

Sunday Evening News No. 101

Week 44 (2018-10-29 / 11-04)

Selected and edited by **BGF** Jany

Dear all,

Due to several requests concerning the AFBV-WGG letter:

Open Letter to Commission President Juncker, Commissioner for Health Andriukaitis, Commissioner for Agriculture Hogan, Commissioner for Research, Science and Innovation Moedas, and Commissioner for Jobs, Growth, Investment and Competitiveness Katainen

The English and French versions of the open letter to the EU Commission can be found as pdf files at the end of the German text.

<https://www.biotech-gm-food.com/afvb-wgg-offener-brief-an-kommission-eugh-urt>

Press releases – media reports

Roubanis I.: **The Netherlands clears the way for agricultural genetic modification**

<https://www.neweurope.eu/article/the-netherlands-clears-the-way-for-agricultural-genetic-modification/>

Miller H.: **Quick FDA approval of GMO human insulin 36 years ago contrasts with today's biotechnology regulatory sclerosis**

<https://geneticliteracyproject.org/2018/11/02/quick-fda-approval-of-gmo-human-insulin-36-years-ago-contrasts-with-todays-biotechnology-regulatory-sclerosis/>

American Society of Plant Biologists: **Gene silencing could help boost rice yields in developing world**

<https://geneticliteracyproject.org/2018/11/02/gene-silencing-could-help-boost-rice-yields-in-developing-world/>

New Food Economy: **America cannot eat without immigrant food workers. These are their stories.**

<https://newfoodeconomy.org/hands-that-feed-us-immigrant-food-workers-in-their-own-words/>

Brennan Z.: **Genome Editing in Animals: FDA Preps for New Flexible Regulatory Approach**

<https://www.raps.org/news-and-articles/news-articles/2018/10/genome-editing-in-animals-fda-preps-for-new-flexi>

Niiler E.: **Why Gene Editing Is the Next Food Revolution**

<https://www.nationalgeographic.com/environment/future-of-food/food-technology-gene-editing/>

Nunes K.: **Ingredients from genome edited crops on the horizon in the United States**

<https://www.foodbusinessnews.net/articles/12786-ingredients-from-genome-edited-crops-on-the-horizon-in-the-united-states>

Mackelprang R. **Organic farming with gene editing? Yes**

<https://www.farmanddairy.com/columns/organic-farming-with-gene-editing-yes/521157.html>

Merlot J.: **Frau Künast trifft den Feind**

<http://www.spiegel.de/wissenschaft/mensch/gentechnik-in-der-landwirtschaft-frau-kuenast-trifft-den-feind-a-1235809.html>

Bioökonomie.de: **CRISPR-Cas: Chancen für die Gentechnik**

<https://biooekonomie.de/nachrichten/crispr-cas-chancen-fuer-die-gentechnik>

Ebi K.: **Climate change and rice: How some of the world's poorest nations may suffer**

<https://geneticliteracyproject.org/2018/10/31/climate-change-and-rice-how-some-of-the-worlds-poorest-nations-may-suffer/>

As always you will find the daily up-date of the press releases at: <https://www.biotech-gm-food.com/presse>

Publications

transkript: “Ein neues Gesetz tut not“ Der WGG-Vorstand Klaus-Dieter Jany sprach exklusiv mit transkript über die erste Umfrage zu den Auswirkungen auf die Forschung. transkript 24, 77-78 (2018)
pdf-file available (German, English version in December)

Karberg S.: **Immun gegen die Schere**. Transkript 24, 71-76 (2018)

Die Genschere CRISPR/Cas9 gilt als die derzeit beste Methode, um künftig krankmachende Gendefekte in menschlichen Zellen korrigieren zu können. Doch das Immunsystem attackiert das Werkzeug offenbar – und gefährdet damit das Konzept des Genome Editing.

https://issuu.com/biocom/docs/tk2018_11-12

and corresponding publication

Wagner D.L., Amini L., Wendering D.J, Burkhardt L-M., Akyüz L., Reinke P., Volk H.-D. & Schmueck-Henneresse M. (2018): **High prevalence of *Streptococcus pyogenes* Cas9-reactive T cells within the adult human population**. *Nature Medicine*

The discovery of the highly efficient site-specific nuclease system CRISPR–Cas9 from *Streptococcus pyogenes* has galvanized the field of gene therapy^{1,2}. The immunogenicity of Cas9 nuclease has been demonstrated in mice^{3,4}. Preexisting immunity against therapeutic gene vectors or their cargo can decrease the efficacy of a potentially curative treatment and may pose significant safety issues^{3,4,5,6}. *S. pyogenes* is a common cause for infectious diseases in humans, but it remains unclear whether it induces a T cell memory against the Cas9 nuclease^{7,8}. Here, we show the presence of a preexisting ubiquitous effector T cell response directed toward the most widely used Cas9 homolog from *S. pyogenes* (SpCas9) within healthy humans. We characterize SpCas9-reactive T cells within the CD4/CD8 compartments for multi-effector potency, cytotoxicity, and lineage determination. In-depth analysis of SpCas9-reactive T cells reveals a high frequency of SpCas9-reactive regulatory T cells that can mitigate SpCas9-reactive effector T cell proliferation and function in vitro. Our results shed light on T cell-mediated immunity toward CRISPR-associated nucleases and offer a possible solution to overcome the problem of preexisting immunity.

<https://www.nature.com/articles/s41591-018-0204-6>

Alkan F., Wenzel A., Anthon C., Havgaard J.H. and Gorodkin J (2018): **CRISPR-Cas9 off-targeting assessment with nucleic acid duplex energy parameters**. *Genome Biology* 19,:177

<https://doi.org/10.1186/s13059-018-1534-x>

DNA–DNA, and RNA–DNA duplexes. Based on this model, two novel off-target assessment methods for gRNA selection in CRISPR–Cas9

Background: Recent experimental efforts of CRISPR–Cas9 systems have shown that off-target binding and cleavage are a concern for the system and that this is highly dependent on the selected guide RNA (gRNA) design. Computational predictions of off-targets have been proposed as an attractive and more feasible alternative to tedious experimental efforts. However, accurate scoring of the high number of putative off-targets plays a key role for the success of computational off-targeting assessment.

Results: We present an approximate binding energy model for the Cas9–gRNA–DNA complex, which systematically combines the energy parameters obtained for RNA–RNA, applications are introduced:CRISPRoff to assign confidence scores to predicted off-targets and CRISPRspec to measure the specificity of the gRNA. We benchmark the methods against current state-of-the-art methods and show that both are in better agreement with experimental results. Furthermore, we show significant evidence supporting the inverse relationship between the on-target cleavage efficiency and specificity of the system, in which introduced binding energies are key components.

Conclusions: The impact of the binding energies provides a direction for further studies of off-targeting mechanisms. The performance of CRISPRoff and CRISPRspec enables more accurate off-target evaluation for gRNA selections, prior to any CRISPR–Cas9 genome-editing application. For given gRNA sequences or all potential gRNAs in a given target region, CRISPRoff-based off-target predictions and CRISPRspec -based specificity evaluations can be carried out through our webserver at <https://rth.dk/resources/crispr/>
<https://genomebiology.biomedcentral.com/track/pdf/10.1186/s13059-018-1534-x>

Kofler N. et al. (2018): **Editing nature: Local roots of global governance**. *Science* 362, Issue 6414, 527-529; DOI: 10.1126/science.aat4612

<http://science.sciencemag.org/content/362/6414/527>

Fatima, M., Zaynab, M., Sharif, Y., Abbas, S., Zaffar, M., & Saleem, T. (2018). **Recent Advances in Plant Biotechnology and Genetic Engineering: Application in Agriculture**. *International Journal of Molecular Microbiology*, 1(2), 40-43.

Increasing population is facing the challenge for food security. Researchers are searching the convenient and fast ways for improving crop production. Basic research provides us with genetic mechanism of plants. Tools have been discovered to manipulate and alter these mechanisms to get the new and desirable products and to incorporate innovative characteristics in plants. Synthetically made promoters, enhancers and repressors for native or transgene expression regulation are some of these tools. Some tools like, transformation of plant with artificially synthesized chromosomes and linked multiple genes are gaining importance. The most advanced one is CRISPR-Cas genome editing system. To assess their implicational potential in addressing agro-environmental problems, such genomic tools should be integrated.

<http://journals.pscpublishers.org/index.php/ijmm/article/view/227/173>

Werner C., Snowdon R. (2018): **Genome-Facilitated Breeding of Oilseed Rape**. In: Liu S., Snowdon R., Chalhoub B. (eds) *The Brassica napus Genome*. Compendium of Plant Genomes. Springer, Cham
Brassica napus ssp. *napus* (rapeseed, oilseed rape, canola) became a major global oilseed crop through intensive breeding during the last five decades. The implementation of large-scale metabolic screening of seeds to identify mutants carrying low seed erucic acid and glucosinolate content, respectively, facilitated the use of these variants in backcrossing programmes which established the species as a “new” global oilseed crop with exceptional oil quality and high meal quality. Divergent ecogeographical forms were adapted to agricultural systems in North America (spring-type canola), Europe (predominantly winter-type oilseed rape) and Asia/Australia (semi-winter rapeseed/canola forms), and the establishment of hybrid breeding systems during the 1990s increased seed yield and yield stability and established *B. napus* as an important cash crop for farmers and breeders. Also around this time, cytogenetic studies and the first genetic maps for *B. napus*, developed with restriction fragment length polymorphism (RFLP) markers, revealed first evidence of unusual rearrangements among homoeologous chromosomes, and evidence grew for complex allohexaploidization among the diploid subgenomes. However, it was not until the *B. napus* genome sequence was deciphered two decades later that the broad extent and consequences of large-scale and small-scale rearrangements in the *B. napus* genome, and the unexpected impact of complex genome structural rearrangements on traits of importance for breeding, became apparent. As more and more *B. napus* genome sequences become available, and new methods for high-throughput screening enable detailed associations of genome features with simple and quantitative traits, breeders are beginning to appreciate the importance of post-polyploidization genome structural variation for a multitude of important traits in this recent allopolyploid crop. The use of genome data, high-throughput genotyping techniques, genomic selection, and genome-based hybrid performance prediction is already changing the way that *B. napus* breeders identify useful diversity and implement it in their breeding programmes. Access to high-quality genome assemblies, vast genomic datasets, and large-scale digital phenomic datasets will play a key role in future implementation of omics-assisted breeding in *B. napus* breeding. This chapter provides an overview of the impact of the *B. napus* genome on breeding progress and the opportunities provided by genomics technologies for future breeding.

https://link.springer.com/chapter/10.1007/978-3-319-43694-4_15

Friedt W., Tu J., Fu T. (2018) **Academic and Economic Importance of *Brassica napus* Rapeseed**. In: Liu S., Snowdon R., Chalhoub B. (eds) *The Brassica napus Genome*. Compendium of Plant Genomes. Springer, Cham

Rapeseed or canola (*B. napus*) is the second most important oilseed crop of the world. It is also a favourite plant for basic and breeding research. Due to its origin and evolution, rapeseed has a complex polyploid genome. Recent sequencing of the corresponding genomes provides the basis for a better understanding and exploitation of the genetic diversity involved in major rapeseed traits. However, directed selection for major quality characteristics, i.e. minimal erucic acid content and low glucosinolate level, has caused genetic bottlenecks limiting genetic variation in the current gene pools of cultivated oilseed rape (OSR). Therefore, broadening genetic diversity is an important aim of research and a necessary prerequisite for further progress by OSR breeding. In agricultural production, rapeseed is nowadays an indispensable component of crop rotations in major growing areas such as Australia, Western Canada, Central China and many countries of the European Union. In many cases, OSR is the only leaf crop among dominating cereal species. Therefore, OSR as a component of crop rotations helps to maintain soil fertility and contributes to sustainable production therefore. As a major cash crop OSR substantially contributes to farmers' incomes and therefore helps to stabilize rural populations. Beyond that, as major globally traded agricultural commodities rapeseed/canola and rapeseed/canola oil and meal significantly input the national products of a number of countries e.g. Canada. Rapeseed/canola is a raw material for vegetable oil and extraction meal as feed, food and fuel. The oil is mainly used as a high-value salad oil for dressings etc. due to its high contents of oleic acid (ca. 60%) and poly-unsaturated linolenic acid (omega-3, ca. 10%). Nevertheless, a large part is also used as a mobility fuel for diesel cars and tractors, particularly in Germany and Europe. The extraction meal (and protein) from oil processing is now recognized as a highly valuable animal feed, particularly for ruminants (cattle) but also for monogastric farm animals (pigs, poultry). Furthermore, the interest in rapeseed protein for the purpose of human nutrition is increasing. Optimal contents of the major compounds mentioned before represent the main requirements for rapeseed/canola varieties today. Consequently, quality characteristics are major criteria for variety testing and registration therefore. Other major requirements for modern rapeseed varieties are yield and various agronomic traits securing seed yield, i.e. resistance against fungal diseases and insect pests. Because of the environmental concerns and the rejection of agrochemicals such as insecticides (e.g. ban of neonicotinoids in the EU), genetic approaches of establishing resistant crop cultivars constantly gain importance. OSR breeding has long been a relatively ordinary process of repeated selection for resistance, quality and yield, the propagation of improved populations and their release as new open pollinated (OP) varieties. Since this approach is not very effective, breeders have been interested in breeding hybrids instead.

Today, F1 hybrids represent the major variety type. They are produced with genetic male sterility systems, most of which are based on cytoplasmic mutations causing male sterility (cms). The higher performance of hybrids is caused by “heterotic effect” which largely depends on the genetic distance between the parents. Therefore, distant genetic pools need to be generated for the development of female and male parents. The future potential of variety design is consequently determined by the usefulness of the genetic pools and the performance of hybrid parents extracted from them. Modern breeding tools based on biotechnology and genomics can substantially contribute to a better exploitation of useful genetic diversity, i.e. specific genes and genetic networks. Better varieties are a precondition for further crop improvement. Future quality OSR cultivars deserve high yield potential, combined with good stability due to disease and pest resistance. This will be the basis for exploiting the great agronomical and industrial advantages of the rapeseed plant.

https://link.springer.com/chapter/10.1007/978-3-319-43694-4_1

Swetha C., Basu D., Pachamuthu K., Tirumalai V., Nair A, Prasad M, and Shivaprasad P.V. (2018): **Major Domestication-Related Phenotypes in Indica Rice are Due to Loss of miRNA-Mediated Laccase Silencing.** *Plant Cell* doi.org/10.1105/tpc.18.00472

Domestication of rice included conversion of perennial wild species with few seeds to short plants that produced abundant seeds. Most domestication-associated changes were due to variations in transcription factors and other key genes such as enzymes. Here, we show that multiple yield-related traits associated with indica rice domestication are linked to micro (mi) RNA mediated regulation. Analysis of small (s) RNA datasets from cultivated indica rice lines, a few landraces and two wild relatives of rice revealed the presence of abundant 22-nucleotide (nt) reads in wild relatives that mapped to miR397 precursors. miR397 expressed at very high levels in wild relatives and at negligible levels in high-yielding cultivated lines. In its genera-specific form of 22-nt, miR397 targeted mRNAs coding for laccases to decay and induce robust secondary cascade silencing in wild species that required RNA-dependent RNA polymerase 6. In wild species of rice, reduced expression of laccases resulted in low lignification. As expected, over-expression of miR397 induced de-domestication phenotypes. Interestingly, nearly 26 unknown QTLs previously implicated for rice yield overlapped with laccases and miR397 genes. These results suggest the involvement of miRNAs in rice domestication-associated phenotypes.

<http://www.plantcell.org/content/plantcell/early/2018/10/19/tpc.18.00472.full.pdf>

American Society of Plant Biologists

Loss of a microRNA molecule boosts rice production

<https://phys.org/news/2018-10-loss-microrna-molecule-boosts-rice.html#iCp>

Scott N.D. (2018) **Magic Bullets II, Genetic Engineering and Technological Pragmatism.** In: Food, Genetic Engineering and Philosophy of Technology 59-78. The International Library of Environmental, Agricultural and Food Ethics, vol 28. Springer, Cham

This chapter builds on the analysis of the magic bullet strategy discussed in the previous chapter. The overuse and misuse of magic bullets have loaded the environment with antibiotics and pesticides that threaten human health and biodiversity. Nonetheless, the magic bullet myth continues to define the goals of powerful public and private institutions in medicine and agriculture. The framework for critically examining the magic bullet strategy developed in the previous chapter to examine the two most economically important genetically engineered traits to date: insect resistance and herbicide resistance. This examination will provide insights into evaluating GE crops, as well as more philosophical insights into the magic bullet myth that could contribute to better understanding the place of biotechnology in a narrative of sustainability.

<https://link.springer.com/book/10.1007/978-3-319-96027-2>

Scott N.D. (2018) **Progress in Crisis, Genetic Engineering and Philosophy of Technology.** In: Food, Genetic Engineering and Philosophy of Technology. The International Library of Environmental, Agricultural and Food Ethics, vol 28. Springer, Cham

This chapter sets the stage for the rest of the book by characterizing central themes and ideas: the narrative of progress, technological optimism, technological pessimism, and precautionary ethics. The chapter begins by developing the idea that the polarized debate over genetic engineering in agriculture is at least in part the result of a narrative crisis created by a clash between technological optimism and technological pessimism. The ultimate goal of the book is to investigate possibilities for moving beyond the current polarized debate over genetic engineering. This chapter aims to start the process of identifying obstacles to, and possibilities for moving beyond the current narrative crisis and to develop a narrative of sustainability. To that end, the chapter investigates and identifies hindrances to research and development in agricultural biotechnology from making greater contributions to creating more just and sustainable societies. I identify three obstacles: (1) costly and time-consuming precautionary regulations, (2) market failures in the private sector and (3) limited public sector funding for social-goods research. Chapter 2 will explore ideas for moving beyond these three obstacles.

https://link.springer.com/content/pdf/10.1007%2F978-3-319-96027-2_1.pdf

Scott N.D. (2018) **Reinterpreting Progress, Genetically Engineered Biofortified Crops and Technological Pragmatism.** In: Food, Genetic Engineering and Philosophy of Technology. The International Library of Environmental, Agricultural and Food Ethics, vol 28. Springer, Cham

https://doi.org/10.1007/978-3-319-96027-2_2

This chapter explores ideas for overcoming the three obstacles identified in the previous chapter. The chapter begins by focusing on fundamental issues in philosophy of technology, arguing that we need to reinterpret the philosophical idea of progress to move beyond the polarized debate over genetic engineering in agriculture. This requires abandoning conflicting metaphysical assumptions found in techno-optimism and techno-pessimism. I argue that environmental ethics needs a pragmatic philosophy of technology with a more limited interpretation of progress. The remainder of the chapter explores the implications of applying pragmatic technological philosophy to overcoming the three obstacles identified in the first chapter. More specifically, the chapter examines possibilities for using genetic engineering for social justice by reducing population-level micronutrient malnutrition with genetically engineered biofortified crops, with particular attention to the controversy over Golden Rice. The chapter ends by exploring the possibility of using a publicly funded, pay-for-performance incentive system to correct defects in the current incentive system, which is leading to market failures and injustices.

https://link.springer.com/content/pdf/10.1007%2F978-3-319-96027-2_2.pdf

Ibrahim K.M. (2018): Integrating Date Palm Biotechnology with community, A Review: Iraqi Journal of Biotechnology 17 (2), 1-12

Date palm (*Phoenix dactylifera* L.) tree is one of the oldest cultivated fruit trees in many regions in Asia and Africa particularly Mesopotamia. The tree has sustained and associated with many human cultures as a source for food, wood, furniture besides the high nutritional value of fruits. The tree has been and still plays a vital role in mitigating harsh environments in the regions where date palm groves are already established. The proposed review focuses on entire utilization of date palm biotechnology in improving the environment, enrichment of flora and fauna diversity, flourishing the tourism, and other aspects of human life. Biotechnology has been integrated almost in all human aspects including the full usefulness of manipulating date palm tree.

Widespread of date groves certainly will encourage the biodiversity enriching the ecosystem with a variety of fauna and flora including birds, butterflies, insects, other plant species, and soil microorganisms. Industry based on date palm pruning remains will also flourish the biofuel production. In the last decades, the advances in horticultural and technological practices have been reflected on the date industry shifting into modern agricultural systems. Although, implementation of this progress in some date palm countries is still a slow process. Major challenges are post-harvest and mechanization technologies that are so crucial for building rural

<https://www.iasj.net/iasj?func=article&aid=150212>

Jin L. et al. (2018): Dominant point mutation in a tetraspanin gene associated with field-evolved resistance of cotton bollworm to transgenic Bt cotton. PNAS;

<https://doi.org/10.1073/pnas.1812138115>

Extensive planting of crops genetically engineered to produce insecticidal proteins from the bacterium *Bacillus thuringiensis* (Bt) has suppressed some major pests, reduced insecticide sprays, enhanced pest control by natural enemies, and increased grower profits. However, rapid evolution of resistance in pests is reducing these benefits. Better understanding of the genetic basis of resistance to Bt crops is urgently needed to monitor, delay, and counter pest resistance. We discovered that a point mutation in a previously unknown tetraspanin gene in the cotton bollworm (*Helicoverpa armigera*), a devastating global pest, confers dominant resistance to Cry1Ac, the sole Bt protein produced by transgenic cotton planted in China. We found the mutation using a genome-wide association study, followed by fine-scale genetic mapping and DNA sequence comparisons between resistant and susceptible strains. CRISPR/Cas9 knockout of the tetraspanin gene restored susceptibility to a resistant strain, whereas inserting the mutation conferred 125-fold resistance in a susceptible strain. DNA screening of moths captured from 23 field sites in six provinces of northern China revealed a 100-fold increase in the frequency of this mutation, from 0.001 in 2006 to 0.10 in 2016. The correspondence between the observed trajectory of the mutation and the trajectory predicted from simulation modeling shows that the dominance of the mutation accelerated adaptation. Proactive identification and tracking of the tetraspanin mutation demonstrate the potential for genomic analysis, gene editing, and molecular monitoring to improve management of resistance.

<http://www.pnas.org/content/early/2018/10/30/1812138115>

University of Arizona

Genetic search reveals key to resistance in global cotton pest

<https://phys.org/news/2018-10-genetic-reveals-key-resistance-global.html#iCp>

VanBuren R., Wai C.M., Pardo J., Giarola V., Ambrosini S., Song X., Bartels D. (2018): Desiccation tolerance evolved through gene duplication and network rewiring in *Lindernia*.

The Plant Cell; <http://www.plantcell.org/content/early/2018/10/25/tpc.18.00517>

Though several resurrection plant genomes have been sequenced, the lack of suitable dehydration-sensitive outgroups has limited genomic insights into the origin of desiccation tolerance. Here, we utilized a comparative system of closely related desiccation-tolerant (*Lindernia brevidens*) and -sensitive (*L. subracemosa*) species to identify gene and pathway level changes associated with the evolution of desiccation tolerance. The two high-quality *Lindernia* genomes we assembled are largely collinear and over 90% of genes are conserved. *L. brevidens* and *L. subracemosa* have evidence of an ancient, shared whole-genome duplication event, and retained genes have neofunctionalized, with desiccation-specific expression in *L. brevidens*. Tandem gene duplicates are also enriched in desiccation-associated functions including a dramatic expansion of early light induced proteins (ELIPs) from 4 to 26 copies in *L. brevidens*. A comparative differential gene co-expression analysis between *L. brevidens* and *L. subracemosa* supports extensive network rewiring across early dehydration, desiccation, and rehydration timecourses. Many LEA genes show significantly higher expression in

L. brevidens compared to their orthologs in L. subracemosa. Co-expression modules uniquely upregulated during desiccation in L. brevidens are enriched with seed-specific and ABA-associated cis regulatory elements. These modules contain a wide array of seed-associated genes that have no expression in the desiccation-sensitive L. subracemosa. Together these findings suggest that desiccation tolerance evolved through a combination of gene duplications and network level rewiring of existing seed desiccation pathways.
<http://www.plantcell.org/content/plantcell/early/2018/10/25/tpc.18.00517.full.pdf>

Nagarathinam, K. et al. (2018): **Outward open conformation of a Major Facilitator Superfamily multidrug/H⁺ antiporter provides insights into switching mechanism.** Nature Communications **9**, Article number:4005 (2018), doi: 10.1038/s41467-018-06306-x
Multidrug resistance (MDR) poses a major challenge to medicine. A principle cause of MDR is through active efflux by MDR transporters situated in the bacterial membrane. Here we present the crystal structure of the major facilitator superfamily (MFS) drug/H⁺ antiporter MdfA from *Escherichia coli* in an outward open conformation. Comparison with the inward facing (drug binding) state shows that, in addition to the expected change in relative orientations of the N- and C-terminal lobes of the antiporter, the conformation of TM5 is kinked and twisted. In vitro reconstitution experiments demonstrate the importance of selected residues for transport and molecular dynamics simulations are used to gain insights into antiporter switching. With the availability of structures of alternative conformational states, we anticipate that MdfA will serve as a model system for understanding drug efflux in MFS MDR antiporters.
<https://www.nature.com/articles/s41467-018-06306-x>
<https://www.nature.com/articles/s41467-018-06306-x.pdf>

IFOAM: POSITION PAPER: **Compatibility of Breeding Techniques in Organic Systems**
Null GM segregants are prohibited
All types of genome editing are prohibited
Protoplast fusion is to be excluded, though traceability issues have not been resolved.
https://www.ifoam.bio/sites/default/files/position_paper_v01_web.pdf

Valverde A.H.P. et al: (2018): **A new methodology for large-scale screening sugarcane resistance to *Mahanarva Fimbriolata* (Hemiptera: Cercopidae):** Bragantia,
<http://dx.doi.org/10.1590/1678-4499.2017403>
The sugarcane spittlebug, *Mahanarva fimbriolata* (Walker) (Hemiptera: Cercopidae) is an economically important pest of sugarcane in Brazil. The purpose of this study was to develop and validate a greenhouse methodology to screen large sugarcane populations for resistance to spittlebug *Mahanarva fimbriolata*. A resistant and a susceptible genotype (H. Kawandang and SP81-3250) were first used to determine adequate days after infestation and levels of infestation (number of nymphs per plant) for comparing the resistance of genotypes. Then, 74 sugarcane genotypes including three susceptible and three resistant controls were screened for resistance. The screening method consists in infesting single-tiller plants supported in a small plant growth unit and assessing the damage by using a 1-5 visual damage score. Our data suggest screening with four to six nymphs per plant and the damage score assessment at least 21 days after infestation. The screening technique was proved reliable as susceptible and resistant controls were placed in their respective resistance category. Three genotypes were classified as resistant while the majority of genotypes were classified as susceptible to spittlebug, indicating the need of breeding for resistance.
http://www.scielo.br/scielo.php?pid=S0006-87052018005012104&script=sci_arttext

Tagungen - Meetings:

Innoplanta-Forum 2018 - **Grüne Biotechnologie - Wahrnehmung und Wirklichkeit**
Freitag, 30. November 2018, 10.00 bis 16.00 Uhr
Julius Kühn-Institut (JKI), Quedlinburg
Programflyer: http://www.innoplanta.de/fileadmin/user_upload/Pdf/Pdf_Innoplanta-Forum/Flyer_InnoPlanta_Forum_2018.pdf

Das Nagoya-Protokoll - Herausforderungen und Perspektiven, Gemeinsamer Workshop von VBU, DECHEMA und VBIO, am 3. Dezember 2018 im DECHEMA-Haus, Frankfurt am Main
http://v-b-u.org/Workshop_Nagoya_Protokoll.html

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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