
Press releases – Presseberichte

Black S.: Not all genome editing tools are equal: CRISPR vs. TALEN [https://www.scienceboard.net/index.aspx?sec=sup&sub=pro&page=dis&ItemID=2045](https://www.scienceboard.net/index.aspx?sec=sup&sub=pro&page=dis&ItemID=2045)


Smyth S.: European regulation has driven innovation away for 20 years [https://www.saifood.ca/eu-regulation-kills-innovation/](https://www.saifood.ca/eu-regulation-kills-innovation/)


Grain Club: Neue Züchtungstechniken unverzichtbar für globale Versorgungssicherheit und eine nachhaltigere Landwirtschaft [https://www.presseportal.de/pm/105718/4820964](https://www.presseportal.de/pm/105718/4820964)

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [here](https://www.eureporter.co/economy/agriculture/2021/01/27/commission-presents-study-on-impact-of-trade-agreements-on-agri-food-sectors/): (January – week 04)

Publications – Publikationen

Jain, S., Shukla, S., Yang, C. et al. (2021): TALEN outperforms Cas9 in editing heterochromatin target sites. Nat Commun 12, 606 | [https://doi.org/10.1038/s41467-020-20672-5](https://doi.org/10.1038/s41467-020-20672-5)

Genome editing critically relies on selective recognition of target sites. However, despite recent progress, the underlying search mechanism of genome-editing proteins is not fully understood in the context of cellular chromatin environments. Here, we use single-molecule imaging in live cells to directly study the behavior of CRISPR/Cas9 and TALEN. Our single-molecule imaging of genome-editing proteins reveals that Cas9 is less efficient in heterochromatin than TALEN because Cas9 becomes encumbered by local searches on non-specific sites in these regions. We find up to a fivefold increase in editing efficiency for TALEN compared to Cas9 in heterochromatin regions. Overall, our results show that Cas9 and TALEN use a combination of 3-D and local searches to identify target sites, and the nanoscopic granularity of local search determines the editing outcomes of the genome-editing proteins. Taken together, our results suggest that TALEN is a more efficient gene-editing tool than Cas9 for applications in heterochromatin.

[https://www.nature.com/articles/s41467-020-20672-5](https://www.nature.com/articles/s41467-020-20672-5)

Ren, Q., Sretenovic, S., Liu, S. et al. (2021): PAM-less plant genome editing using a CRISPR–SpRY toolbox. Nat. Plants 7, 25–33 | [https://doi.org/10.1038/s41477-020-00827-4](https://doi.org/10.1038/s41477-020-00827-4)

The rapid development of the CRISPR–Cas9, –Cas12a and –Cas12b genome editing systems has greatly fuelled basic and translational plant research. DNA targeting by these Cas nuclease is restricted by their preferred protospacer adjacent motifs (PAMs). The PAM requirement for the most popular Streptococcus pyogenes Cas9 (SpCas9) is NGG (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 pdf-file available


Public engagement in science with diverse cross-sections of the community is considered a critical aspect of responsible biotechnological innovation. While the research community shows willingness to engage with both ambivalent and supportive audiences about potentially disruptive technological advances, there is less enthusiasm for engaging with groups who hold deeply opposing views to such advances. ‘Playing God’ and ‘tampering with nature’ are popular examples of intrinsic objections often made in opposition to the development or use of novel genetic technologies. Historically appearing in arguments against the pursuit of genetically modified organisms in agriculture and food industries, intrinsic objections have previously been labelled by the science community as inconsistent, non-scientific, and vague. Now found in a range of innovation contexts, the domain of synthetic biology appears to attract such objections consistently. We present the findings from a large Australian study (N = 4593) which suggests ‘playing God’ objections and their variants can be multi layered and, at times, accompanied by meaningful information about risk perceptions. We use qualitative analysis of open ended responses from an online survey to show how these objections are articulated in response to selected synthetic biology applications across environmental and health domains.

Our research invites a rethink of how the synthetic biology community perceives, and engages with, people who express intrinsic objections. These people may additionally hold extrinsic concerns that may be potentially addressed, or at least reasonably considered, through dialogue. We offer some concluding remarks for engaging with publics who employ these types of arguments to communicate unease with aspects of technology development and use.


The looming effects of climate change and the intensification of European climate activism show that it is both scientifically necessary and politically possible to reinterpret the Precautionary Principle and change EU regulation of plant gene editing.

EU regulation of gene editing does not consider its value for tackling climate change.

Climate change presents scientific reason to reinterpret the Precautionary Principle.

Political shifts and activism show a pathway to change EU gene editing decision.


Genetically modified organisms (GMOs) or genetically modified technology is currently considered an “excluded method” not allowed to be used in, or added to, organic agricultural products under the US Code of Federal Regulations. Despite evidence that GMOs may serve as a safe alternative to conventional crops, they are frequently associated with harmful and unsustainable agricultural practices. We discuss the economic, environmental, nutritional, and food safety concerns of GMOs in organic agriculture, and how GMO technology could benefit it. We propose (1) allowing the use of genetic modification in organic agriculture and (2) an enhanced effort to disseminate science-based information to consumers.


Genetically engineered (GE) livestock were first reported in 1985, and yet only a single GE food animal, the fast-growing AquAdvantage salmon, has been commercialized. There are myriad interconnected reasons for the slow progress in this once-promising field, including technical issues, the structure of livestock industries, lack of public research funding and investment, regulatory obstacles, and concern about public opinion. This review focuses on GE livestock that have been produced and documents the difficulties that researchers and developers have encountered enroute. Additionally, the costs associated with delayed commercialization of GE livestock were modeled using three case studies: GEmastitis-resistant dairy cattle, genome edited porcine reproductive and respiratory syndrome virus–resistant pigs, and the AquAdvantage salmon. Delays of 5 or 10
years in the commercialization of GE livestock beyond the normative 10-year GE product evaluation period were associated with billions of dollars in opportunity costs and reduced global food security. https://www.annualreviews.org/doi/10.1146/annurev-animal-061220-023052


Delivery of the CRISPR/Cas9 components to the plant cells is a key step in its application as a genome editing tool. Here, we compared Agrobacterium-mediated transformation and protoplast transfection with CRISPR/Cas9 components for potato genome editing. Two sgRNAs were designed to simultaneously direct Cas9 to the StPPO2 gene encoding for a tuber polyphenol oxidase (PPO). A binary vector (CR-PPO) was utilized for either Agrobacterium-mediated transformation or for transient expression in protoplasts, while ribonucleoprotein complexes (RNP-PPO) were additionally assayed in protoplasts. Editing efficiency varied, yielding 9.6%, 18.4% and 31.9% of edited lines from Agrobacterium-mediated transformation, RNP-PPO and CR-PPO transient expression in protoplasts, respectively. Furthermore, only the CR-PPO transient expression resulted in lines edited in all four StPPO2 alleles, observed in 46% of the edited lines and confirmed by tuber PPO activity and enzymatic browning analysis. Lines with on-target DNA insertions were found from all three approaches and characterized by sequencing. The dual-sgRNA strategy resulted in a low incidence of the targeted deletion, likely due to contrasting efficiencies between sgRNAs, that was partially evident in the in silico analysis. Our results demonstrate that gene editing efficiency in potato depends on the CRISPR/Cas9 delivery strategy and p https://link.springer.com/article/10.1007/s11240-020-02008-9

Jin, R., Klasfeld, S., Zhu, Y. et al.(2021): LEAFY is a pioneer transcription factor and licenses cell reprogramming to floral fate. Nat Commun 12, 626 | https://doi.org/10.1038/s41467-020-20883-w

Master transcription factors reprogram cell fate in multicellular eukaryotes. Pioneer transcription factors have prominent roles in this process because of their ability to contact their cognate binding motifs in closed chromatin. Reprogramming is pervasive in plants, whose development is plastic and tuned by the environment, yet little is known about pioneer transcription factors in this kingdom. Here, we show that the master transcription factor LEAFY (LFY), which promotes floral fate through upregulation of the floral commitment factor APETALA1 (AP1), is a pioneer transcription factor. In vitro, LFY binds to the endogenous AP1 target locus DNA assembled into a nucleosome. In vivo, LFY associates with nucleosome occupied binding sites at the majority of its target loci, including AP1. Upon binding, LFY ‘unlocks’ chromatin locally by displacing the H1 linker histone and by recruiting SWI/SNF chromatin remodelers, but broad changes in chromatin accessibility occur later. Our study provides a mechanistic framework for patterning of inflorescence architecture and uncovers striking similarities between LFY and animal pioneer transcription factor. https://www.nature.com/articles/s41467-020-20883-w

Tran, NH.T., Oguchi, T., Matsunaga, E. et al. (2021): Evaluation of potential impacts on biodiversity of the salt-tolerant transgenic Eucalyptus camaldulensis harboring an RNA chaperonic RNA-Binding-Protein gene derived from common ice plant. Transgenic Res | https://doi.org/10.1007/s11248-020-02027-6

We recently reported that a genetic transformation of the RNA-Binding-Protein (McRBP), an RNA chaperone gene derived from common ice plant (Mesembryanthemum crystallinum), alleviated injury and loss of biomass production by salt stress in Eucalyptus camaldulensis in a semi-confined screen house trial. In this study, we assessed the potential environmental impact of the transgenic Eucalyptus in a manner complying with Japanese bio-safety regulatory framework required for getting permission for experimental confined field trials. Two kinds of bioassays for the effects of allelopathic activity on the growth of other plants, i.e., the sandwich assay and the succeeding crop assay, were performed for three transgenic lines and three non-transgenic lines. No significant differences were observed between transgenic and non-transgenic plants. No significant difference in the numbers of cultivable microorganisms analyzed by the spread plate method were observed among the six transgenic and non-transgenic lines. These results suggested that there is no significant difference in the potential impact on biodiversity between the transgenic McRBP-E. camaldulensis lines and their non-transgenic comparators. https://link.springer.com/article/10.1007/s11248-020-02027-6


New genetic tools can potentially mitigate the decline of biodiversity. Democratisation of science mandates public opinion be considered while new technologies are in development. We conducted eleven focus groups in New Zealand to explore three questions about novel technologies (gene drive and two others for comparison of pest control tools): (1) what are the risks/benefits? (2) how do they compare to current methods? and (3) who should be represented on a panel that evaluates the tools and what factors should they consider? Findings from the content analysis of the risks/benefits revealed three main considerations that were of social concern –
Environmental, Practical, and Ethical. Most participants were self-aware of their insufficient knowledge to compare the different technologies. Unanimously, respondents wanted the available information provided throughout the tool development process and saw multi-sector panel oversight as essential. Scientists and policy makers should match the public's willingness to engage collaboratively https://www.tandfonline.com/doi/full/10.1080/03036758.2020.1850481.

Vázquez-Barrios, V., Boege, K., Sosa-Fuentes, T.G. et al. (2021): Ongoing ecological and evolutionary consequences by the presence of transgenes in a wild cotton population. Sci Rep 11, 1959 | https://doi.org/10.1038/s41598-021-81567-z

After 25 years of genetically modified cotton cultivation in Mexico, gene flow between transgenic individuals and their wild relatives represents an opportunity for analysing the impacts of the presence of novel genes in ecological and evolutionary processes in natural conditions. We show comprehensive empirical evidence on the physiological, metabolic, and ecological effects of transgene introgression in wild cotton, Gossypium hirsutum. We report that the expression of both the cry and cp4-epsps genes in wild cotton under natural conditions altered extrafloreal nectar inducibility and thus, its association with different ant species: the dominance of the defensive species Camponotus planatus in Bt plants, the presence of cp4-epsps without defence role of Monomorium ebeninum ants, and of the invasive species Paratrechina longicornis in wild plants without transgenes. Moreover, we found an increase in herbivore damage to cp4-epsps plants. Our results reveal the influence of transgene expression on native ecological interactions. These findings can be useful in the design of risk assessment methodologies for genetically modified organisms and the in situ conservation of G. hirsutum metapopulations.
https://www.nature.com/articles/s41598-021-81567-z


Non-target effects of genetically engineered (GE) plants on aquatic Daphnia magna have been studied by feeding the species with different maize materials containing insecticidal Cry proteins from Bacillus thuringiensis (Bt). The results of those studies were often difficult to interpret, because only one GE plant was compared to one related non-GE control. In such a setting, effects of the Cry proteins cannot be distinguished from plant background effects, in particular when the test species is nutritionally stressed. In the present study, we tested the suitability of three different maize materials, i.e., flour, leaves and pollen, from five diverse non-GE maize lines (including EXP 258, a breeding line that is closely related to a SmartStax Bt maize) as exclusive food sources for D. magna. The parameters recorded included survival, sublethal endpoints such as body size, number of molts to first offspring, time to first offspring, number of individuals in first clutch, total number of clutches, total number of offspring, average number of offspring per clutch, and population measures such as net reproductive rate R0, generation time T and intrinsic rate of increase rm. The results showed that D. magna can survive, grow and reproduce when fed only maize materials, although the performance was poorer than when fed algae, which indicates nutritional stress. Large differences in life table and population parameters of D. magna were observed among the different maize lines. Our results suggest that confounding effects caused by nutritional stress and plant background might explain some of the conflicting results previously published on the effects of Bt crops on D. magna. Using 95% confidence intervals for the means of the five maize lines for all measured parameters of D. magna performance in our study, we captured the natural range of variation. This information is useful for the interpretation of observed differences in D. magna performance between a GE plant and its non-GE comparator as it helps judging whether observed effects are of biological relevance. If differences between a GE and comparator line are observed and their biological relevance needs to be assessed in future risk assessments of GE maize, 1) the data on natural variation of the different parameters generated by previous studies can be informative (e.g. data from our study for maize fed D. magna); 2) for additional experiments the inclusion of multiple unrelated non-GE comparators should be considered; In addition, it should be taken into account that nutritional stress can affect the outcome of the study.


Reinforcing the high-dose/refuge strategy with releases of transgenic insects has been suggested as a method for simultaneously managing agricultural pest populations and resistance to transgenic crops. Theoretical and empirical studies have shown that these approaches can work when deployed against closed populations and the assumptions of the HDR strategy are met. However, field-evolved resistance is often linked to non-recessive resistance or refuge non-compliance, and pest management regimes are likely to take place at the landscape-level. It is therefore important to understand how effective such strategies are when resistance is non-recessive, and how they could be employed in agricultural landscapes. We developed a spatially-explicit model to investigate the efficacy of strategies combining refuges with transgenic insect releases to manage a pest with non-recessive resistance in agricultural landscapes. We compared two release strategies, area-wide releases and localised releases targeted at population hotspots, and analysed the effects of refuge and release
parameters on population and resistance dynamics. Area-wide releases reliably achieved landscape-level pest eradication. Localised releases also eradicated the pest when low release thresholds were combined with high release ratios, and maintained the pest at low densities when insufficient to achieve extinction. Reinforcing refuges with localised releases also greatly enhanced the probability of resistance extinction. However, when resistance remained in the population, localised releases prevented resistance from reaching fixation rather than greatly delaying or reversing resistance evolution. Our work indicates that combining refuges with simple release policies is effective for landscape-level pest suppression when the HDR assumptions are violated, but more nuanced release strategies may be required to enhance the benefits to resistance management.  


Histone modifications play pivotal roles within the intricate protein networks that underlie transcription and gene silencing in eukaryotic genomes. The enzymes that deposit them undergo spatiotemporal fine-tuning of their catalytic activity; one example is trans-histone cross-talk, in which one histone modification activates an enzyme responsible for another histone modification. Valencia-Sánchez et al. show that histone H4 lysine 16 acetylation (H4K16ac), a hallmark of decondensed, transcriptionally permissive chromatin, directly stimulates the Dot1 histone H3 lysine 79 methyltransferase. Structural, biochemical, and cellular data explain Dot1’s regulation by H4K16ac and show how it coordinates with a second positive regulator of Dot1, histone H2B ubiquitination.  
https://science.sciencemag.org/content/371/6527/eabc6663

Mesnage R., Teixeira M.; Mandrioli D.; Falcioni L. et al. (2021): Use of Shotgun Metagenomics and Metabolomics to Evaluate the Impact of Glyphosate or Roundup MON 52276 on the Gut Microbiota and Serum Metabolome of Sprague-Dawley Rats Environmental Health Perspective  
https://doi.org/10.1289/EHP6990


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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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