* is a wild tomato species related to the domesticated *Solanum lycopersicum*.

https://solgenomics.net/organism/Solanum_lycopersicoides/genome

Frederic Strobl F., Anderl A. and Stelzer E.H.K. (2018): **A universal vector concept for a direct genotyping of transgenic organisms and a systematic creation of homozygous lines.** *eLife* DOI: [10.7554/eLife.31677](https://doi.org/10.7554/eLife.31677)

Diploid transgenic organisms are either hemi- or homozygous. Genetic assays are, therefore, required to identify the genotype. Our AGameOfClones vector concept uses two clearly distinguishable transformation markers embedded in interweaved, but incompatible Lox site pairs. Cre-mediated recombination leads to hemizygous individuals that carry only one marker. In the following generation, heterozygous descendants are identified by the presence of both markers and produce homozygous progeny that are selected by the lack of one marker. We prove our concept in *Tribolium castaneum* by systematically creating multiple functional homozygous transgenic lines suitable for long-term fluorescence live imaging. Our approach saves resources and simplifies transgenic organism handling. Since the concept relies on the universal Cre-Lox system, it is expected to work in all diploid model organisms, for example, insects, zebrafish, rodents and plants. With appropriate adaptations, it can be used in knock-out assays to preselect homozygous individuals and thus minimize the number of wasted animals.

<https://elifesciences.org/articles/31677>

and

Goethe University Frankfurt am Main: **Identification of transgenic organisms**

<https://phys.org/news/2018-03-identification-transgenic.html#jCp>

Gonzalez E. et al. (2018): **Trees, fungi and bacteria: tripartite metatranscriptomics of a root microbiome responding to soil contamination.** *Microbiome*, 2018 DOI: [10.1186/s40168-018-0432-5](https://doi.org/10.1186/s40168-018-0432-5)

Background: One method for rejuvenating land polluted with anthropogenic contaminants is through phytoremediation, the reclamation of land through the cultivation of specific crops. The capacity for phytoremediation crops, such as *Salix* spp., to tolerate and even flourish in contaminated soils relies on a highly complex and predominantly cryptic interacting community of microbial life.

Methods: Here, Illumina HiSeq 2500 sequencing and de novo transcriptome assembly were used to observe gene expression in washed *Salix purpurea* cv. 'Fish Creek' roots from trees pot grown in petroleum hydrocarbon-contaminated or non-contaminated soil. All 189,849 assembled contigs were annotated without a priori assumptions to sequence origin and differential expression was assessed.

Results: The 839 contigs differentially expressed (DE) and annotated from *S. purpurea* revealed substantial increases in transcripts encoding abiotic stress response equipment, such as glutathione S-transferases, in roots of contaminated trees as well as the hallmarks of fungal interaction, such as SWEET2 (Sugars Will Eventually Be Exported Transporter). A total of 8252 DE transcripts were fungal in origin, with contamination conditions resulting in a community shift from Ascomycotata Basidiomycota genera. In response to contamination, 1745 Basidiomycota transcripts increased in abundance (the majority uniquely expressed in contaminated soil) including major monosaccharide transporter MST1, primary cell wall and lamella CAZy enzymes, and an ectomycorrhiza-upregulated exo- β -1,3-glucanase (GH5). Additionally, 639 DE polycistronic transcripts from an uncharacterised Enterobacteriaceae species were uniformly in higher abundance in contamination conditions and comprised a wide spectrum of genes cryptic under laboratory conditions but considered putatively involved in eukaryotic interaction, biofilm formation and dioxygenase hydrocarbon degradation.

Conclusions: Fungal gene expression, representing the majority of contigs assembled, suggests out-competition of white rot Ascomycota genera (dominated by *Pyronema*), a sometimes ectomycorrhizal (ECM) Ascomycota

(Tuber) and ECM Basidiomycota (Hebeloma) by a poorly characterised putative ECM Basidiomycota due to contamination. Root and fungal expression involved transcripts encoding carbohydrate/amino acid (C/N) dialogue whereas bacterial gene expression included the apparatus necessary for biofilm interaction and direct reduction of contamination stress, a potential bacterial currency for a role in tripartite mutualism. Unmistakable within the metatranscriptome is the degree to which the landscape of rhizospheric biology, particularly the important but predominantly uncharacterised fungal genetics, is yet to be discovered.
<https://microbiomejournal.biomedcentral.com/track/pdf/10.1186/s40168-018-0432-5>

Potapova N.A., Andrianova M.A., Bazykin, G.A. and Kondrashov A.S. (2018): **Are Nonsense Alleles of *Drosophila melanogaster* Genes under Any Selection?** *Genome Biology and Evolution* (2018). DOI: [10.1093/gbe/evy032](https://doi.org/10.1093/gbe/evy032)

A gene which carries a *bona fide* loss-of-function mutation effectively becomes a functionless pseudogene, free from selective constraint. However, there is a number of molecular mechanisms that may lead to at least a partial preservation of the function of genes carrying even drastic alleles. We performed a direct measurement of the strength of negative selection acting on nonsense alleles of protein-coding genes in the Zambian population of *Drosophila melanogaster*. Within those exons that carry nonsense mutations, negative selection, assayed by the ratio of missense over synonymous nucleotide diversity levels, appears to be absent, consistent with total loss of function. In other exons of nonsense alleles, negative selection was deeply relaxed but likely not completely absent, and the per site number of missense alleles declined significantly with the distance from the premature stop codon. This pattern may be due to alternative splicing which preserves function of some isoforms of nonsense alleles of genes.

<https://academic.oup.com/gbe/advance-article/doi/10.1093/gbe/evy032/4841996>

and Lomonosov Moscow State University

Bioinformaticians studied the evolution of broken genes in a fruit fly

<https://phys.org/news/2018-03-bioinformaticians-evolution-broken-genes-fruit.html#iCp>

Cantine M. D. and Fournier G.P. (2017): **Environmental Adaptation from the Origin of Life to the Last Universal Common Ancestor**, *Origins of Life and Evolution of Biospheres* 48 (1),35–54; DOI: [10.1007/s11084-017-9542-5](https://doi.org/10.1007/s11084-017-9542-5)

Extensive fundamental molecular and biological evolution took place between the prebiotic origins of life and the state of the Last Universal Common Ancestor (LUCA). Considering the evolutionary innovations between these two endpoints from the perspective of environmental adaptation, we explore the hypothesis that LUCA was temporally, spatially, and environmentally distinct from life's earliest origins in an RNA world. Using this lens, we interpret several molecular biological features as indicating an environmental transition between a cold, radiation-shielded origin of life and a mesophilic, surface-dwelling LUCA. Cellularity provides motility and permits Darwinian evolution by connecting genetic material and its products, and thus establishing heredity and lineage. Considering the importance of compartmentalization and motility, we propose that the early emergence of cellularity is required for environmental dispersal and diversification during these transitions. Early diversification and the emergence of ecology before LUCA could be an important pre-adaptation for life's persistence on a changing planet.

<https://link.springer.com/article/10.1007%2Fs11084-017-9542-5>

and Charles Q. Choi, Astrobio.net

Early life had evolutionary power to survive radical

<https://phys.org/news/2018-03-early-life-evolutionary-power-survive.html#iCp>

Reboredo-Rodríguez, P; Gonzalez-Barreiro, C; Cancho-Grande, B; Simal-Gandara, J; Trujillo, I. (2018): **Genotypic and phenotypic identification of olive cultivars from north-western Spain and characterization of their extra virgin olive oils in terms of fatty acid composition and minor compounds.** *Scientia Horticulturae* 232, 269-279

Galicia (NW Spain) is emerging as a new olive-growing region. Galician oil producers are currently striving to recover old autochthonous cultivars with a view to obtaining high quality extra virgin olive oil (EVOO). In this work, a total of 32 trees were studied in order to established their identity and genetic relationships to the main cultivated material in the Iberian Peninsula. The analysis of 11 morphological features of the endocarp and 14 microsatellite markers allowed three different cultivars to be identified among the sampled trees. Comparison with the morphological and molecular profiles available in the World Olive Germplasm Bank of Cordoba (WOGBC) revealed that 24 trees (75%) were of the 'Brava' cultivar and 7 (22%) of the 'Mansa' cultivar. The other tree, labelled as Picuda, matched no specific cultivar in WOGBC. Characterizing the oils obtained from the studied cultivars revealed a high potential for producing high-quality EVOOs of specific origin.

<https://www.sciencedirect.com/science/article/pii/S0304423818300219>

and University of Córdoba

Study characterizes two new Galician olive varieties for the first time

<https://phys.org/news/2018-03-characterizes-galician-olive-varieties.html#iCp>

Gopinarayanan V. E. & Nikhil U. Nai N.U. (2018): **A semi-synthetic regulon enables rapid growth of yeast on xylose.** *Nature Communications*, DOI: [10.1038/s41467-018-03645-7](https://doi.org/10.1038/s41467-018-03645-7)

Nutrient assimilation is the first step that allows biological systems to proliferate and produce value-added products. Yet, implementation of heterologous catabolic pathways has so far relied on constitutive gene expression without consideration for global regulatory systems that may enhance nutrient assimilation and cell growth. In contrast, natural systems prefer nutrient-responsive gene regulation (called regulons) that control multiple cellular functions necessary for cell survival and growth. Here, in *Saccharomyces cerevisiae*, by partially- and fully uncoupling galactose (GAL)-responsive regulation and metabolism, we demonstrate the significant growth benefits conferred by the GAL regulon. Next, by adapting the various aspects of the GAL regulon for a non-native nutrient, xylose, we build a semi-synthetic regulon that exhibits higher growth rate, better nutrient consumption, and improved growth fitness compared to the traditional and ubiquitous constitutive expression strategy. This work provides an elegant paradigm to integrate non-native nutrient catabolism with native, global cellular responses to support fast growth.

<https://www.nature.com/articles/s41467-018-03645-7.pdf>

and Tufts University

Let them eat xylose: Yeast engineered to grow efficiently on novel nutrients

<https://phys.org/news/2018-03-xylose-yeast-efficiently-nutrients.html#jCp>

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.

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