

Sunday Evening News No. 112

Week 05 (2019-28-01 – 2019-03-02)

Selected and edited by **BGF** Jany

Dear all,

Here again my subjective selection of press releases and publications.

Cox K.: **Academics across the country say agribusiness has outsize influence on their research**

https://newfoodeconomy.org/agriculture-industry-influence-money-academic-research/?utm_source=New+Food+Economy+Subscribers&utm_campaign=632140d9de-EMAIL_CAMPAIGN_2019_01_31_09_20&utm_medium=email&utm_term=0_75a28a0eaf-632140d9de-511579245 and

<https://www.theguardian.com/environment/2019/jan/31/us-academics-feel-the-invisible-hand-of-politicians-and-big-agriculture>

Le Page M.: **Virus lurking inside banana genome has been destroyed with CRISPR**

<https://www.newscientist.com/article/2192461-virus-lurking-inside-banana-genome-has-been-destroyed-with-crispr/>

Le Page M.: **CRISPR used to fight virus hiding inside banana genome**

<https://geneticliteracyproject.org/2019/02/01/crispr-used-to-fight-virus-hiding-inside-banana-genome/>

Publications see below "bananas!"

GMWatch : **New research confirms GM causes massive off-target damage to plant genomes**

<https://www.gmwatch.org/en/news/latest-news/18730>

Jupe F. et al.: **The complex architecture and epigenomic impact of plant T-DNA insertions**

PLOS Genetics: <https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1007819>

GM-Watch: **New study claimed to show safety of CRISPR shows the opposite**

<https://www.gmwatch.org/en/news/latest-news/18731> please have a look on: Tang X. et al.: **A large-scale whole-genome sequencing analysis reveals highly specific genome editing by both Cas9 and Cpf1 (Cas12a) nucleases in rice.** Genome Biology (2018) 19:84 | <https://doi.org/10.1186/s13059-018-1458-5>

Miller H. I. and Kershen D.L.: **This May Be the Worst Regulation Ever**

A USDA rule about labels on 'bioengineered' food costs hundreds of millions and has no benefits.

<http://www.henrymillermd.org/22301/this-may-be-the-worst-regulation-ever>

in part comparable about the discussion "without gene engineering" in Germany. Products containing rDNA can be labelled as GMO free.

The Social Democratic Party (SPD) has its back to the wall and is now seeking every opportunity to win votes.

Miersch M.: **Mein Interview in der AGRA-EUROPE vom 28.01.2019**

<https://www.matthias-miersch.de/2019/01/29/mein-interview-in-der-agra-europe-vom-28-01-2019/>

Lehmann N.: **SPD-Fraktionsvize droht mit Blockade von Agrargesetzen**

Die SPD-Fraktion will Bundeslandwirtschaftsministerin Klöckner zum "Paradigmenwechsel" in der Agrarpolitik zwingen. Andernfalls droht der Koalitionspartner mit einer Blockade.

<https://www.agrarheute.com/politik/spd-fraktionsvize-droht-blockade-agrargesetzen-551240>

Glyphosate

BfR: **Offener Brief Plagiatsvorwurf**

<https://www.bfr.bund.de/cm/343/offener-brief-des-bfr-an-do-z-dr-stefan-weber-sachverstaendiger-fuer-plagiatspruefung.pdf>

The daily up-date of the press releases: <https://www.biotech-gm-food.com/presse>

Publications

Bananas

Tripathi J.N., Ntui V.O., Ron M., Muiruri S.K., Britt A. & Leena Tripathi L. (2019): **CRISPR/Cas9 editing of endogenous banana streak virus in the B genome of *Musa* spp. overcomes a major challenge in banana breeding.** COMMUNICATIONS BIOLOGY 2:46 | <https://doi.org/10.1038/s42003-019-0288-7>

Presence of the integrated endogenous banana streak virus (eBSV) in the B genome of plantain (AAB) is a major challenge for breeding and dissemination of hybrids. As the eBSV activates into infectious viral particles under stress, the progenitor *Musa balbisiana* and its derivants, having at least one B genome, cannot be used as parents for crop improvement. Here, we report a strategy to inactivate the eBSV by editing the virus sequences. The regenerated genome-edited events of Gonja Manjaya showed mutations in the targeted sites with the potential to prevent proper transcription or/and translational into functional viral proteins. Seventy-five percent of the edited events remained asymptomatic in comparison to the non-edited control plants under water stress conditions, confirming inactivation of eBSV into infectious viral particles. This study paves the way for the improvement of B genome germplasm and its use in breeding programs to produce hybrids that can be globally disseminated.

<https://www.nature.com/articles/s42003-019-0288-7>

Dale J., Paul J-Y., Dugdale B. and Harding R. (2017): Review: **Modifying Bananas: From Transgenics to Organics?** Sustainability 2017, 9, 333; doi:10.3390/su9030333

Bananas are one of the top ten world food crops. Unlike most other major food crops, bananas are difficult to genetically improve. The challenge is that nearly all banana cultivars and landraces are triploids, with high levels of male and female infertility. There are a number of international conventional breeding programs and many of these are developing new cultivars. However, it is virtually impossible to backcross bananas, thus excluding the possibility of introgressing new traits into a current cultivar. The alternative strategy is to “modify” the cultivar itself. We have been developing the capacity to modify Cavendish bananas and other cultivars for both disease resistance and enhanced fruit quality. Initially, we were using transgenes; genes that were derived from species outside of the *Musa* or banana genus. However, we have recently incorporated two banana genes (cisgenes) into Cavendish; one to enhance the level of pro-vitamin A and the other to increase the resistance to Panama disease. Modified Cavendish with these cisgenes have been employed in a field trial. Almost certainly, the next advance will be to edit the Cavendish genome, to generate the desired traits. As these banana cultivars are essentially sterile, transgene flow and the outcrossing of modified genes into wild *Musa* species. are highly unlikely and virtually impossible in other triploid cultivars. Therefore, genetic changes in bananas may be compatible with organic farming.

<https://www.mdpi.com/2071-1050/9/3/333>

Tang X. et al.: **A large-scale whole-genome sequencing analysis reveals highly specific genome editing by both Cas9 and Cpf1 (Cas12a) nucleases in rice.** Genome Biology (2018) 19:84 | <https://doi.org/10.1186/s13059-018-1458-5>

Background: Targeting specificity has been a barrier to applying genome editing systems in functional genomics, precise medicine and plant breeding. In plants, only limited studies have used whole-genome sequencing (WGS) to test off-target effects of Cas9. The cause of numerous discovered mutations is still controversial. Furthermore, WGS based off-target analysis of Cpf1 (Cas12a) has not been reported in any higher organism to date.

Results: We conduct a WGS analysis of 34 plants edited by Cas9 and 15 plants edited by Cpf1 in T0 and T1 generations along with 20 diverse control plants in rice. The sequencing depths range from 45× to 105× with read mapping rates above 96%. Our results clearly show that most mutations in edited plants are created by the tissue culture process, which causes approximately 102 to 148 single nucleotide variations (SNVs) and approximately 32 to 83 insertions/deletions (indels) per plant. Among 12 Cas9 single guide RNAs (sgRNAs) and three Cpf1 CRISPR RNAs (crRNAs) assessed by WGS, only one Cas9 sgRNA resulted in off-target mutations in T0 lines at sites predicted by computer programs. Moreover, we cannot find evidence for bona fide off-target mutations due to continued expression of Cas9 or Cpf1 with guide RNAs in T1 generation.

Conclusions: Our comprehensive and rigorous analysis of WGS data across multiple sample types suggests both Cas9 and Cpf1 nucleases are very specific in generating targeted DNA modifications and off-targeting can be avoided by designing guide RNAs with high specificity.

<https://www.biorxiv.org/content/10.1101/292086v1>

Champer J, Chung J., Lee J.Y., Liu C., Yang E., Wen Z., Clark A.G., Messer P.W. (2019): **Molecular safeguarding of CRISPR gene drive experiments.** eLife | DOI:

10.7554/eLife.41439 <<http://dx.doi.org/10.7554/eLife.41439>

CRISPR-based gene drives have sparked both enthusiasm and deep concerns due to their potential for genetically altering entire species. This raises the question about our ability to prevent the unintended spread of such drives from the laboratory into a natural population. Here, we experimentally demonstrate the suitability of synthetic target sites and split drives as flexible safeguarding strategies for gene drive experiment

<https://www.biorxiv.org/content/biorxiv/early/2018/09/08/411876.full.pdf>

Editorial: **Genomics and our future food security**

Ensuring that agricultural production meets the goal of feeding a world experiencing continued human population growth and increasingly severe effects from climate change is an urgent challenge. Genomics has a role to play in maximizing the utility, diversity and yield of resources, as well as in contributing to sustained food security in the future.

Nature Genetics 51,197 (2019) | <https://doi.org/10.1038/s41588-019-0352-8>

Milner S.G. et al. (2019): **Genebank genomics highlights the diversity of a global barley collection.** *Nature Genetics* 51, 319–326 | <https://doi.org/10.1038/s41588-018-0266-x>

Genebanks hold comprehensive collections of cultivars, landraces and crop wild relatives of all major food crops, but their detailed characterization has so far been limited to sparse core sets. The analysis of genome-wide genotyping-by-sequencing data for almost all barley accessions of the German ex situ genebank provides insights into the global population structure of domesticated barley and points out redundancies and coverage gaps in one of the world's major genebanks. Our large sample size and dense marker data afford great power for genome-wide association scans. We detect known and novel loci underlying morphological traits differentiating barley gene pools, find evidence for convergent selection for barbless awns in barley and rice and show that a major-effect resistance locus conferring resistance to bymovirus infection has been favored by traditional farmers. This study outlines future directions for genomics-assisted genebank management and the utilization of germplasm collections for linking natural variation to human selection during crop evolution. <https://www.nature.com/articles/s41588-018-0266-x> pdf-file available

McPhetres, J., Rutjens, B. T., Weinstein, N., & Brisson, J. (2019): **Modifying attitudes about modified foods: increased knowledge leads to more positive attitudes.**

<https://doi.org/10.31234/osf.io/h5dpg>

Genetically modified (GM) foods are often met with harsh public opposition, though little research has attempted to understand why this is. The research that does exist has focused on identifying the role of immutable beliefs, such as morality and politics, which are difficult to change. Therefore, research may benefit from identifying mutable predictors of science rejection—predictors which can be modified through interventions—so efforts can be made to increase public support for scientific advancements. Here we present four studies in which we investigate a lack of domain-specific science literacy—literacy of GM technology—as a strong and unique predictor of GM food skepticism. Results from Studies 1 and 2 demonstrated that knowledge of GM technology is a unique predictor of GM food attitudes above general science knowledge and demographic controls. Study 3 (preregistered) demonstrates that the unique predictive value of GM-specific knowledge replicates in the US, the UK, and the Netherlands. In Study 4, we sought to overcome this lack of knowledge by teaching people the basic science behind GM technology using a five-week, longitudinal experimental design. Results showed that learning about the science behind GM technology leads to more positive explicit attitudes towards GM foods, greater willingness to eat GM products, and lowered perceptions of GM foods as risky. Thus, the present results provide some support for the deficit model of science attitudes within the context of GM foods. These results also provide a relatively simple mold for future interventions to overcome GM skepticism, suggesting that researchers and scientists may wish to focus on communicating the basic science behind GM technology and increasing science literacy. <https://psyarxiv.com/h5dpg/>

Romeis J., Naranjo S.E., Meissle M., Shelton A.M. (2019): **Genetically engineered crops help support conservation biological control.** *Biological Control* 130 (2019) 136–154

Genetically engineered (GE) crops producing insecticidal proteins from *Bacillus thuringiensis* (Bt) (mainly Cry proteins) have become a major control tactic for a number of key lepidopteran and coleopteran pests, mainly in maize, cotton, and soybean. As with any management tactic, there is concern that using GE crops might cause adverse effects on valued non-target species, including arthropod predators and parasitoids that contribute to biological control. Such potential risks are addressed prior to the commercial release of any new GE plant. Over the past 20+ years, extensive experience and insight have been gained through laboratory and field-based studies of the non-target effects of crops producing Cry proteins. Overall, the vast majority of studies demonstrates that the insecticidal proteins deployed today cause no unintended adverse effects to natural enemies. Furthermore, when Bt crops replace synthetic chemical insecticides for target pest control, this creates an environment supportive of the conservation of natural enemies. As part of an overall integrated pest management (IPM) strategy, Bt crops can contribute to more effective biological control of both target and non-target pests. The growing use of insecticidal seed treatments in major field crops (Bt or not) may dampen the positive gains realized through reductions in foliar and soil insecticides. Nonetheless, Bt technology represents a powerful tool for IPM.

<https://www.sciencedirect.com/science/article/pii/S1049964418305103>

Taylor S. A. and Larson E.L. (2019): **Insights from genomes into the evolutionary importance and prevalence of hybridization in nature.** *Nature Ecology & Evolution* 3, 170–177

Hybridization is an evolutionary phenomenon that has fascinated biologists for centuries. Prior to the advent of whole-genome sequencing, it was clear that hybridization had played a role in the evolutionary history of many extant taxa, particularly plants. The extent to which hybridization has contributed to the evolution of Earth's biodiversity has, however, been the topic of much debate. Analyses of whole genomes are providing further

insight into this evolutionary problem. Recent studies have documented ancient hybridization in a diverse array of taxa including mammals, birds, fish, fungi, and insects. Evidence for adaptive introgression is being documented in an increasing number of systems, though demonstrating the adaptive function of introgressed genomic regions remains difficult. And finally, several new homoploid hybrid speciation events have been reported. Here we review the current state of the field and specifically evaluate the additional insights gained from having access to whole-genome data and the challenges that remain with respect to understanding the evolutionary relevance and frequency of ancient hybridization, adaptive introgression, and hybrid speciation in nature.

<https://www.nature.com/articles/s41559-018-0777-y>

Hamlin J.A.P. and Moyle L.C. (2019): Spatial proximity determines post-speciation introgression in *Solanum*. <https://www.biorxiv.org/content/10.1101/529115v1>

An increasing number of phylogenomic studies have documented a clear footprint of post-speciation introgression among closely-related species. Nonetheless, systematic genome-wide studies of factors influencing the likelihood of introgression remain rare. Here, we use an a priori hypothesis-testing framework, and introgression statistics, to evaluate the prevalence and frequency of introgression. Specifically, with whole genome sequences from 32 lineages of wild tomato species, we assess the effect of three factors on introgression: genetic relatedness, geographical proximity, and mating system differences. Using multiple trios within the ABBA-BABA test, we find that one of our factors, geographic proximity, is consistently associated with evidence for recent introgression between species. Of 14 species pairs with proximate versus distant population comparisons, 12 showed evidence of introgression; in ten of these cases, this was more prevalent between geographically-closer populations. We found no evidence that introgression varies systematically with increasing genetic divergence between lineages or with mating system differences, although we have limited power to address the latter effect. While our analysis indicates that recent post-speciation introgression is frequent in this group, estimated levels of genetic exchange are modest (0.05-1.5% of the genome), so the relative importance of hybridization in shaping the evolutionary trajectories of these species could be limited. Regardless, similar clade-wide analyses of genomic introgression would be valuable for disentangling the major ecological, reproductive, and historical determinants of post-speciation gene flow, and for assessing the relative importance of introgression as a source of evolutionary change.

<https://www.biorxiv.org/content/biorxiv/early/2019/01/24/529115.full.pdf>

Conklin B.R. (2019): On the road to a gene drive in mammals

A method for making a version of a gene more likely to be inherited than normal, generating what is called a gene drive, might be used to control insect populations. It has now been reported to work in mammals, too. Nature | <https://doi.org/10.1038/d41586-019-00185-y>
<https://www.nature.com/articles/d41586-019-00185-y>

Grunwald H.A., Gantz V.M., Poplawski G., Xu X-R.S, Bier E. & L. Cooper K.L. (2019): Super-Mendelian inheritance mediated by CRISPR-Cas9 in the female mouse germline.

Nature | <https://doi.org/10.1038/s41586-019-0875-2>

Vandersteen W E., Leggatt R., Sundström L.F. & Robert H. Devlin R.H. (2019): Importance of Experimental Environmental Conditions in Estimating Risks and Associated Uncertainty of Transgenic Fish Prior to Entry into Nature. Scientific Reports 9:406 | DOI:10.1038/s41598-018-35826-1

Salmonids show a high degree of phenotypic plasticity that can differ among genotypes, and this variation is one of the major factors contributing to uncertainty in extrapolating laboratory-based risk assessment data to nature. Many studies have examined the relative growth and survival of transgenic and non-transgenic salmonids, and the results have been highly variable due to genotype × environment interactions. The relative survival of fast- and slow-growing strains can reverse depending on the environment, but it is not clear which specific environmental characteristics are driving these responses. To address this question, two experiments were designed where environmental conditions were varied to investigate the contribution of rearing density, food amount, food type, habitat complexity, and risk of predation on relative growth and survival of fast-growing transgenic and slow-growing wild-type coho salmon. The first experiment altered density (high vs. low) and food amount (high vs. low). Density impacted the relative growth of the genotypes, where transgenic fish grew more than non-transgenic fish in low density streams, regardless of food level. Density also affected survival, with high density causing increased mortality for both genotypes, but the mortality of transgenic relative to non-transgenic fish was lower within the high-density streams, regardless of food level. The second experiment altered habitat complexity (simple vs. complex), food type (artificial vs. natural), amount of food (normal vs. satiation), and risk of predation (present vs. absent). Results from this experiment showed that genotype affected growth and survival, but genotype effects were modulated by one or more environmental factors. The effect of genotype on survival was influenced by all examined environmental factors, such that no predictable trend in relative survival of transgenic versus non-transgenic fry emerged. This was primarily due to variations in survival of non-transgenic fish under different environmental conditions (nontransgenic fry had highest survival in hatchery conditions, and lowest survival in complex conditions with natural food fed at a normal level with or without predators). Transgenic fry survival was only significantly influenced by predator presence. The effects of genotype on mass and length were significantly modulated by food type only. Transgenic fry were able to gain a large size advantage over non-transgenic fish when fed artificial food under

all habitat types. These experiments support the observations of dynamic responses in growth and survival depending on the environment, and demonstrate the challenge of applying laboratory-based experiments to risk assessment in nature.

<https://www.nature.com/articles/s41598-018-35826-1>

Pan Y. et al. (2019): **The molecular evolution of feathers with direct evidence from fossils.** PNAS (2019). www.pnas.org/cgi/doi/10.1073/pnas.1815703116

Dinosaur fossils possessing integumentary appendages of various morphologies, interpreted as feathers, have greatly enhanced our understanding of the evolutionary link between birds and dinosaurs, as well as the origins of feathers and avian flight. In extant birds, the unique expression and amino acid composition of proteins in mature feathers have been shown to determine their biomechanical properties, such as hardness, resilience, and plasticity. Here, we provide molecular and ultrastructural evidence that the pennaceous feathers of the Jurassic nonavian dinosaur *Anchiornis* were composed of both feather β -keratins and α -keratins. This is significant, because mature feathers in extant birds are dominated by β -keratins, particularly in the barbs and barbules forming the vane. We confirm here that feathers were modified at both molecular and morphological levels to obtain the biomechanical properties for flight during the dinosaur–bird transition, and we show that the patterns and timing of adaptive change at the molecular level can be directly addressed in exceptionally preserved fossils in deep time.

North Carolina State University: **Molecular analysis of anchiornis feather gives clues to origin of flight**

<https://phys.org/news/2019-01-molecular-analysis-anchiornis-feather-clues.html#jCp>

EFSA:

Marco Daniele Parenti, Aurelia Santoro, Alberto Del Rio, Claudio Franceschi (2019):

Literature review in support of adjuvanticity/immunogenicity assessment of proteins EFSA

supporting publication 2019:EN-1551. 68pp. | doi:10.2903/sp.efsa.2019.EN-1551

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/sp.efsa.2019.EN-1551>

European Food Safety Authority (EFSA), 2019. **EFSA statement on the risk posed to humans by a vitamin B2 produced by a genetically modified strain of *Bacillus subtilis* used as a feed additive** EFSA Journal 2019;17(1):5615, 11 pp.

https://www.efsa.europa.eu/sites/default/files/scientific_output/ON-5615.pdf

Meetings

4th International Congress Hidden Hunger:

Hidden hunger and the transformation of food systems: How to combat the double burden of malnutrition?

February 27 - March 1, 2019; University of Hohenheim Stuttgart, Germany

<https://hiddenhunger.uni-hohenheim.de/en>

Vortrag von Urs Niggli zum Thema Biolandbau und Gene Editing.

<https://www.boku.ac.at/ethikplattform/biolandbau-und-gene-editing-eine-un-moegliche-kombination/>

oder direkt zu You Tube: <https://t.co/zWM6kYCmx>

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.

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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