

Sunday Evening News

Week 09 (2018-02-26 / 03-04)

Selected and edited by **BGF** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,

66% der SPD-Mitglieder haben der Bildung einer großen Koalition mit der CDU zugestimmt. Damit steht der Bildung einer neuen Regierung (fast) nichts mehr im Wege. In Deutschland können nun die Ministerien den Ausstieg aus Glyphosat und das generelle Anbauverbot von gv-Pflanzen auf den Weg bringen und in Europa können wieder Entscheidungen getroffen werden.

Hier noch eine Auswahl von Pressemeldungen und Medienberichten. Wie immer alle Beiträge <https://www.biotech-gm-food.com/presse>

Dear all,

66% of the members of the social party (SPD) have agreed to a formation of the grand coalition with the Christian party (CDU). Now the way is open to build up a new government. In Germany, the ministries can now initiate on legal basis the phasing out of glyphosate and the general ban for the cultivation of GM crops.

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

New book

Transgenic Plants and Beyond, Volume 86

<https://www.elsevier.com/books/transgenic-plants-and-beyond/kuntz/978-0-12-809447-1>

O'Malley B.: The question of trust in science requires many answers

<http://www.universityworldnews.com/article.php?story=20180302092229937>

Prime Sarmiento: **Australia, New Zealand approval of GM rice questioned**

A Munich-based research institute warns of public safety issues over a genetically modified golden rice variety approved for commercial sale by Australia and New Zealand.

<http://www.eco-business.com/news/australia-new-zealand-approval-of-gm-rice-questioned/>

Testbiotech comments on risk assessment of FSANZ

Data on 'Golden Rice' not sufficient to show health safety and indicate low benefits

<https://www.testbiotech.org/en/node/2151>

Nochmals Statements EuGH-Generalanwalt Bobek und NBTs

Transcript: **Unbeobachtet im Pflanzengenom** transcript 3.2018, 44-45

Deter A. – topagrar: **Neue Gentechnik-Verfahren: "Trennlinie zwischen Züchtung und Gentechnik zu unklar definiert "**

<https://www.topagrar.com/news/Acker-Agrarwetter-Ackernews-Neue-Gentechnik-Verfahren-Trennlinie-zwischen-Zuechtung-und-Gentechnik-zu-unklar-definiert-9075803.html>

TestBiotech: **Genome editing: Legal expert criticises opinion of Attorney General of the EuCJ**

<https://www.eubusiness.com/Members/testbiotech/genome-editing>

und entsprechendes Gutachten

The genome editing technique is covered by Directive 2001/18 - Comment on Advocate Bobeks Opinion in case C-528/16

https://www.testbiotech.org/sites/default/files/Legal%20dossier_GMO%20-%20genome%20editing_2018.pdf

EFSA: **Neonicotinoids: risks to bees confirmed**

Most uses of neonicotinoid pesticides represent a risk to wild bees and honeybees, according to assessments published today by EFSA. The Authority has updated its risk assessments of three neonicotinoids – clothianidin,

imidacloprid and thiamethoxam – that are currently subject to [restrictions](#) in the EU because of the threat they pose to bees.

<https://www.efsa.europa.eu/en/press/news/180228>

OTS Wirtschaft: IGP: EFSA-Einschätzungen basieren auf nicht ratifizierten Leitlinien

Europäische Landwirtschaft erleidet nachhaltigen Schaden im internationalen Wettbewerb

<https://boerse-express.com/news/articles/igp-efsa-einschaetzungen-basieren-auf-nicht-ratifizierten-leitlinien-5378>

National Law Review: New EFSA Report Finds Antimicrobial Resistance Persists in Humans, Animals and Food

<https://www.natlawreview.com/article/new-efsa-report-finds-antimicrobial-resistance-persists-humans-animals-and-food>

and the report

<http://onlinelibrary.wiley.com/doi/10.2903/j.efsa.2018.5182/full>

Current GMO Crops

https://gmoanswers.com/current-gmo-crops?mc_cid=419b33dbf8&mc_eid=b89825d9e5

Scientific References

Wang W, Pan Q., He F., Akhunova A., Chao S., Trick H. and Akhunov E. (2018):

Transgenerational CRISPR-Cas9 Activity Facilitates Multiplex Gene Editing in Allopolyploid Wheat. The CRISPR Journal 1, (1) DOI: 10.1089/crispr.2017.0010

The CRISPR-Cas9-based multiplexed gene editing (MGE) provides a powerful method to modify multiple genomic regions simultaneously controlling different agronomic traits in crops. We applied the MGE construct built by combining the tandemly arrayed tRNA-gRNA units to generate heritable mutations in the TaGW2, TaLpx-1, and TaMLO genes of hexaploid wheat. The knockout mutations generated by this construct in all three homoeologous copies of one of the target genes, TaGW2, resulted in a substantial increase in seed size and thousand grain weight. We showed that the non-modified gRNA targets in the early generation plants can be edited by CRISPR-Cas9 in the following generations. Our results demonstrate that transgenerational gene editing activity can serve as the source of novel variation in the progeny of CRISPR-Cas9-expressing plants and suggest that the Cas9-inducible trait transfer for crop improvement can be achieved by crossing the plants expressing the gene editing constructs with the lines of interest.

<http://online.liebertpub.com/doi/pdf/10.1089/crispr.2017.0010>

News- Nature: Powerful enzyme could make CRISPR gene-editing more versatile

Revamped Cas9 protein could work on more sites in the genome, and with fewer unwanted effects.

<https://www.nature.com/articles/d41586-018-02540-x>

Hu J.H. et al. (2018): Evolved Cas9 variants with broad PAM compatibility and high DNA specificity. Nature, doi:10.1038/nature26155

A key limitation to the use of CRISPR-Cas9 proteins for genome editing and other applications is the requirement that a protospacer adjacent motif (PAM) be present at the target site. For the most commonly used Cas9 from *Streptococcus pyogenes* (SpCas9), the required PAM sequence is NGG. No natural or engineered Cas9 variants shown to function efficiently in mammalian cells offer a PAM less restrictive than NGG. Here we used phage-assisted continuous evolution (PACE) to evolve an expanded PAM SpCas9 variant (xCas9) that can recognize a broad range of PAM sequences including NG, GAA, and GAT. The PAM compatibility of xCas9 is the broadest reported to date among Cas9s active in mammalian cells, and supports applications in human cells including targeted transcriptional activation, nuclease-mediated gene disruption, and both cytidine and adenine base editing. Remarkably, despite its broadened PAM compatibility, xCas9 has much greater DNA specificity than SpCas9, with substantially lower genome-wide off-target activity at all NGG target sites tested, as well as minimal off-target activity when targeting genomic sites with non-NGG PAMs. These findings expand the DNA targeting scope of CRISPR systems and establish that there is no necessary trade-off between Cas9 editing efficiency, PAM compatibility, and DNA specificity.

<https://www.nature.com/articles/nature26155>

Ricroch A.E, Guillaume-Hofnung M., and Kuntz M. (2018): The ethical concerns about transgenic crops. Biochemical Journal, 475, (4) 803-811; DOI: 10.1042/BCJ20170794 2018,

It is generally accepted that transgenesis can improve our knowledge of natural processes, but also leads to agricultural, industrial or socio-economical changes which could affect human society at large and which may, consequently, require regulation. It is often stated that developing countries are most likely to benefit from plant biotechnology and are at the same time most likely to be affected by the deployment of such new

technologies. Therefore, ethical questions related to such biotechnology probably also need to be addressed. We first illustrate how consequentialist and non-consequentialist theories of ethics can be applied to the genetically modified organism debate, namely consequentialism, autonomy/consent ethics (i.e. self-determination of people regarding matters that may have an effect on these people) and virtue ethics (i.e. whether an action is in adequacy with ideal traits). We show that these approaches lead to highly conflicting views. We have then refocused on moral 'imperatives', such as freedom, justice and truth. Doing so does not resolve all conflicting views, but allows a gain in clarity in the sense that the ethical concerns are shifted from a technology (and its use) to the morality or amorality of various stakeholders of this debate.
<http://www.biochemj.org/content/475/4/803>
<http://www.marcel-kuntz-ogm.fr/2018/03/ethical-concerns-about-transgenic-crops.html>

Navarro A. R., and Francis Narin F. (2018): **European Paradox or Delusion—Are European Science and Economy Outdated?** *Science and Public Policy*, 45(1), 2018, 14–23
doi: 10.1093/scipol/scx021

The European Union (EU) seems to presume that the mass production of European research papers indicates that Europe is a leading scientific power, and the so-called European paradox of strong science but weak technology is due to inefficiencies in the utilization of this top level European science by European industry. We fundamentally disagree, and will show that Europe lags far behind the USA in the production of important, highly cited research. We will show that there is a consistent weakening of European science as one ascends the citation scale, with the EU almost twice as effective in the production of minimal impact papers, while the USA is at least twice as effective in the production of very highly cited scientific papers, and garnering Nobel prizes. Only in the highly multinational, collaborative fields of Physics and Clinical Medicine does the EU seem to approach the USA in top scale impact.

<https://academic.oup.com/spp/article-abstract/45/1/14/3788009> pdf-file available

White P.J., Pongrac P., Sneddon C.C., Jacqueline A. Thompson J.A., and Gladys Wright G. (2018): **Limits to the Biofortification of Leafy Brassicas with Zinc.** *Agriculture* 8 (3), 32;
doi:[10.3390/agriculture8030032](https://doi.org/10.3390/agriculture8030032)

Many humans lack sufficient zinc (Zn) in their diet for their wellbeing and increasing Zn concentrations in edible produce (biofortification) can mitigate this. Recent efforts have focused on biofortifying staple crops. However, greater Zn concentrations can be achieved in leafy vegetables than in fruits, seeds, or tubers. Brassicas, such as cabbage and broccoli, are widely consumed and might provide an additional means to increase dietary Zn intake. Zinc concentrations in brassicas are limited primarily by Zn phytotoxicity. To assess the limits of Zn biofortification of brassicas, the Zn concentration in a peat:sand (v/v 75:25) medium was manipulated to examine the relationship between shoot Zn concentration and shoot dry weight (DW) and thereby determine the critical shoot Zn concentrations, defined as the shoot Zn concentration at which yield is reduced below 90%. The critical shoot Zn concentration was regarded as the commercial limit to Zn biofortification.

Experiments were undertaken over six successive years. A linear relationship between Zn fertiliser application and shoot Zn concentration was observed at low application rates. Critical shoot Zn concentrations ranged from 0.074 to 1.201 mg Zn g⁻¹ DW among cabbage genotypes studied in 2014, and between 0.117 and 1.666 mg Zn g⁻¹ DW among broccoli genotypes studied in 2015–2017. It is concluded that if 5% of the dietary Zn intake of a population is currently delivered through brassicas, then the biofortification of brassicas from 0.057 to > 0.100 mg Zn g⁻¹ DW through the application of Zn fertilisers could increase dietary Zn intake substantially.
<http://www.mdpi.com/2077-0472/8/3/32>

Fahse L., Papastefanou P. and Mathias Otto M. (2018): **Estimating acute mortality of Lepidoptera caused by the cultivation of insect-resistant Bt maize – The LepiX model.** *Ecological Modelling* 371, 50-59, <https://doi.org/10.1016/j.ecolmodel.2018.01.006>

The cultivation of *Bt* maize, genetically modified to be resistant to [insect pests](#), has led to intense scientific and political debate about its possible adverse impacts on biodiversity. To better address this question we developed an individual-based simulation model (*LepiX*). *LepiX* considers the temporal dynamics of maize pollen shedding and larval [phenology](#), and pollen deposition on host plants related to distance from the maize field, in order to estimate mortality of lepidopteran larvae exposed to toxic *Bt* pollen. We employed a refined exposure analysis, comparison to previous approaches, using recent evidence on leaf pollen deposition and accounting for the spatial heterogeneity of pollen on leaves. Moreover, we used a stochastic approach, considering literature data on a minimum dataset for butterfly biology in combination with historic data on temporal pollen deposition to predict the coincidence between larval phenology and pollen deposition. Since conservation management actions may act at the level of the individual for protected species, *LepiX*, as an individual based spatially explicit model, is suited to assist both risk assessment and management measures based on threshold mortalities. We tested our model using *Inachis io* (Lepidoptera: Nymphalidae) as butterfly species and the cultivation of insect resistant MON810 maize. In accordance to predictions based on other models we identified mortality risks of *I. io* larvae for the second larval generation. An analysis of the sensitivity of input parameters stressed the importance of both the slope and the LC₅₀ value of the dose-response curve

as well as the earliest day of larval hatching. Using different published data to characterize the dose-response of MON810 pollen to *I. io* we revealed consequences due to uncertainties in ecotoxicological parameters and thus highlight the importance of key biological parameters for reliable estimates of effects, and decision making (e.g. isolation distances) in risk assessment.

<https://www.sciencedirect.com/science/article/pii/S0304380018300152?via%3Dihub>

Saeki I., Hirao A.S., Kenta T., Nagamitsu T., Hiura T. (2018): **Landscape genetics of a threatened maple, *Acer miyabei* : Implications for restoring riparian forest connectivity**, *Biological Conservation* 220, 299–307; DOI: [10.1016/j.biocon.2018.01.018](https://doi.org/10.1016/j.biocon.2018.01.018)

Because forest fragmentation affects ecological connectivity, establishing corridors is increasingly important in conserving biodiversity. Conserving the connectivity of riparian forests should be a priority because they often support rich and unique biota but are greatly modified by humans. *Acer miyabei* is a threatened maple which grows in floodplain ecosystems in northern Japan. We examined the effects of forest fragmentation on its genetic connectivity and identified candidate areas to be restored as riparian forest corridors. We collected leaf samples from 290 of *A. miyabei* individuals in 13 populations and determined pairwise genetic distances among the populations using 12 microsatellite loci. We also calculated geographic and resistance distances; the latter was quantified by least-cost path and circuit theory models by designating forested or riparian forested areas as having lower resistance than other types of land use. According to multiple regression analyses, genetic distance showed significant positive relationships with resistance distance but was not significantly related to geographic distance. The results indicate that forest fragmentation impedes gene flow of the species. Genetic differentiation among populations was greater in the smaller tree group than in larger one, suggesting that more recently established individuals are exposed to greater genetic isolation than the mature individuals owing to increasing forest fragmentation over time. Reduction of genetic connectivity was conspicuous in and around deforested areas. Such areas can be targeted for promoting connectivity of riparian habitats in future landscape planning.

<https://www.sciencedirect.com/science/article/pii/S0006320717312636>

and

University of Tsukuba: Landscape genetics branches out to help conserve riverside forests

<https://phys.org/news/2018-02-landscape-genetics-riverside-forests.html#jCp>

Yinping Jiao et al. (2018): **MSD1 regulates pedicellate spikelet fertility in sorghum through the jasmonic acid pathway**, *Nature Communications*. DOI: [10.1038/s41467-018-03238-4](https://doi.org/10.1038/s41467-018-03238-4)

Grain number per panicle (GNP) is a major determinant of grain yield in cereals. However, the mechanisms that regulate GNP remain unclear. To address this issue, we isolate a series of sorghum [*Sorghum bicolor* (L.) Moench] multiseeded (msd) mutants that can double GNP by increasing panicle size and altering floral development so that all spikelets are fertile and set grain. Through bulk segregant analysis by next-generation sequencing, we identify MSD1 as a TCP (Teosinte branched/Cycloidea/PCF) transcription factor. Whole-genome expression profiling reveals that jasmonic acid (JA) biosynthetic enzymes are transiently activated in pedicellate spikelets. Young msd1 panicles have 50% less JA than wild-type (WT) panicles, and application of exogenous JA can rescue the msd1 phenotype. Our results reveal a new mechanism for increasing GNP, with the potential to boost grain yield, and provide insight into the regulation of plant inflorescence architecture and development.

<https://www.nature.com/articles/s41467-018-03238-4.pdf>

<https://phys.org/news/2018-02-secret-tripling-grains-sorghum-staple.html#jCp>

Livshultz T. et al. (2018): **Evolution of pyrrolizidine alkaloid biosynthesis in Apocynaceae: revisiting the defence de-escalation hypothesis**, *New Phytologist* (2018). DOI: [10.1111/nph.15061](https://doi.org/10.1111/nph.15061)

Plants produce specialized metabolites for their defence. However, specialist herbivores adapt to these compounds and use them for their own benefit. Plants attacked predominantly by specialists may be under selection to reduce or eliminate production of co-opted chemicals: the defence de-escalation hypothesis. We studied the evolution of pyrrolizidine alkaloids (PAs) in Apocynaceae, larval host plants for PA-adapted butterflies (Danainae, milkweed and clearwing butterflies), to test if the evolutionary pattern is consistent with de-escalation. We used the first PA biosynthesis specific enzyme (homospermidine synthase, HSS) as tool for reconstructing PA evolution. We found hss orthologues in diverse Apocynaceae species, not all of them known to produce PAs. The phylogenetic analysis showed a monophyletic origin of the putative hss sequences early in the evolution of one Apocynaceae lineage (the APSA clade). We found an hss pseudogene in *Asclepias syriaca*, a species known to produce cardiac glycosides but no PAs, and four losses of an HSS amino acid motif. APSA clade species are significantly more likely to be Danainae larval host plants than expected if all Apocynaceae species were equally likely to be exploited. Our findings are consistent with PA de-escalation as an adaptive response to specialist attack.

<http://onlinelibrary.wiley.com/doi/10.1111/nph.15061/epdf>

and

Drexel University: Plants evolve away from obsolete defenses when attacked by immune herbivores, study shows

<https://phys.org/news/2018-02-evolve-obsolete-defenses-immune-herbivores.html#iCp>

Blüher D. et al. (2017): **A 1-phytase type III effector interferes with plant hormone signaling**. Nature Communications Volume 8, 2159 (2017), doi: [10.1038/s41467-017-02195-8](https://doi.org/10.1038/s41467-017-02195-8)

Most Gram-negative phytopathogenic bacteria inject type III effector (T3E) proteins into plant cells to manipulate signaling pathways to the pathogen's benefit. In resistant plants, specialized immune receptors recognize single T3Es or their biochemical activities, thus halting pathogen ingress. However, molecular function and mode of recognition for most T3Es remains elusive. Here, we show that the *Xanthomonas* T3E XopH possesses phytase activity, i.e., dephosphorylates phytate (*myo*-inositol-hexakisphosphate, InsP₆), the major phosphate storage compound in plants, which is also involved in pathogen defense. A combination of biochemical approaches, including a new NMR-based method to discriminate inositol polyphosphate enantiomers, identifies XopH as a naturally occurring 1-phytase that dephosphorylates InsP₆ at C1. Infection of *Nicotiana benthamiana* and pepper by *Xanthomonas* results in a XopH-dependent conversion of InsP₆ to InsP₅. 1-phytase activity is required for XopH-mediated immunity of plants carrying the *Bs7* resistance gene, and for induction of jasmonate- and ethylene-responsive genes in *N. benthamiana*.

<https://www.nature.com/articles/s41467-017-02195-8.pdf>

Westwood J. H. et al. (2018): **Weed Management in 2050: Perspectives on the Future of Weed Science**. Weed Sci. ; <https://doi.org/10.1017/wsc.2017.78>

The discipline of weed science is at a critical juncture. Decades of efficient chemical weed control have led to a rise in the number of herbicide-resistant weed populations, with few new herbicides with unique modes of action to counter this trend and often no economical alternatives to herbicides in large-acreage crops. At the same time, the world population is swelling, necessitating increased food production to feed an anticipated 9 billion people by the year 2050. Here, we consider these challenges along with emerging trends in technology and innovation that offer hope of providing sustainable weed management into the future. The emergence of natural product leads in discovery of new herbicides and biopesticides suggests that new modes of action can be discovered, while genetic engineering provides additional options for manipulating herbicide selectivity and creating entirely novel approaches to weed management. Advances in understanding plant pathogen interactions will contribute to developing new biological control agents, and insights into plant-plant interactions suggest that crops can be improved by manipulating their response to competition. Revolutions in computing power and automation have led to a nascent industry built on using machine vision and global positioning system information to distinguish weeds from crops and deliver precision weed control. These technologies open multiple possibilities for efficient weed management, whether through chemical or mechanical mechanisms. Information is also needed by growers to make good decisions, and will be delivered with unprecedented efficiency and specificity, potentially revolutionizing aspects of extension work. We consider that meeting the weed management needs of agriculture by 2050 and beyond is a challenge that requires commitment by funding agencies, researchers, and students to translate new technologies into durable weed management solutions. Integrating old and new weed management technologies into more diverse weed management systems based on a better understanding of weed biology and ecology can provide integrated weed management and resistance management strategies that will be more sustainable than the technologies that are now failing.

[https://www.cambridge.org/core/services/aop-cambridge-](https://www.cambridge.org/core/services/aop-cambridge-core/content/view/51F98001554CADCE9866699E976562D1/S0043174517000789a.pdf/weed_management_in_2050_perspectives_on_the_future_of_weed_science.pdf)

[core/content/view/51F98001554CADCE9866699E976562D1/S0043174517000789a.pdf/weed_management_in_2050_perspectives_on_the_future_of_weed_science.pdf](https://www.cambridge.org/core/content/view/51F98001554CADCE9866699E976562D1/S0043174517000789a.pdf/weed_management_in_2050_perspectives_on_the_future_of_weed_science.pdf)

DeBruyn J. M. et al. (2016): **Field-grown transgenic switchgrass (*Panicum virgatum* L.) with altered lignin does not affect soil chemistry, microbiology, and carbon storage potential**, GCB Bioenergy. DOI: [10.1111/gcbb.12407](https://doi.org/10.1111/gcbb.12407)

<http://onlinelibrary.wiley.com/doi/10.1111/gcbb.12407/epdf>

and

US Department of Energy

Modified switchgrass has no negative effect on soils

<https://phys.org/news/2018-03-switchgrass-negative-effect-soils.html#iCp>

Sivaram V. (2018): **The race to invent the artificial leaf**

<https://www.technologyreview.com/s/610177/the-race-to-invent-the-artificial-leaf/>

Nyamugenda E. et al. (2018): **Charged residues on the side of the nucleosome contribute to normal Spt16-gene interactions in budding yeast**. Epigenetics 13 (1), 1-7;

<https://doi.org/10.1080/15592294.2017.1418132>

Previous work in *Saccharomyces cerevisiae* identified three residues located in close proximity to each other on the side of the nucleosome whose integrity is required for proper association of the Spt16 component of the FACT complex across transcribed genes. In an effort to gain further insights into the parameters that control

Spt16 interactions with genes *in vivo*, we tested the effects of additional histone mutants on Spt16 occupancy across two constitutively transcribed genes. These studies revealed that mutations in several charged residues in the vicinity of the three residues originally identified as important for Spt16-gene interactions also significantly perturb normal association of Spt16 across genes. Based on these and our previous findings, we propose that the charge landscape across the region encompassed by these residues, which we refer to as the Influences Spt16-Gene Interactions or ISGI region, is an important contributor to proper Spt16-gene interactions *in vivo*.

<https://www.tandfonline.com/doi/pdf/10.1080/15592294.2017.1418132?needAccess=true>

Hannah T. Reynolds .T., Vijayakumar V., Gluck-Thaler E., Korotkin H.B., Matheny P.B., and Slot J.C. (2018): **Horizontal gene cluster transfer increased hallucinogenic mushroom diversity**, *EVOLUTION LETTERS*, doi:10.1002/evl3.42

Secondary metabolites are a heterogeneous class of chemicals that often mediate interactions between species. The tryptophan-derived secondary metabolite, psilocin, is a serotonin receptor agonist that induces altered states of consciousness. A phylogenetically disjunct group of mushroom-forming fungi in the Agaricales produce the psilocin prodrug, psilocybin. Spotty phylogenetic distributions of fungal compounds are sometimes explained by horizontal transfer of metabolic gene clusters among unrelated fungi with overlapping niches. We report the discovery of a psilocybin gene cluster in three hallucinogenic mushroom genomes, and evidence for its horizontal transfer between fungal lineages. Patterns of gene distribution and transmission suggest that synthesis of psilocybin may have provided a fitness advantage in the dung and late wood-decay fungal niches, which may serve as reservoirs of fungal indole-based metabolites that alter behavior of mycophagous and wood-eating invertebrates. These hallucinogenic mushroom genomes will serve as models in neurochemical ecology, advancing the (bio)prospecting and synthetic biology of novel neuropharmaceuticals

<http://onlinelibrary.wiley.com/doi/10.1002/evl3.42/epdf>

Kacar B., Ge X. Sanyal S., Eric A., Gaucher E.A. (2017): **Experimental Evolution of Escherichia coli Harboring an Ancient Translation Protein**. *Journal of Molecular Evolution* (2017). 84,(2–3), 69–84, DOI: [10.1007/s00239-017-9781-0](https://doi.org/10.1007/s00239-017-9781-0)

The ability to design synthetic genes and engineer biological systems at the genome scale opens new means by which to characterize phenotypic states and the responses of biological systems to perturbations. One emerging method involves inserting artificial genes into bacterial genomes and examining how the genome and its new genes adapt to each other. Here we report the development and implementation of a modified approach to this method, in which phylogenetically inferred genes are inserted into a microbial genome, and laboratory evolution is then used to examine the adaptive potential of the resulting hybrid genome. Specifically, we engineered an approximately 700-million-year-old inferred ancestral variant of *tufB*, an essential gene encoding elongation factor Tu, and inserted it in a modern *Escherichia coli* genome in place of the native *tufB* gene. While the ancient homolog was not lethal to the cell, it did cause a twofold decrease in organismal fitness, mainly due to reduced protein dosage. We subsequently evolved replicate hybrid bacterial populations for 2000 generations in the laboratory and examined the adaptive response via fitness assays, whole genome sequencing, proteomics, and biochemical assays. Hybrid lineages exhibit a general adaptive strategy in which the fitness cost of the ancient gene was ameliorated in part by upregulation of protein production. Our results suggest that an ancient–modern recombinant method may pave the way for the synthesis of organisms that exhibit ancient phenotypes, and that laboratory evolution of these organisms may prove useful in elucidating insights into historical adaptive processes.

<https://link.springer.com/content/pdf/10.1007%2Fs00239-017-9781-0.pdf>

and

Arnold C., *Astrobiology Magazine*

What happens when you put evolution on replay?

<https://phys.org/news/2018-02-evolution-replay.html#jCp>

Handberg-Thorsager M. et al. (2018): **The ancestral retinoic acid receptor was a low-affinity sensor triggering neuronal differentiation**, *Science Advances* 21 (4), no. 2, eaao1261; DOI: [10.1126/sciadv.aao1261](https://doi.org/10.1126/sciadv.aao1261)

<https://phys.org/news/2018-03-ancestral-function-retinoic-acid-essential.html#jCp>

EFSA - Scientific Report

The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 201

The data on antimicrobial resistance in zoonotic and indicator bacteria in 2016, submitted by 28 EU Member States (MSs), were jointly analysed by the EFSA and ECDC. Resistance in bacterial isolates of zoonotic *Salmonella* and *Campylobacter* from humans, animals and food, and resistance in indicator *Escherichia coli* as well as in meticillin-resistant *Staphylococcus aureus* from animals and food were addressed. 'Microbiological' resistance was assessed using epidemiological cut-off (ECOFF) values; for some countries, qualitative data on isolates from humans were interpreted in a way that corresponds closely to ECOFF-defined 'microbiological'

resistance. In *Salmonella* from humans, the occurrence of resistance to ampicillin, sulfonamides and tetracyclines was high, whereas resistance to third-generation cephalosporins was low. In *Salmonella* and *E. coli* isolates from broilers, fattening turkeys and their meat, resistance to ampicillin, (fluoro)quinolones, tetracyclines and sulfonamides was frequently high, whereas resistance to third-generation cephalosporins was rare. The occurrence of ESBL-/AmpC producers was low in *Salmonella* and *E. coli* from poultry and in *Salmonella* from humans. The prevalence of ESBL-/AmpC-producing *E. coli*, assessed in poultry and its meat for the first time, showed marked variations among MSs. Fourteen presumptive carbapenemase-producing *E. coli* were detected from broilers and its meat in two MSs. Resistance to colistin was observed at low levels in *Salmonella* and *E. coli* from poultry and meat thereof and in *Salmonella* from humans. In *Campylobacter* from humans, broilers and broiler meat, resistance to ciprofloxacin and tetracyclines was high to extremely high, whereas resistance to erythromycin was low to moderate. Combined resistance to critically important antimicrobials in isolates from both humans and animals was generally uncommon, but very high to extremely high multidrug resistance levels were observed in certain *Salmonella* serovars. Specific serovars of *Salmonella* (notably Kentucky) from both humans and animals exhibited high-level resistance to ciprofloxacin, in addition to findings of ESBL.

<http://onlinelibrary.wiley.com/doi/10.2903/j.efsa.2018.5182/full>

Naturwissenschaften - Tagungsband

Gene Drive – eine Technik für die Manipulation wilder Populationen

[https://naturwissenschaften.ch/uuid/8d47aaa1-5c23-5ae8-80b1-](https://naturwissenschaften.ch/uuid/8d47aaa1-5c23-5ae8-80b1-cdba5a029222?r=20170706115333_1516007593_3780257b-02b4-59e3-994c-b6f215085505)

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https://naturwissenschaften.ch/topics/synbio/applications/gene_drive/99518-tagungsbericht-gene-drive---eine-technik-fuer-die-manipulation-wilder-populationen-

Veranstaltung:

DLG Rahmenprogramm im Forum Current topics of the food industry

Wo: Forum Themen, Trends, Technologien – Das bewegt die Lebensmittelbranche, Halle 9, D 98

Wann: Freitag, 23.03.2018, 13.00– 15.00 Uhr

► [Programm](#): Genome Editing: New techniques for better food products

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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