Press releases – Presseberichte

The Commission authorises eight genetically modified crops for use as food and feed

Today, the Commission has authorised five genetically modified crops (3 maize and 2 soybeans) and renewed the authorisation for three maize crops used for food and feed. All of these GMOs have gone through a comprehensive and stringent authorisation procedure, including a favourable scientific assessment by the European Food Safety Authority (EFSA). The authorisation decisions do not cover cultivation. Member States did not reach a qualified majority either in favour or against at the Standing Committee and at the subsequent Appeal Committee. The European Commission has therefore the legal duty to proceed with the authorisations. The authorisations are valid for 10 years, and any product produced from these GMOs will be subject to the EU’s strict labelling and traceability rules.


Authorisation:

Maize:
- MON87427 x MON89034 x MIR162 x NK603
- MON87427 x MON87460 x MON89034 x MIR162xNK603
- MON87427 × MON 89034 × MIR162 × MON 87411

Soybeans:
- SYNHT0H2
- MON 87751 × MON 87701 × MON 87708 × MON 89788

Renewal: Maize
- MIR 604
- MON 88017
- MON 89034

The press release says almost everything. Despite great resistance from the EU Parliament, the Commission has fulfilled its legal obligation in a timely manner.

More, but in German:


Phase 4: Risikomanagement

Reuters Staff: France backs non-GMO regulation for crop gene-editing in EU

Trompiz G.: CRISPR crops ‘aren’t GMOs,’ France says, challenging EU’s strict gene-editing regulations

These press releases surprised many and they rubbed their eyes in disbelief. This press release was not taken up further and there were no further enquiries. One could think it was fake news. No, it was the (private) opinion of the French Minister of Agriculture, an agronomist. His statement is not a government position. Similar to Germany, there are still conflicts between the Ministry of Agriculture and the Ministry of Environment and there were no statements from this ministry. Nevertheless, this statement is encouraging and perhaps a rethink will begin in France and activate other member states.

GM Watch: France has not backed deregulation of gene-edited crops
USDA: USDA approves GM petunias engineered to produce orange flowers  
https://geneticliteracyproject.org/2021/01/20/usda-approves-gm-petunias-engineered-to-produce-orange-flowers/  
https://content.govdelivery.com/accounts/USDAAPHIS/bulletins/2ba11c9

The orange petunias are back.  
see also publication part: USDA:

This would hardly be possible in the EU; it would require several years of research into the potential environmental risks. Especially in view of the fact that these petunias have already been released in the EU, unauthorised but without causing any damage.  
More in German:  

see also:  
https://geneticliteracyproject.org/2017/10/19/gmo-petunias-ridiculousness-exposed-explained/  
https://www.wsj.com/articles/attack-of-the-killer-petunias-1497307595

TestBiotech: Risk assessment of GE plants in the EU: Taking a look at the ‘dark side of the moon’  
New report provides evidence that EFSA systematically ignores specific risks  

Preston C.J. and Antonsen T.: Ethicists: We need more flexible tools for evaluating gene-edited food  

BÖLW: BÖLW-Grundsatzpapier zur Bundestagswahl 2021  
https://www.boelw.de/themen/gentechnik/lebensmittel/artikel/boelw-grundsatzpapier-zur-bundestagswahl-2021/

aiz: Frankreich: Neue Regeln für 'ohne Gentechnik'  

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are ► here: (January – week 02)

Publications – Publikationen


Growing global demands for food, bioenergy, and specialty products, along with the threat posed by various environmental changes, present substantial challenges for agricultural production. Agricultural biotechnology offers a promising avenue for meeting these challenges; however, ethical and sociocultural concerns must first be addressed, to ensure widespread public trust and uptake. To be effective, we need to develop solutions that are ethically responsible, socially responsive, relevant to people of different cultural and social backgrounds, and conveyed to the public in a convincing and straightforward manner. Here, we highlight how ethical approaches, principled decision-making strategies, citizen stakeholder participation, effective science communication, and bioethics education should be used to guide responsible use of agricultural biotechnology.  
https://www.cell.com/trends/plant-science/fulltext/S1360-1385(20)30392-7  
pdf-file available


Climate change impacts imply that the stabilization and improvement of agricultural production systems using technological innovations has become vital. Improvements in plant breeding are integral to such innovations. In the context of German crop breeding programs, the economic impact of exchanging genetic material has yet to be determined. To this end, we analyze in this impact assessment the economic effects on German winter
wheat production that are attributable to exchanging parental material amongst breeders in the breeding process. This exchange is supported by the breeders’ exemption, which is an integral part of the German plant variety protection legislation. It ensures that breeders can freely use licensed varieties created by other breeders for their own breeding activities and aims to speed up the development of improved varieties. For our analysis, we created a unique data set that combines variety-specific grain yield, adoption, and pedigree information of 133 winter wheat varieties. We determined the parental pedigree of each variety to see if a variety was created by interbreeding varieties that are internal or external to its specific breeder. Our study is the first that analyzes the economic impact of exchanging genetic material in German breeding programs. We found that more than 90% of the tested varieties were bred with exchanged parental material, whereby the majority had two external parents. Also, these varieties were planted on an 8.5 times larger area than the varieties that were bred with two internal parents. Due to lower adoption, these only contributed 11% to the overall winter wheat production in Germany, even though they yielded more. We used an economic surplus model to measure the benefits of exchanging parental breeding material on German winter wheat production. This resulted in an overall estimated economic surplus of 19.2 to 22.0 billion EUR from production year 1972 to 2018. This implies tremendous returns to using the breeder’s exemption, which, from an economic perspective, is almost cost-free for the breeder. We conclude that the exchange of breeding material contributes to improving Germany’s agricultural production and fosters the development of climate-resilient production systems and global food security.


A grand challenge facing plant scientists today is to find innovative solutions to increase global crop production in the context of an increasingly warming climate. A major roadblock to global food sufficiency is persistent loss of crops to plant diseases and insect infestations. The United Nations has declared 2020 as the International Year of Plant Health. For historical reasons, molecular studies of plant-biotic interactions in the past several decades have not paid enough attention to how variable climate conditions affect plant-biotic interactions. Here, we highlight a few recent studies that begin to reveal how major climatic drivers impact the plant immune system, particularly secondary messenger and defense hormone signaling, and discuss possible approaches toward engineering climate-resilient plant immunity as part of an ongoing global effort to design ‘dream’ crops of the future.


Genetic engineering (GM) has great potential to improve maize productivity, but rises some concerns on unintended effects, and equivalent as their comparators. There are some limitations through targeted analysis to detect the UE in genetically modified organisms in many previous studies. We here reported a case-study on the effects of introducing herbicides and insect resistance (HIR) gene cassette on molecular profiling (transcripts and metabolites) in a popular maize variety Zhengdan958 (ZD958) in China. We found that introducing HIR gene cassette bring a limited numbers of differential abundant genes (DAGs) or differential abundant metabolites (DAMs) between transgenic events and non-transgenic control. In contrast, averaged 10 times more DAGs and DAMs were observed when performed comparison under different growing environments in three different ecological regions of China than the numbers induced by gene effects. Major biological pathways relating to stress response or signaling transduction could explain somehow the effects of growing environments. We further compared two transgenic events plants mediated ZD958 (GM-ZD958) with either transgenic parent GM-Z58, and other genetic background nonGM-Z58, nonGM-ZD958, and Chang7-2. We found that the numbers of DAGs and DAMs between GM-ZD958 and its one parent maize variety, Z58 or GM-Z58 is equivalent, but not Chang7-2. These findings suggest that greater effects due to different genetic background on altered molecular profiling than gene modification itself. This study provides a case evidence indicating marginal effects of gene pleiotropic effects, and environmental effects should be emphasized.


USDA: Preliminary Determination1 of Nonregulated Status for Westhoff Petunias containing the A1 gene of Maize (A1-DFR Petunias)
are declining in Europe due to the effects of several environmental stressors, both natural and of anthropic origin. The ecological service they provide to crops, and the direct economic revenues from apiculture. Bee populations

Science | Ecological and environmental services in pollinators and their ecosystems: current approach and further development in the EU

Arpaia S., Smagghe G., Sweet J.B. (2021)


The rapid development of the CRISPR–Cas9, –Cas12a and –Cas12b genome editing systems has greatly fuelled basic and translational plant research. The key for these systems is a protospacer adjacent motif (PAM) restriction barrier for DNA targeting by these Cas nucleases is restricted by their preferred protospacer adjacent motifs (PAMs). The PAM requirement for the most popular Streptococcus pyogenes Cas9 (SpCas9) is NNG (N = A, T, C, G), limiting its targeting scope to GC-rich regions. Here, we demonstrate genome editing at relaxed PAM sites in rice (a monocot) and the Dahurian larch (a coniferous tree), using an engineered SpRY Cas9 variant. Highly efficient targeted mutagenesis can be readily achieved by SpRY at relaxed PAM sites in the Dahurian larch protoplasts and in rice transgenic lines through non-homologous end joining (NHEJ). Furthermore, an SpRY-based cytosine base editor was developed and demonstrated by directed evolution of new herbicide resistant OsALS alleles in rice. Similarly, a highly active SpRY adenine base editor was developed based on ABE8e (ref. 3) and SpRY-ABE8e was able to target relaxed PAM sites in rice plants, achieving up to 79% editing efficiency with high product purity. Thus, the SpRY toolbox breaks a PAM restriction barrier in plant genome engineering by enabling DNA editing in a PAM-less fashion. Evidence was also provided for secondary off-target effects by de novo generated single guide RNAs (sgRNAs) due to SpRY-mediated transfer DNA self-editing, which calls for more sophisticated programmes for designing highly specific sgRNAs when implementing the SpRY genome editing toolbox.

https://www.nature.com/articles/s41477-020-00827-4


Genome editing has transformed the life sciences and has exciting prospects for use in treating genetic diseases. Our laboratory developed base editing to enable precise and efficient genome editing while minimizing undesired by products and toxicity associated with double-stranded DNA breaks. Adenine and cytosine base editors mediate targeted A•T-to-G•C or C•G-to-T•A base pair changes, respectively, which can theoretically address most human disease-associated single-nucleotide polymorphisms. Current base editors can achieve high editing efficiencies—for example, approaching 100% in cultured mammalian cells or 70% in adult mouse neurons in vivo. Since their initial description, a large set of base editor variants have been developed with different on-target and off-target editing characteristics. Here, we describe a protocol for using base editing in cultured mammalian cells. We provide guidelines for choosing target sites, appropriate base editor variants and delivery strategies to best suit a desired application. We further describe standard base-editing experiments in HEK293T cells, along with computational analysis of base-editing outcomes using CRISPResso2. Beginning with target DNA site selection, base-editing experiments in mammalian cells can typically be completed within 1–3 weeks and require only standard molecular biology techniques and readily available plasmid constructs.

https://www.nature.com/articles/s41596-020-00450-9


Plant abiotic stresses negative affects growth and development, causing a massive reduction in global agricultural production. Rapeseed (Brassica napus L.) is a major oilseed crop because of its economic value and oilseed production. However, its productivity has been reduced by many environmental adversities. Therefore, it is a prime need to grow rapeseed cultivars, which can withstand numerous abiotic stresses. To understand the various molecular and cellular mechanisms underpinning the abiotic stress tolerance and improvement in rapeseed, omics approaches have been extensively employed in recent years. This review summarized the recent advancement in genomics, transcriptomics, proteomics, metabolomics, and their implication in abiotic stress regulation in rapeseed. Some persisting bottlenecks have been highlighted, demanding proper attention to fully explore the omics tools. Further, the potential prospects of the CRISPR/Cas9 system for genome editing to assist molecular breeding in developing abiotic stress-tolerant rapeseed genotypes have also been explained. In short, the combination of integrated omics, genome editing, and speed breeding can alter rapeseed production worldwide.


Bee pollinators are an integral and vital pollinating guild delivering a fundamental input to European agriculture, due to the ecological service they provide to crops, and the direct economic revenues from apiculture. Bee populations are declining in Europe due to the effects of several environmental stressors, both natural and of anthropic origin. Efforts are ongoing in the European Union to improve monitoring and managing pollinator populations.
to arrest further declines. Genetically modified (GM) crops are currently cultivated on a limited area in Europe, an environmental risk assessment (ERA) is required prior to their authorization for cultivation. The possible impacts of GM crops on pollinators are deemed relevant for the ERA. Existing eco-toxicological studies indicated that traits currently expressed in insect resistant GM plants are unlikely to represent a risk for pollinators. However new mechanisms of insect resistance are being introduced into GM plants, including novel combinations of Cry toxins and dsRNA, and an ERA is required to consider lethal and sub-lethal effects of these new products on non-target species, including insect pollinators. The evaluation of indirect effects linked to the changes in management practices (e.g. for herbicide-tolerant GM crops) is an important component of European Union regulations and a requirement for ERA. This paper reviews current approaches used to test the sensitivity of pollinators to GM plants and their products to determine whether sufficient data is being provided on novel GM plants for satisfying the EU risk assessment requirements.


Present in many industrial effluents and as common degradation product of organic matter, phenol is a widespread compound which may cause serious environmental problems, due to its toxicity to animals and humans. Degradation of phenol from the environment by mesophilic bacteria has been studied extensively over the past decades, but only little is known about phenol biodegradation at high temperatures or low pH. In this work we studied phenol degradation in the thermoacidophilic archaeon *Saccharolobus solfataricus* P2 (basonym: *Sulfolobus solfataricus*) under extreme conditions (80°C, pH 3.5). We combined metabolomics and transcriptomics together with metabolic modeling to elucidate the organism’s response to growth with phenol as sole carbon source. Although *S. solfataricus* is able to utilize phenol for biomass production, the carbon source induces profound stress reactions, including genome rearrangement as well as a strong intracellular accumulation of polyamines. Furthermore, computational modeling revealed a 40% higher oxygen demand for substrate oxidation, compared to growth on glucose. However, only 16.5% of oxygen is used for oxidation of phenol to catechol, resulting in a less efficient integration of carbon into the biomass. Finally, our data underlines the importance of the phenol *meta*-degradation pathway in *S. solfataricus* and enables us to predict enzyme candidates involved in the degradation processes downstream of 2-hydroxymuconic acid. https://www.frontiersin.org/articles/10.3389/fmicb.2020.587032/full


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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