Dear all,
due to the Whitsun holidays, you receive the Sunday Evening News on Monday evening this
time.

**Report on new genomic technique:**

The statements of the Commission in its report on the status of new genomic techniques are
mainly based on the analysis of the written surveys of stakeholders (107 requested, 58
responded), Member States and competent authorities. The report largely reflects the
opinions of the respondents and presents a comprehensive state of affairs on the new
genomic techniques and their applications in the entire economic sector (industrial
biotechnology, medicine and pharmaceuticals, as well as in agriculture and food production).
Evaluating the different opinions, the Commission concludes that the new genomic
techniques have
- show high innovative potential, especially in the field of plant biotechnology,
- facilitate the achievement of the Green Deal objectives,
- cannot be regulated appropriately and in a differentiated manner with the current legal
provisions.

However, the Commission does not make any concrete proposals as to what a regulation
could look like, although this was also desired by the Council at the time.

However, the Commission also notes that there is a lack of clarity for some terms and that
they are interpreted differently. Therefore, these should be clearly clarified or defined in the
further consultations. These include
- mutagenesis,
- conventionally used in a number of applications; or long safe use,
- altered genetic material; modification of genetic material,
- recombinant nucleic acid molecules,
- use of recombinant nucleic acid molecules.
- transformation event

It can be seen from the report that the Commission is considering new genomic techniques
for applications to
- regulate separately in the medical and pharmaceutical sectors,
- initially continue applying the existing laws on micro-organisms and animals,
- prepare a new or separate regulation for plants.

The letter to the Portuguese Council President makes it clear that the Commission is focusing
on directed mutagenesis, cisgenesis and intragenesis, is striving for an intensive exchange of
information with all parties involved and wants to carry out a technology assessment with a
sustainability assessment in the near future.

**Agriculture and Fisheries Council, 26-27 May 2021: Agenda highlights - New genomic
techniques**

New genomic techniques are capable of changing the genetic material of an organism
and have **wide-ranging existing and potential applications in the agri-food, industrial and pharmaceutical sectors.**

In 2019, the Council requested the Commission to submit a study on the status of
new genomic techniques. The Commission submitted the study in April 2021.
Ministers will hold a debate on the conclusions of the study and possible future policy
actions.


The Taxonomy Regulation establishes six environmental objectives:
1. Climate change mitigation
2. Climate change adaptation
3. The sustainable use and protection of water and marine resources
4. The transition to a circular economy
5. Pollution prevention and control
6. The protection and restoration of biodiversity and ecosystems

Implementing and delegated acts


**Webinar:**

GRAIN-Club und Verbände: **CRISPR/Cas & Co – Warum Europa ein zeitgemäßes Gentechnikrecht braucht.**

2. Juni 2021 | 14:30 – 16:00 Uhr

https://mailer.genius.de/archive/UBbvhkyAfO/tqAuuSuWNU/MxibceHmJh

DLG-Think Food 2021: Online-Konferenz

Alternative Proteinquellen und Enzymtechnologie

15. 06. – 16.06.2021

https://www.dlg.org/de/lebensmittel/veranstaltungen/dlg-think-food-2021

**Press Releases and Media Reports**

**BMEL: Deutschland, wie es isst** - Der BMEL-Ernährungsreport 202


**BRAIN Biotech AG: Genome Editing Tool Developed by BRAIN**

https://www.dgap.de/dgap/News/corporate/brain-biotech-genome-editing-tool-developed-brain/?newsID=1442839

**Universität zu Köln: Eine Symbiose mit Pilzen ermöglichte pflanzliches Leben auf der Erde**

https://idw-online.de/de/news769264

**Testbiotech: Die Gen-Schere unter Kontrolle halten!**

https://www.testbiotech.org/aktuelles/die-gen-schere-unter-kontrolle-halten

**Keep gene scissors under control!**

Agriculture & Progress: **EU Commission study opens the door to an adapted regulatory framework for NGTs:**
An important step in the right direction requiring rapid follow-up action by the EU Commission

Reis A.: **EU report supports the use of gene editing techniques in plants**

MEUNIER E.: **OGM : vers un affaiblissement de l’étiquetage en Europe ?**

Carey T.: **This New Gene Editing Technology Rivals CRISPR**
https://www.freethink.com/articles/gene-editing-technology

Sharratt L.: **Health Canada considers abandoning safety assessments for new genetically engineered foods**

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ►here: (May – week 19)

**Publications – Publikationen**


Symbiosis with arbuscular mycorrhizal fungi (AMF) improves plant nutrition in most land plants, and its contribution to the colonization of land by plants has been hypothesized. Here, we identify a conserved transcriptomic response to AMF among land plants, including the activation of lipid metabolism. Using gain of function, we show the transfer of lipids from the liverwort *Marchantia paleacea* to AMF and its direct regulation by the transcription factor WRINKLED (WRI). Arbuscules, the nutrient-exchange structures, were not formed in loss-of-function wri mutants in *M. paleacea*, leading to aborted mutualism. Our results show the orthology of the symbiotic transfer of lipids across land plants and demonstrate that mutualism with arbuscular mycorrhizal fungi was present in the most recent ancestor of land plants 450 million years ago.
https://science.sciencemag.org/content/372/6544/864

Mottl O., Suzette G. A. Flantua S.G.A., Bhatta K.P. et al. (2021): **Global acceleration in rates of vegetation change over the past 18,000 years.** Science 372 (Issue 6544), 860-864 | DOI: 10.1126/science.abg1685

Global vegetation over the past 18,000 years has been transformed first by the climate changes that accompanied the last deglaciation and again by increasing human pressures; however, the magnitude and patterns of rates of vegetation change are poorly understood globally. Using a compilation of 1181 fossil pollen sequences and newly developed statistical methods, we detect a worldwide acceleration in the rates of vegetation compositional change beginning between 4.6 and 2.9 thousand years ago that is globally unprecedented over the past 18,000 years in both magnitude and extent. Late Holocene rates of change equal or exceed the deglacial rates for all continents, which suggests that the scale of human effects on terrestrial ecosystems exceeds even the climate-driven transformations of the last deglaciation. The acceleration of biodiversity change demonstrated in ecological datasets from the past century began millennia ago.
https://science.sciencemag.org/content/372/6544/860

Serra-Garcia M. and Gneezy U. (2021): **Nonreplicable publications are cited more than replicable ones.** Science Advances 7 (21), eabd1705 | DOI: 10.1126/sciadv.abd1705

We use publicly available data to show that published papers in top psychology, economics, and general interest journals that fail to replicate are cited more than those that replicate. This difference in citation does not change after the publication of the failure to replicate. Only 12% of postreplication citations of nonreplicable findings acknowledge the replication failure. Existing evidence also shows that experts predict well which papers will be replicated. Given this prediction, why are nonreplicable papers accepted for publication in the first place? A possible answer is that the review team faces a trade-off. When the results are more “interesting,” they apply lower standards regarding their reproducibility.
https://advances.sciencemag.org/content/7/21/eabd1705.full
For thousands of years, humans have been improving crops to better suit their needs. These enhancements are driven by changes in the genetic makeup of the plant. While this was initially unintentional, there has been a steady push to increase the pace and precision of crop breeding, something that has occurred alongside a growing understanding of genetics and an escalating capacity to thoroughly assess genomes at the molecular level. With the advent and rapid uptake of molecular breeding techniques, such as transgenics and genome editing over the past few decades, there has been much trepidation regarding the possibility of off-target effects derived from unanticipated mutations at loci other than those intended for alteration, and the unintended risks that this might confer. These concerns persist regardless of the fact that a growing number of studies indicate that the occurrence of off-target mutations derived from newer biotechnological breeding techniques are negligible compared to what is observed with many conventional breeding approaches, and even spontaneously from one generation to the next. Given the impending food security crisis that we are facing in the short-term, there is a critical need to implement a wide range of breeding tools as a means of meeting growing demand, withstanding climate change-related pressures, increasing nutrition, and providing environmental benefits. While food safety is clearly of the utmost importance, now is certainly not the time to prevent the use of particular breeding technologies based on unfounded doubts. Therefore, in this review, we attempt to shed light on these apprehensions by putting purported “risks” into the context of plant breeding as a whole by comparing frequencies of spontaneous mutations with those (both anticipated and unanticipated) that occur through various conventional and biotechnological breeding approaches, including transgenics and genome editing. We then consider how these changes may, or may not, translate into unanticipated risk, and discuss the current global regulatory asynchrony surrounding genome edited crops. https://www.tandfonline.com/doi/full/10.1080/07352689.2021.1883826


A presentation of the results is available


Sugarcane (Saccharum spp.) is one of the most important industrial cash crops, contributing to the world sugar industry and biofuel production. It has been cultivated and improved from prehistoric times through natural selection and conventional breeding and, more recently, using the modern tools of genetic engineering and biotechnology. However, the heterogeneity, complex polyan euploid genome and susceptibility of sugarcane to different biotic and abiotic stresses represent impediments that require us to pay greater attention to the improvement of the sugarcane crop. Compared to traditional breeding, recent advances in breeding technologies (molecular marker assisted breeding, sugarcane transformation, genome editing and multiple omics technologies) can potentially improve sugarcane, especially against environmental stressors. This article will focus on efficient modern breeding technologies, which provide crucial clues for the engineering of sugarcane cultivars resistant to environmental stresses. https://www.mdpi.com/2073-4395/11/6/1042


Gene editing technology provides important technical basics for the research in plant functional genes and crop genetic improvement. CRISPR/Cas9-mediated gene editing is an effective experimental tool for crop genome directed editing in recent years, which has been widely used in many crops as rice, wheat and other crops. CRISPR/Cas9 system was expected to be a powerful experimental tool in genetic improvement and molecular design breeding of rapeseed. This paper, which based on the development history and the latest research of CRISPR/Cas9-mediated gene editing technology in rapeseed, summarized the progress of CRISPR/Cas9 including plant type improvement, yield traits, quality improvement, disease and stress resistance improvement, yellow seed creation and other utilizes at present. The application scope, development direction and target analysis method of this technology in rape were focused. The problems of CRISPR/cas9 system in rapeseed breeding were analyzed and the improvement strategies were discussed. Finally, views on direction of rapeseed breeding by gene editing were emphasized. https://www.sciencedirect.com/science/article/pii/S2096242821000245

Banana (Musa spp.) is an important staple food crop and a source of income for resource-poor farmers in more than 136 tropical and sub-tropical countries with an annual production of 155 million tons (FAOSTAT, 2018). Many diseases severely constrain banana production, particularly where many pathogens co-exist (Tripathi et al., 2020). Banana Xanthomonas wilt (BXW) caused by Xanthomonas campestris pv. musacearum (Xcm) is considered among the most destructive banana diseases in East and Central Africa (Tripathi et al., 2009). All the cultivated banana varieties are susceptible, and only the wild-type progenitor, Musa balbisiana, is resistant to BXW disease (Tripathi et al., 2019). Overall economic losses from BXW were estimated at US$ 2-8 billion over a decade. The use of disease-resistant varieties is one of the most effective strategies to manage diseases. Recent advances in CRISPR/Cas-based genome-editing can accelerate banana improvement. The availability of reference genome-sequences and the CRISPR/Cas9-editing system has made it possible to develop disease-resistant banana by precisely editing the endogenous genes (Ntui et al., 2020).


Background: In angiosperms the transition to flowering is controlled by a complex set of interacting networks integrating a range of developmental, physiological, and environmental factors optimizing transition time for maximal reproductive efficiency. The molecular mechanisms comprising these networks have been partially characterized and include both transcriptional and post-transcriptional regulatory pathways. Florigen, encoded by FLOWERING LOCUS T (FT) orthologs, is a conserved central integrator of several flowering time regulatory pathways. To characterize the molecular mechanisms involved in controlling cacao flowering time, we have characterized a cacao candidate florigen gene, TcFLOWERING LOCUS T (TcFT). Understanding how this conserved flowering time regulator affects cacao plant’s transition to flowering could lead to strategies to accelerate cacao breeding.

Results: BLAST searches of cacao genome reference assemblies identified seven candidate members of the CENTRORADIALIS/TERMINAL FLOWER1/SELF PRUNING gene family including a single florigen candidate. cDNA encoding the predicted cacao florigen was cloned and functionally tested by transgenic genetic complementation in the Arabidopsis ft-10 mutant. Transgenic expression of the candidate TcFT cDNA in late flowering Arabidopsis ft-10 partially rescues the mutant to wild-type flowering time. Gene expression studies reveal that TcFT is spatially and temporally expressed in a manner similar to that found in Arabidopsis, specifically, TcFT mRNA is shown to be both developmentally and diurnally regulated in leaves and is most abundant in floral tissues. Finally, to test interspecies compatibility of florigens, we transformed cacao tissues with AtFT resulting in the remarkable formation of flowers in tissue culture. The morphology of these in vitro flowers is normal, and they produce pollen that germinates in vitro with high rates.

Conclusion: We have identified the cacao CETS gene family, central to developmental regulation in angiosperms. The role of the cacao’s single FT-like gene (TcFT) as a general regulator of determinate growth in cacao was demonstrated by functional complementation of Arabidopsis ft-10 late-flowering mutant and through gene expression analysis. In addition, overexpression of AtFT in cacao resulted in precocious flowering in cacao tissue culture demonstrating the highly conserved function of FT and the mechanisms controlling flowering in cacao.


The maturation of green fleshy fruit to become colourful and flavoursome is an important strategy for plant reproduction and dispersal. In tomato (Solanum lycopersicum) and many other species, fruit ripening is intimately linked to the biogenesis of chromoplasts, the plastids that are abundant in ripe fruit and specialized for the accumulation of carotenoid pigments. Chromoplasts develop from pre-existing chloroplasts in the fruit, but the mechanisms underlying this transition are poorly understood. Here, we reveal a role for the chloroplast-associated protein degradation (CHLORAD) proteolytic pathway in chromoplast differentiation. Knockdown of the plastid ubiquitin E3 ligase SP1, or its homologue SPL2, delays tomato fruit ripening, whereas overexpression of SP1 accelerates ripening, as judged by colour changes. We demonstrate that SP1 triggers broader effects on fruit ripening, including fruit softening, and gene expression and metabolism changes, by promoting the chloroplast-to-chromoplast transition. Moreover, we show that tomato SP1 and SPL2 regulate leaf senescence, revealing conserved functions of CHLORAD in plants. We conclude that SP1 homologues control plastid transitions during fruit ripening and leaf senescence by enabling reconfiguration of the plastid protein import machinery to effect proteome reorganization. The work highlights the critical role of chromoplasts in fruit ripening, and provides a theoretical basis for engineering crop improvements.

Url: https://www.nature.com/articles/s41477-021-00916-y.epdf?sharing_token=Hn878Jhv8yGyHfZsbEaOro8Ngr8NoJAJwlel9jB30tvOMPWExwxyxxyxkg2C3JHcRIQJPH3hUdV7TWyHaoVbF87CTwMV1g8304aUeneQqsCnKQVZ5s2mL-0q4k54seHilhywMjimJ5C3Sbfw8W818-rh420NMMnvsCSxSHw1%3D

5

Traditional breeding or genetically modified organisms (GMOs) have for a long time been the sole approaches to effectively cope with biotic and abiotic stresses and implement the quality traits of crops. However, emerging diseases as well as unpredictable climate changes affecting agriculture over the entire globe force scientists to find alternative solutions required to quickly overcome seasonal crises. In this review, we first focus on cisgenesis and genome editing as challenging biotechnological approaches for breeding crops more tolerant to biotic and abiotic stresses. In addition, we take into consideration a toolbox of new techniques based on RNA interference and epigenome modifications, which can be adopted for improving plant resilience. Recent advances in these biotechnological applications are mainly reported for non-model plants and woody crops in particular. Indeed, the characterization of RNAi machinery in plants is fundamental to transform available information into biologically or biotechnologically applicable knowledge. Finally, here we discuss how these innovative and environmentally friendly techniques combined with traditional breeding can sustain a modern agriculture and be of potential contribution to climate change mitigation.


Zabel F., Müller C., Elliott J., Minoli S. et al. (2021): **Large potential for crop production adaptation depends on available future varieties.** Glob Change Biol | [https://doi.org/10.1111/gcb.15649](https://doi.org/10.1111/gcb.15649)

Climate change affects global agricultural production and threatens food security. Faster phenological development of crops due to climate warming is one of the main drivers for potential future yield reductions. To counter the effect of faster maturity, adapted varieties would require more heat units to regain the previous growing period length. In this study, we investigate the effects of variety adaptation on global caloric production under four different future climate change scenarios for maize, rice, soybean, and wheat. Thereby, we empirically identify areas that could require new varieties and areas where variety adaptation could be achieved by shifting existing varieties into new regions. The study uses an ensemble of seven global gridded crop models and five CMIP6 climate models. We found that 39% (SSP5-8.5) of global cropland could require new crop varieties to avoid yield loss from climate change by the end of the century. At low levels of warming (SSP1-2.6), 85% of currently cultivated land can draw from existing varieties to shift within an agro-ecological zone for adaptation. The assumptions on available varieties for adaptation have major impacts on the effectiveness of variety adaptation, which could more than half in SSP5-8.5. The results highlight that region-specific breeding efforts are required to allow for a successful adaptation to climate change.


Regulation of seed size is a key strategy for improving crop yield, and is also a basic biological question, but how plants determine their seed size remains elusive. Here we report that the GW2-WG1-OsbZIP47 regulatory module controls grain width and weight in rice. WG1, which encodes a glutaredoxin protein, promotes grain growth by increasing cell proliferation. WG1 interacts with the transcription factor OsbZIP47 and represses its transcriptional activity by associating with the transcriptional co-repressor ASP1. Indicating that WG1 may act as adaptor protein to recruit the transcriptional co-repressor. OsbZIP47 restricts grain growth by decreasing cell proliferation. Further results reveal that the E3 ubiquitin ligase GW2 ubiquitinates WG1 and targets it for degradation. Genetic analyses support that GW2, WG1 and OsbZIP47 function in a common pathway to control grain growth. Thus, our findings reveal a genetic and molecular framework for the GW2-WG1-OsbZIP47 regulatory module-mediated control of grain size and weight, opening new perspectives for using this regulatory pathway for improvement of seed size and weight in crops.


The lysine specific demethylase 1 (LSD1) plays a pivotal role in cellular differentiation by regulating the expression of key developmental genes in concert with different coregulatory proteins. This process is impaired in different cancer types and incompletely understood. To comprehensively identify functional coregulators of LSD1, we established a novel tractable fluorescent reporter system to monitor LSD1 activity in living cells. Combining this reporter system with a state-of-the-art multiplexed RNAi screen, we identify the DEAD-box helicase 19A (DDX19A) as a novel coregulator and demonstrate that suppression of Ddx19a results in an increase of R-loops and reduced LSD1-mediated gene silencing. We further show that DDX19A binds to trimethylated lysine 27 of histone 3 (H3K27me3) and it regulates gene expression through the removal of
transcription promoting R-loops. Our results uncover a novel transcriptional regulatory cascade where the downregulation of genes is dependent on the LSD1 mediated demethylation of histone H3 lysine 4 (H3K4). This allows the polycomb repressive complex 2 (PRC2) to methylate H3K27, which serves as a binding site for DDX19A. Finally, the binding of DDX19A leads to the efficient removal of R-loops at active promoters, which further de-represses LSD1 and PRC2, establishing a positive feedback loop leading to a robust repression of the target gene.

https://academic.oup.com/nar/article/49/8/4350/6212757

Wen N., Chen J., Chen G., Du L. et al. (2021): The overexpression of insect endogenous microRNA in transgenic rice inhibits the pupation of Chilo suppressalis and Cnaphalocrois medinalis

Pest Manag Sci 2021 Jothibasu K., Dhar D.W.; Rakesh S. (2021): Recent developments in microalgal genome editing for enhancing lipid accumulation and biofuel recovery. Biomass and Bioenergy 150, 106093

https://doi.org/10.1016/j.biombioe.2021.106093

Microalgae based biofuel has been extensively researched with huge investment over more than a past decade. However, integration of lipid accumulation and recovery needs to be optimized for economical production of biofuel. Microalgae are promising feedstocks for carbon-neutral biofuels and their commercialization depends on strain improvement by targeted inhibition of desired gene to increase lipid content. The current review describes the triacylglycerol, phospholipid, fatty acid, starch biosynthetic pathway and target gene for metabolic engineering. Further, it focuses on genome editing techniques viz., Clustered Regularly Interspaced Short Palindromic Repeats, RNA Interference, Transcription Activator-Like Effector Nucleases, Mutation and chemical inhibitor to enhance triacylglycerol content together with cultivation and biomass harvesting for fuel precursor extraction. It also highlights the latest development, challenges for integrating single cell oil accumulation and extraction methods like, biomass pretreatment, solvent based cell lysis and solvent free green lipid conversion. Future efforts on microalgal extracellular matrix organelle membrane biology, continuous production of oil and non-destructive oil recovery from growth media need to be addressed for large scale commercial production of biofuel.


WHO: Guidance framework for testing of genetically modified mosquitoes, second edition

https://www.who.int/publications/i/item/9789240025233

EFSA: Novel food applications: regulations and guidance


As always, I thank you all for hints and for publications. Most of the pdf files can be downloaded directly from the links.