Sunday Evening News No. 90

Week 29 (2018-07-16 / 07-22)

Selected and edited by ***BGF*** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,

Dear all,

The open letter to EU President Juncker and the commissioners concerned is now really public on the websites in German, English and French.

https://www.biotech-gm-food.com/aktuelles

https://www.biotech-gm-food.com/NBTs-EuGH-kommissionpraesident-juncker-brief

https://www.wgg-ev.de/info/korrespondenz-national/

http://www.biotechnologies-vegetales.com/lettre-ouverte-au-president-de-la-commission-juncker

Here are also listed all signatories, who gave their consent until 07-18-2018. There is still the possibility to sign the letter. We, AFBV and WGG, have decided to send an annex with signatory to the president. We would be glad, if many would sign the letter. A short e-mail to kd.jany@t-online.de or philippe.dumont@wanadoo.fr is sufficient.

In the German press this week was the expected ECJ judgment on the mutagenesis techniques "genetic engineering yes or no" a main topic. In addition, publishing in open access journals was discussed as "fake science". Partially very uncritical and no distinction was made between "really good science" and "pseudoscience". The term "fake science" should be avoided.

Genome Editing – expected ECJ judgement

Gmwatch: **Battle lines drawn as EU court weighs fate of gene-edited crops**
Reuters gets it wrong on genome edited foods
https://www.gmwatch.org/en/news/latest-news/18360

Holly Reeve: **EU set to decide on the future of genetically modified crops**
https://www.mirror.co.uk/science/eu-set-decide-future-genetically-12951686

Forschung und Lehre: **Verhärtete Fronten vor Urteil zu neuer Gentechnik**
Der Europäische Gerichtshof soll über neue Verfahren wie CRISPR entscheiden. Muss das strenge Gentechnikrecht gelten? Die Meinungen sind umstritten.

Bitte beachten Sie auch die links zu dem Interview mit Then-TestBiotech, als wissenschaftliche Fachstelle und dem Beitrag von Dabrock und Braun
https://www.forschung-und-lehre.de/recht/verhaertete-fronten-vor-urteil-zu-neuer-gentechnik-842/

Julia Eder, agrarheute: **EuGH urteilt über neue Gentechnik: 7 Fakten zu Genome Editing**
https://www.agrarheute.com/pflanze/eugh-urteilt-ueber-neue-gentechnik-7-fakten-genome-editing-546706

Johann Grolle: **Wer hat Angst vorm Blumenkohl?**
https://magazin.spiegel.de/SP/2018/30/158500383/?utm_source=spon&utm_campaign=centerpage

BVL: **Monitoring Bericht des BVL, JKI und FLI zu Neuen Molekularen Techniken**
http://www.bvl.bund.de/bericht_molekulare_techniken

RND: **Umweltministerin Schulze: Keine Gentechnik durch die Hintertür**
http://www.haz.de/Nachrichten/Politik/Deutschland-Welt/Umweltministerin-Schulze-Keine-Gentechnik-durch-die-Hintertuer

Joachim Müller-Jung: **Werden Gene langsam salonfähig?**

http://www.faz.net/aktuell/wissen/leben-gene/werden-gene-langsam-salonfaehig-15683053.html

Christiane Grefe und Andreas Sentker: **Europäischer Gerichtshof: Ist das Gentechnik?**
https://www.zeit.de/2018/30/europaeischer-gerichtshof-luxemburggentechnik/komplettansicht

Marcus Overmann - BR-24: **Unternehmen und Bürger: Gemeinsam gegen Gentechnik**
https://www.br.de/nachrichten/unternehmen-und-buerger-gemeinsam-gegen-gentechnik-100.html

An excellent video - surprisingly produced in Austria - on green genetic engineering and genome editing
https://www.youtube.com/watch?v=JUxt1LWBLf8

Testbiotech: **Risiken der neuen Gentechnik: der „CRISPR-Giftpilz“**
Video-Clip über mögliches Zukunftsszenario
https://www.youtube.com/watch?v=i7QP_j6gx4Y
http://www.testbiotech.org/node/2239
and the English version: http://www.testbiotech.org/en/node/2241
almost **fake science**! That is an independent and objective information, scientific based!

Fake Science
Robert Gast: »Fake Science«: Dieser Begriff kann der Wissenschaft nur schaden
In der Präsentation ihrer Ergebnisse schießen die Journalisten aber übers Ziel hinaus. Ein Kommentar.
https://www.spektrum.de/kolumne/dieser-begriff-kann-der-wissenschaft-nur-schaden/1579216?utm_medium=newsletter&utm_source=sdw-nl&utm_campaign=sdw-nl-daily&utm_content=kolumne

Carsten Könneker: **Das »Publish or perish«-Diktat muss enden**
https://www.spektrum.de/kolumne/das-publish-or-perish-diktat-muss-enden/1579710?utm_medium=newsletter&utm_source=sdw-nl&utm_campaign=sdw-nl-daily&utm_content=kolumne

NDR: Dossier: Das Geschäft mit der Wissenschaft
https://www.ndr.de/nachrichten/investigation/Dossier-Das-Geschaeft-mit-der-Wissenschaft,fakesciencedossier100.html

https://www.sueddeutsche.de/wissen/wissenschaft-tausende-forscher-publizieren-in-pseudo-journalen-1.4061005
http://www.tagesschau.de/inland/fakescience-101.html
https://www.mdr.de/nachrichten/vermischtes/fake-science-wissenschaftler-zweifelhafte-verlage-100.html

India: https://indianexpress.com/article/india/inside-indias-fake-research-paper-shops-pay-publish-profit-5265402/

France: https://www.lemonde.fr/sciences/article/2018/07/19/alerte-mondiale-a-la-fausse-science_5333374_1650684.html

In respect to the Nature Biotechnology publication: **Repair of double-strand breaks induced by CRISPR–Cas9 leads to large deletions and complex rearrangements**.

Sascha Karberg: **Die Axt im Gen-Walde**
https://www.tagesspiegel.de/wissen/genome-editing-mit-crispr-nicht-immer-praezise-die-axt-im-gen-walde/22806870.html

Jan Osterkamp: **Falsche Schnitte der CRISPR-Genscheren**
Das Original der Gentechnikwaffe CRISPR/Cas9 altert rapide: Es kann einfach zu große Schäden anrichten. Davon kann man aber lernen - um sichere Alternativen zu finden.
https://www.spektrum.de/news/falsche-schnitte-der-crispr-genscheren/1578338

AFP: Gene-editing damages DNA more than previously thought: study
https://www.nation.co.ke/lifestyle/health/Gene-editing-damages-DNA-more-than-previously-thought/1954202-4667202-k3hkfj/index.html

As always, you will find the daily up-to-date press reports here:
https://www.biotech-gm-food.com/presse

Scientific papers:

Kosicki M., Tomberg K. & Bradley A. (2018): **Repair of double-strand breaks induced by CRISPR–Cas9 leads to large deletions and complex rearrangements**. Nature Biotechnology advance online publication; doi:10.1038/nbt.4192
CRISPR–Cas9 is poised to become the gene editing tool of choice in clinical contexts. Thus far, exploration of Cas9-induced genetic alterations has been limited to the immediate vicinity of the target site and distal off-target sequences, leading to the conclusion that CRISPR–Cas9 was reasonably specific. Here we report significant on-target mutagenesis, such as large deletions and more complex genomic rearrangements at the targeted sites in mouse embryonic stem cells, mouse hematopoietic progenitors and a human differentiated cell line. Using long-read sequencing and long-range PCR genotyping, we show that DNA breaks introduced by single-guide RNA/Cas9 frequently resolved into deletions extending over many kilobases. Furthermore, lesions distal to the cut site and crossover events were identified. The observed genomic damage in mitotically active cells caused by CRISPR–Cas9 editing may have pathogenic consequences.
https://www.nature.com/articles/Nbt.4192

Expert reaction to study looking at deletions and rearrangements due to the CRISPR/Cas9 genome editing technique
http://www.sciencemediacentre.org/expert-reaction-to-study-looking-at-deletions-and-rearrangements-due-to-the-crispr-cas9-genome-editing-technique/

NAP: Science Breakthroughs to Advance Food and Agricultural Research by 2030
https://www.nap.edu/download/25059

Nuffield Council on Bioethics (2018): **Genome editing and human reproduction: social and ethical issues**
http://nuffieldbioethics.org/wp-content/uploads/Genome-editing-and-human-reproduction-FINAL-website.pdf

Nigel Hawkes (2018): ***Human genome editing is not unethical, says Nuffield Council***
BMJ 2018; 362 doi: https://doi.org/10.1136/bmj.k3140 (Published 17 July 2018) Cite this as: BMJ 2018;362: k3140
There is no moral or ethical objection to making changes to the human genome that would pass down to future generations, as long as certain preconditions are met, the Nuffield Council for Bioethics has concluded. Germline engineering, as the technique is sometimes called, was for a long time the red line in biology. Any changes made would become part of the genome of the individual, to be passed on to future generations. The uncertainties and risks were deemed so great that it should never be attempted. But attitudes have shifted so much that the Nuffield report does not even attempt to restrict the technique to therapeutic uses. It says, rather, that it could be ethically acceptable if it contributes to the welfare of the person born as a consequence and does not increase …
https://www.bmj.com/content/362/bmj.k3140

Charles M. Benbrook C. M. (2018): **Why Regulators Lost Track and Control of Pesticide Risks: Lessons From the Case of Glyphosate-Based Herbicides and Genetically Engineered-Crop Technology.** Current Environmental Health Reports; https://doi.org/10.1007/s40572-018-0207-y
Purpose of Review: The approval of genetically engineered (GE) crops in the late 1990s triggered dramatic changes in corn, soybean, and cotton pest management systems, as well as complex, novel regulatory challenges. Lessons learned are reviewed and solutions described.
Recent Findings: Government-imposed resistance management provisions can work and adapt to changing circumstances, but within the private sector, pressures to gain and hold market share have thus far trumped the widely recognized need for resistance management. Risks arising from the use of formulated pesticides often exceed by a wide margin those in regulatory risk assessments based on data derived from studies on nearly 100% pure active ingredients.
Summary: Innovative policy changes are needed in four problem areas: excessive faith in the accuracy of pre-market risk assessments and regulatory thresholds; post-approval monitoring of actual impacts; risk arising from formulated pesticides, rather than just pure active ingredient; challenges inherent in assessing and mitigating the combined impacts of all GE traits and associated pesticides on agroecosystems, as opposed to each trait or pesticide alone; and, tools to deal with failing pest management systems.
https://link.springer.com/content/pdf/10.1007%2Fs40572-018-0207-y.pdf

Ellstrand NC (2018) **"Born to Run"? Not Necessarily: Species and Trait Bias in Persistent Free-Living Transgenic Plants.** Front. Bioeng. Biotechnol. 6: 88. doi: 10.3389/fbioe.2018.00088

The possibility of transgenes from engineered plants ending up in unmanaged populations with undesirable consequences has been a long-term biosafety concern. Experience with traditionally improved plants reveals that most cases of such gene escape have been of little consequence, but on occasion they have led to the evolution of problematic plants or have resulted in an increased extinction risk for wild taxa. Three decades have passed since the first environmental release of transgenic plants, andmore than two decades since their first commercialization. Examples of transgenes gone astray are increasingly commonplace. Transgenic individuals have been identified in more than a thousand free-living plant populations. Here I review 14 well-documented consolidated "cases" in which transgenes have found their way into free-living plant populations. Some as transient volunteers; others appear to be persistent transgenic populations. The species involved in the latter are not representative of the current commercialized transgenic crops as whole. They tend to share certain traits that are absent or rare in the transgenic crops that do not exist as persistent populations. The traits commonly occurring in species with persistent transgenic free-living populations are the following, in descending order of importance: (1) a history of occurring as non-transgenic free-living plants, (2) fruits fully or partially shattering prior to harvest, (3) have small or otherwise easily dispersed seeds, either spontaneously or by seed spillage along the supply chain from harvest to consumer, (4) ability to disperse viable pollen, especially to a kilometre or more, (5) perennial habit, and (6) the transgene's fitness effects in the recipient environment are beneficial or neutral. Based on these observations, a thought experiment posits which species might be the next to be reported to occur as free-living transgenic populations.
https://www.frontiersin.org/articles/10.3389/fbioe.2018.00088/full

Douglass A P, Offei B, Braun-Galleani S, Coughlan A Y, Martos A A R, Ortiz-Merino R A, et al. (2018): **Population genomics shows no distinction between pathogenic Candida krusei and environmental Pichia kudriavzev: One species, four names**. PLoS Pathog 14(7): e1007138. https://doi.org/10.1371/journal.ppat.1007138

We investigated genomic diversity of a yeast species that is both an opportunistic pathogen and an important industrial yeast. Under the name *Candida krusei*, it is responsible for about 2% of yeast infections caused by *Candida* species in humans. Bloodstream infections with *C. krusei* are problematic because most isolates are fluconazole-resistant. Under the names *Pichia kudriavzevii*, *Issatchenkia orientalis* and *Candida glycerinogenes*, the same yeast, including genetically modified strains, is used for industrial-scale production of glycerol and succinate. It is also used to make some fermented foods. Here, we sequenced the type strains of *C. krusei* (CBS573^T) and *P. kudriavzevii* (CBS5147^T), as well as 30 other clinical and environmental isolates. Our results show conclusively that they are the same species, with collinear genomes 99.6% identical in DNA sequence. Phylogenetic analysis of SNPs does not segregate clinical and environmental isolates into separate clades, suggesting that *C. krusei* infections are frequently acquired from the environment. Reduced resistance of strains to fluconazole correlates with the presence of one gene instead of two at the *ABC11-ABC1* tandem locus. Most isolates are diploid, but one-quarter are triploid. Loss of heterozygosity is common, including at the mating-type locus. Our PacBio/Illumina assembly of the 10.8 Mb CBS573^T genome is resolved into 5 complete chromosomes, and was annotated using RNAseq support. Each of the 5 centromeres is a 35 kb gene desert containing a large inverted repeat. This species is a member of the genus *Pichia* and family Pichiaceae (the methylotrophic yeasts clade), and so is only distantly related to other pathogenic *Candida* species.
http://journals.plos.org/plospathogens/article/file?id=10.1371/journal.ppat.1007138&type=printable

Drabsch T., Gatzemeier J., Pfadenhauer L., Hauner H., Holzapfel C. (2018): **Associations between Single Nucleotide Polymorphisms and Total Energy, Carbohydrate, and Fat Intakes: A Systematic Review**. *Advances in Nutrition*, 9 (4): 425-453; DOI: 10.1093/advances/nmy024

A better understanding of the genetic underpinning of total energy, carbohydrate, and fat intake is a prerequisite to develop personalized dietary recommendations. For this purpose, we systematically reviewed associations between single nucleotide polymorphisms (SNPs) and total energy, carbohydrate, and fat intakes. Four databases were searched for studies that assessed an association between SNPs and total energy, carbohydrate, and fat intakes. Screening of articles and data extraction was performed independently by 2 reviewers. Articles in English or German language, published between 1994 and September 2017, on human studies in adults and without specific populations were considered for the review. In total, 39 articles, including 86 independent loci, met the inclusion criteria. The fat mass and obesity–associated (FTO) gene as well as the melanocortin 4 receptor (MC4R) locus were most frequently studied. Limited significant evidence of an association between the FTO SNP rs9939609 and lower total energy intake and between the MC4R SNP rs17782313 and higher total energy intake was reported. Most of the other identified loci showed inconsistent results. In conclusion, there is no consistent evidence that the investigated SNPs are associated with and predictive for total energy, carbohydrate, and fat intakes.
https://academic.oup.com/advances/article/9/4/425/5055951

Yan Y., Liu Q., Zang X., Yuan S., Bat-Erdene U., Nguyen C., Gan J., Zhou J., Jacobsen S.E. & Tang Y.(2018): **Resistance-gene-directed discovery of a natural-product herbicide with a new mode of action.** *Nature* **559**, 415–418

Bioactive natural products have evolved to inhibit specific cellular targets and have served as lead molecules for health and agricultural applications for the past century[1,2,3]. The post-genomics era has brought a renaissance in the discovery of natural products using synthetic-biology tools[4,5,6]. However, compared to traditional bioactivity-guided approaches, genome mining of natural products with specific and potent biological activities remains challenging[4]. Here we present the discovery and validation of a potent herbicide that targets a critical metabolic enzyme that is required for plant survival. Our approach is based on the co-clustering of a self-resistance gene in the natural-product biosynthesis gene cluster[7,8,9], which provides insight into the potential biological activity of the encoded compound. We targeted dihydroxy-acid dehydratase in the branched-chain amino acid biosynthetic pathway in plants; the last step in this pathway is often targeted for herbicide development[10]. We show that the fungal sesquiterpenoid aspterric acid, which was discovered using the method described above, is a sub-micromolar inhibitor of dihydroxy-acid dehydratase that is effective as a herbicide in spray applications. The self-resistance gene *astD* was validated to be insensitive to aspterric acid and was deployed as a transgene in the establishment of plants that are resistant to aspterric acid. This herbicide-resistance gene combination complements the urgent ongoing efforts to overcome weed resistance[11]. Our discovery demonstrates the potential of using a resistance-gene-directed approach in the discovery of bioactive natural products.

https://www.nature.com/articles/s41586-018-0319-4

Naim F., Dugdale B., Kleidon J., Brinin A., Shand K., Waterhouse P., Dale J. (2018): **Gene editing the phytoene desaturase alleles of Cavendish banana using CRISPR/Cas9.** Transgenic Res; https://doi.org/10.1007/s11248-018-0083-0

Bananas are a staple food source and a major export commodity worldwide. The Cavendish dessert banana is a triploid AAA genome type and accounts for around 47% of global production. Being essentially sterile, genetic modification is perhaps the only pathway available to improve this cultivar. In this study, we used the CRISPR/Cas9 gene editing system to deliver a self-cleaving polycistronic guide RNA (gRNA) designed to target exon 1 of the Phytoene desaturase (PDS) gene in the Cavendish cultivar ''Williams''. Genotyping of 19 independent events showed a 100% PDS modification rate primarily in the form of insertions (1–105 nt) or deletions (1–55 nt) (indels) at the predicted cleavage site. Tri-allelic disruptive modifications were observed in 63% of plants and resulted in both albinism and dwarfing. Pale green (16%) and wildtype green (21%) phenotypes generally correlated with in-frame indels in at least one of the three PDS alleles. Editing efficiency was dependent on both target site selection and Cas9 abundance. This is the first report of a highly effective CRISPR/Cas9 modification system using a polycistronic gRNA in Cavendish banana. Such an editing platform will be of considerable utility for the development of disease resistance and novel agrotraits in this commercially important cultivar into the future.

https://link.springer.com/content/pdf/10.1007%2Fs11248-018-0083-0.pdf

Giraldo, P.A., Elliott, C., Badenhorst, P. et al. (2018): **Evaluation of endophyte toxin production and its interaction with transgenic perennial ryegrass (Lolium perenne L.) with altered expression of fructosyltransferases** Transgenic Res (2018). https://doi.org/10.1007/s11248-018-0087-9

Alkaloid concentration of perennial ryegrass herbage is affected by endophyte strain and host plant genotype. However, previous studies suggest that associations between host and endophyte also depends on environmental conditions, especially those affecting nutrient reserves and that water-soluble carbohydrate (WSC) concentration of perennial ryegrass plants may influence grass-endophyte associations. In this study a single transgenic event, with altered expression of fructosyltransferase genes to produce high WSC and biomass, has been crossed into a range of cultivar backgrounds with varying *Epichloë* endophyte strains. The effect of the association between the transgenic trait and alkaloid production was assessed and compared with transgene free control populations. In the vast-majority of comparisons there was no significant difference between alkaloid concentrations of transgenic and non-transgenic plants within the same cultivar and endophyte backgrounds. There was no significant difference between GOI+ (gene of interest positive) and GOI− (gene of interest negative) populations in Janthritrem response. Peramine concentration was not different between GOI+ and GOI− for 10 of the 12 endophytes-cultivar combinations. Cultivar Trojan infected with NEA6 and Alto with SE (standard endophyte) exhibited higher peramine and lolitrem B (only for Alto SE) concentration, in the control GOI− compared with GOI+. Similarly, cultivar Trojan infected with NEA6 and Alto with NEA3 presented higher ergovaline concentration in GOI−. Differences in alkaloid concentration may be attributable to an indirect effect in the modulation of fungal biomass. These results conclude that the presence of this transgenic insertion, does not alter the risk (toxicity) of the endophyte–grass associations. Endophyte–host interactions are complex and further research into associations with high WSC plant should be performed in a case by case basis.

https://link.springer.com/article/10.1007/s11248-018-0087-9

Flórez L.V., Scherlach K., Miller I.J., Rodrigues A, Kwan J.C., Hertweck C. & Kaltenpoth M. (2018): **An antifungal polyketide associated with horizontally acquired genes supports symbiont-mediated defense in Lagria villosa beetles**, *Nature Communications* (2018). DOI: 10.1038/s41467-018-04955-6

Microbial symbionts are often a source of chemical novelty and can contribute to host defense against antagonists. However, the ecological relevance of chemical mediators remains unclear for most systems. *Lagria* beetles live in symbiosis with multiple strains of *Burkholderia* bacteria that protect their offspring against pathogens. Here, we describe the antifungal polyketide lagriamide, and provide evidence supporting that it is produced by an uncultured symbiont, *Burkholderia gladioli* Lv-StB, which is dominant in field-collected *Lagria villosa*. Interestingly, lagriamide is structurally similar to bistramides, defensive compounds found in marine tunicates. We identify a gene cluster that is probably involved in lagriamide biosynthesis, provide evidence for horizontal acquisition of these genes, and show that the naturally occurring symbiont strains on the egg are protective in the soil environment. Our findings highlight the potential of microbial symbionts and horizontal gene transfer as influential sources of ecological innovation.
https://www.nature.com/articles/s41467-018-04955-6.pdf

Universitaet Mainz
Lateral gene transfer enables chemical protection of beetles against antagonistic fungi
https://phys.org/news/2018-07-lateral-gene-enables-chemical-beetles.html#jCp

Blei F., Baldeweg F. Fricke J. and Hoffmeister D. (2018): **Biocatalytic Production of Psilocybin and Derivatives in Tryptophan Synthase-Enhanced Reactions**, Chemistry – A European Journal, https://onlinelibrary.wiley.com/doi/full/10.1002/chem.201801047.

Psilocybin (4-phosphoryloxy-*N*,*N*-dimethyltryptamine) is the main alkaloid of the fungal genus *Psilocybe*, the so-called "magic mushrooms." The pharmaceutical interest in this psychotropic natural product as a future medication to treat depression and anxiety is strongly re-emerging. Here, we present an enhanced enzymatic route of psilocybin production by adding TrpB, the tryptophan synthase of the mushroom *Psilocybe cubensis*, to the reaction. We capitalized on its substrate flexibility and show psilocybin formation from 4-hydroxyindole and l-serine, which are less cost-intensive substrates, compared to the previous method. Furthermore, we show enzymatic production of 7-phosphoryloxytryptamine (isonorbaeocystin), a non-natural congener of the *Psilocybe* alkaloid norbaeocystin (4-phosphoryloxytryptamine), and of serotonin (5-hydroxytryptamine) by means of the same in vitro approach.
https://onlinelibrary.wiley.com/doi/full/10.1002/chem.201801047

Hoefgen S. et al. (2018): **Facile assembly and fluorescence-based screening method for heterologous expression of biosynthetic pathways in fungi.** Metabolic Engineering, https://doi.org/10.1016/j.ymben.2018.05.014.

Heterologous expression of multi-gene biosynthetic pathways in eukaryotic hosts is limited by highly regulated individual monocistrons. Dissimilar to prokaryotes, each eukaryotic gene is strictly controlled by its own regulatory elements, such as promoter and terminator. Consequently, parallel transcription can occur only when a group of genes is synchronously activated. A strategy to circumvent this limitation is the concerted expression of multiple genes as a polycistron. By exploiting the "stop-carry on" mechanism of picornaviruses, we have designed a sophisticated, yet easy-to-assemble vector system to heterologously express multiple genes under the control of a single promoter. For facile selection of correctly transformed colonies by basic fluorescence microscopy, our vector includes a split gene for a fluorescent reporter protein. This method was successfully applied to produce the psychotropic mushroom alkaloid psilocybin in high yields by heterologous expression of the entire biosynthetic gene cluster in the mould *Aspergillus* nidulans.
https://www.sciencedirect.com/science/article/pii/S1096717618301228?via%3Dihub

Waller R. F. et al. (2018): S**trength in numbers: Collaborative science for new experimental model systems,** *PLOS Biology* (2018). DOI: 10.1371/journal.pbio.2006333

Our current understanding of biology is heavily based on a small number of genetically tractable model organisms. Most eukaryotic phyla lack such experimental models, and this limits our ability to explore the molecular mechanisms that ultimately define their biology, ecology, and diversity. In particular, marine protists suffer from a paucity of model organisms despite playing critical roles in global nutrient cycles, food webs, and climate. To address this deficit, an initiative was launched in 2015 to foster the development of ecologically and taxonomically diverse marine protist genetic models. The development of new models faces many barriers, some technical and others institutional, and this often discourages the risky, long-term effort that may be required. To lower these barriers and tackle the complexity of this effort, a highly collaborative community-based approach was taken. Herein, we describe this approach, the advances achieved, and the lessons learned by participants in this novel community-based model for research.
http://journals.plos.org/plosbiology/article/file?id=10.1371/journal.pbio.2006333&type=printable
Stony Brook University

Scientists explore new experimental model systems to advance biology
https://phys.org/news/2018-07-scientists-explore-experimental-advance-biology.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. M*ost of the pdf files can be downloaded directly from the links.

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