

# Sunday Evening News No. 96

Week 39 (2018-09-24 / 09-30)

Selected and edited by **BGF** Jany

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Dear colleagues, friends  
Dear all,

This week the publication "Glyphosate perturbs the gut microbiota of honey bees" filled the pages of the media. It was interpreted as further evidence of the dangers of glyphosate and is intended to serve as a global ban on glyphosate. Possible effects of the CJEU-ruling on mutagenesis procedures played only a minor role.

## Press releases and media reports

### CJEU-ruling

Laborjournalal:

#### „Es sollte keine pauschale juristische Festlegung geben“

Auch der Bioökonomierat hat sich inzwischen zum EuGH-Urteil über *Genome Editing* geäußert. Wir sprachen mit den Ratsmitgliedern Christine Lang und Hannelore Daniel.

<https://www.laborjournal.de/editorials/1600.lasso>

Eric MEUNIER

#### New GMOs: the European Commission in no hurry to act

<https://www.infogm.org/6634-new-gmos-european-commission-in-no-hurry-to-act>

SLU-News: (translation of the Swedish text)

#### EU decision threatens necessary plant research

"We, as vice-chancellors of Swedish universities and higher education institutions, are very critical of a decision by the Court of Justice of the European Union.

<https://www.slu.se/en/ew-news/2018/9/eu-decision-gene-editing/>

Pieter Devuyst

#### ECJ ruling on new breeding techniques "creates more confusion", says MEP

<https://iegpolicy.agribusinessintelligence.informa.com/PL217772/ECJ-ruling-on-new-breeding-techniques-creates-more-confusion-says-MEP>

ESA Statement

#### ESA Statement on ECJ Ruling C-528/16

<https://www.euroseeds.eu/esa-statement-ecj-ruling-c-52816>

Ministries of agriculture from Argentina, Brazil, Chile, Paraguay and Uruguay

#### Gene editing declaration Argentina, Brazil, Chile, Paraguay and Uruguay

<http://consejocas.org/wp-content/uploads/2018/09/XXXVI-RO-CAS-Declaraci%C3%B3n-II.-T%C3%A9cnicas-de-Edici%C3%B3n-G%C3%A9nica.pdf>

#### Japan: Environment Ministry Proposes Policy for Regulating Genome Editing

On August 29, 2018, the "Advisory Panel on Genetically Modified Organisms" of Japan's Ministry of Environment held its second meeting to review recommendations made by the expert committee on the handling of genome editing technology under the Cartagena Protocol. The advisory panel concluded that any living organism with foreign nucleotide(s) remained in the host genome should be regulated regardless of whether the foreign nucleotide(s) is detectable. As a result, only "Site-directed nucleases-1" will fall outside the scope of existing regulations on genetically engineered organisms in Japan. This proposal has been made available for public comment until October 19, 2018.

[https://gain.fas.usda.gov/Recent%20GAIN%20Publications/Environment%20Ministry%20Proposes%20Policy%20for%20Regulating%20Genome%20Editing%20Tokyo%20Japan\\_9-25-2018.pdf](https://gain.fas.usda.gov/Recent%20GAIN%20Publications/Environment%20Ministry%20Proposes%20Policy%20for%20Regulating%20Genome%20Editing%20Tokyo%20Japan_9-25-2018.pdf)

see also

<https://mainichi.jp/english/articles/20180821/p2a/00m/0na/033000c>

John J. Cahrssen and Henry I. Miller

#### We Need Smarter Regulation of Food and Agricultural Biotechnology

Regulation has been unscientific and excessive for 30 years. It's past time for reform.

<http://www.henrymillermd.org/21648/we-need-smarter-regulation-of-food>

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## Glyphosate

Siobhán Dunphy

### **A common and highly controversial herbicide may be harming bees**

<https://www.europeanscientist.com/en/agriculture/a-common-and-highly-controversial-herbicide-may-be-harming-bees/>

The Guardian

### **Monsanto's global weedkiller harms honeybees, research finds**

Glyphosate – the most used pesticide ever – damages the good bacteria in honeybee guts, making them more prone to deadly infections

<https://www.theguardian.com/environment/2018/sep/24/monsanto-weedkiller-harms-bees-research-finds>

Wissenschaft.de

### **Unkrautvernichter schädigt Bienen indirekt**

Streitfall Glyphosat – wegen möglicher Gefahren für die menschliche Gesundheit steht das Unkrautvernichtungsmittel seit Jahren im kritischen Blick der Forschung. Wenigstens den Bienen kann der Wirkstoff nichts anhaben, hieß es bislang. Doch dies war offenbar ein Trugschluss, geht nun aus einer Studie hervor: Glyphosat bedroht die Insekten indirekt und zwar über ihre Darmflora. Es schädigt demnach bestimmte günstige Darmbakterien der Bienen und macht sie dadurch anfällig für Krankheitserreger. Möglicherweise spielt dieser Effekt eine Rolle beim sogenannten Bienensterben, sagen die Forscher.

<https://www.wissenschaft.de/umwelt-natur/unkrautvernichter-schaedigt-bienen-indirekt/>

Joachim Müller-Jung

### **Glyphosat und die Immunschwäche der Bienen**

<http://www.faz.net/aktuell/wissen/glyphosat-und-die-immunschwaeche-der-bienen-15805798.html?GEPC=s5>

Agrar heute

### **Kommentar: "Glyphosatstudie - neue Sau durchs Dorf getrieben"**

<https://www.agrarheute.com/pflanze/kommentar-glyphosatstudie-neue-sau-durchs-dorf-getrieben-548274>

### **Glyphosat – Pro und Contra**

Thoralf Kuchler: Die Diskussion um Glyphosat ist nicht sachlich

Johannes G. Zaller: Entscheidungen nach dem Vorsorgeprinzip sind gefordert

Nachrichten aus der Chemie 66, 992-993 2018

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Alfons Deter

### **EU-Parlament legt Berichtsentwurf für die Zulassung von Pflanzenschutzmitteln vor**

<https://www.topagrar.com/news/Acker-Agrarwetter-Ackernews-EU-Parlament-legt-Berichtsentwurf-fuer-die-Zulassung-von-Pflanzenschutzmitteln-vor-9818873.html>

Sarantis Michalopoulos

### **Business confidentiality: The 'hot potato' of new EU transparency rules on food**

EU stakeholders are playing ping-pong with the body that will be responsible for deciding whether or not to break business confidentiality and make industry studies public, in line with the terms of the new transparency rules on food safety. EURACTIV.com reports from Parma.

<https://www.euractiv.com/section/agriculture-food/news/sr-mon-business-confidentiality-the-hot-potato-of-new-eu-transparency-rules-on-food/>

The complete overview about press releases and media reports: <https://www.biotech-gm-food.com/presse>

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## **Publications:**

### **CJEU-Ruling**

Seitz C: (2018): **Modifiziert oder nicht? – Regulatorische Rechtsfragen zur Genoptimierung durch neue biotechnologische Verfahren.** EuZW 2018, 757

Am 25.7.2018 hat der EuGH in einem vielbeachteten Grundsatzurteil entschieden, dass durch Mutagenese gewonnene Organismen genetisch veränderte Organismen („GVO“) darstellen und grundsätzlich den in der GVO-Richtlinie vorgesehenen Verpflichtungen unterliegen. Der EuGH stellte fest, dass durch Mutagenese gewonnene Organismen GVO sind, da sie durch die Verfahren und Methoden der Mutagenese eine auf natürliche Weise nicht mögliche Veränderung am genetischen Material eines Organismus vorgenommen wird. Als Ergebnis fallen diese Organismen grundsätzlich in den Anwendungsbereich der GVO-Richtlinie und unterliegen den dort genannten Verpflichtungen. Die GVO-Richtlinie gilt nicht für Organismen aus bestimmten

Mutagenese-Verfahren, die herkömmlich in einer Reihe von Anwendungen verwendet wurden und seit Langem als sicher gelten. Im Hinblick auf Organismen, die mit Mutagenese-Verfahren gewonnen werden, die erst nach dem Erlass der GVO-Richtlinie entstanden sind, entschied der EuGH, dass die mit dem Einsatz dieser neuen Mutagenese-Verfahren verbundenen Risiken vergleichbar mit den Risiken aus der Erzeugung und Verbreitung von GVO mittels Transgenese-Verfahren sind. Aufgrund der gemeinsamen Gefahren würde der Ausschluss dieser Organismen aus der GVO-Richtlinie deren Ziel beeinträchtigen, schädliche Auswirkungen auf die menschliche Gesundheit und die Umwelt zu verhindern und würde dem Vorsorgeprinzip widersprechen.  
[pdf-file available](#)

Spranger T.M. (2018): **Neue Techniken und Europäisches Gentechnikrecht.** NJW 2018, 2929  
[pdf-file available](#)

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## Glyphosate - Bees

Motta E.V.S., Raymann K., and Moran N.A. (2018): **Glyphosate perturbs the gut microbiota of honey bees.** PNAS; <http://www.pnas.org/content/early/2018/09/18/1803880115>

Glyphosate, the primary herbicide used globally for weed control, targets the 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) enzyme in the shikimate pathway found in plants and some microorganisms. Thus, glyphosate may affect bacterial symbionts of animals living near agricultural sites, including pollinators such as bees. The honey bee gut microbiota is dominated by eight bacterial species that promote weight gain and reduce pathogen susceptibility. The gene encoding EPSPS is present in almost all sequenced genomes of bee gut bacteria, indicating that they are potentially susceptible to glyphosate. We demonstrated that the relative and absolute abundances of dominant gut microbiota species are decreased in bees exposed to glyphosate at concentrations documented in the environment. Glyphosate exposure of young workers increased mortality of bees subsequently exposed to the opportunistic pathogen *Serratia marcescens*. Members of the bee gut microbiota varied in susceptibility to glyphosate, largely corresponding to whether they possessed an EPSPS of class I (sensitive to glyphosate) or class II (insensitive to glyphosate). This basis for differences in sensitivity was confirmed using in vitro experiments in which the EPSPS gene from bee gut bacteria was cloned into *Escherichia coli*. All strains of the core bee gut species, *Snodgrassella alvi*, encode a sensitive class I EPSPS, and reduction in *S. alvi* levels was a consistent experimental result. However, some *S. alvi* strains appear to possess an alternative mechanism of glyphosate resistance. Thus, exposure of bees to glyphosate can perturb their beneficial gut microbiota, potentially affecting bee health and their effectiveness as pollinators.

<http://www.pnas.org/content/pnas/early/2018/09/18/1803880115.full.pdf>

This article contains supporting information online at

[www.pnas.org/lookup/suppl/doi:10.1073/pnas.1803880115/-/DCSupplemental](http://www.pnas.org/lookup/suppl/doi:10.1073/pnas.1803880115/-/DCSupplemental).

Zhu YC, Yao J, Adamczyk J, Luttrell R. (2017): **Feeding toxicity and impact of imidacloprid formulation and mixtures with six representative pesticides at residue concentrations on honey bee physiology (*Apis mellifera*).** PLoS ONE 12(6): e0178421.

<https://doi.org/10.1371/journal.pone.0178421>

Imidacloprid is the most widely used insecticide in agriculture. In this study, we used feeding methods to simulate in-hive exposures of formulated imidacloprid (Advise® 2FL) alone and mixtures with six representative pesticides for different classes. Advise, fed at 4.3 mg/L (equal to maximal residue detection of 912 ppb active ingredient [a.i.] in pollen) induced 36% mortality and 56% feeding suppression after 2-week feeding. Treatments with individual Bracket (acephate), Karate ( $\lambda$ -cyhalothrin), Vydate (oxamyl), Domark (tetraconazole), and Roundup (glyphosate) at residue level had a mortality range of 1.3±13.3%, statistically similar to that of control ( $P>0.05$ ). The additive/synergistic toxicity was not detected from binary mixtures of Advise with different classes of pesticides at residue levels. The feeding of the mixture of all seven pesticides increased mortality to 53%, significantly higher than Advise only but still without synergism. Enzymatic data showed that activities of invertase, glutathione S-transferase, and acetylcholinesterase activities in imidacloprid-treated survivors were mostly similar to those found in control. Esterase activity mostly increased, but was significantly suppressed by Bracket (acephate). The immunity-related phenoloxidase activity in imidacloprid-treated survivors tended to be lower, but most treatments were statistically similar to the control. Increase of cytochrome P450 activity was correlated with Advise concentrations and reached significant difference at 56 mg/L (12 ppm a.i.). Our data demonstrated that residue levels of seven pesticide in pollens/hive may not adversely affect honey bees, but long term exclusive ingestion of the maximal residue levels of imidacloprid (912 ppb) and sulfoxaflor (3 ppm a.i.) may induce substantial bee mortality. Rotating with other insecticides is a necessary and practical way to reduce the residue level of any given pesticide.

<https://journals.plos.org/plosone/article/file?id=10.1371/journal.pone.0178421&type=printable>

Ricroch A., Akkoyunlu S., Martin-Laffon J, Kuntz M. (2018): **Assessing the Environmental Safety of Transgenic Plants: Honey Bees as a Case Study.** Advances in Botanical Research 86, 111-167; <https://doi.org/10.1016/bs.abr.2017.11.004>

Bees play an important role in the pollination of a wide range of plants and are likely to encounter genetically engineered crops (often termed “genetically modified” or “GM”) during their foraging period, especially insect-resistant crops since these crops have been cultivated worldwide. Thus, it is important to assess potential impacts of these crops on the nontarget organism honey bee (*Apis mellifera* L.), the most important pollinator species worldwide. In the present study, we gathered all scientific data related to the effects of insect-resistant

GM crops (mostly corn and cotton, and also oilseed rape, rice, soybean, and wheat) on honey bees. Assessments included feeding honey bees with purified insecticidal toxins or transgenic pollen collected from GM crops producing such toxins, namely protease inhibitors (PIs), Cry or VIP toxins from *Bacillus thuringiensis*. RNAi-producing and herbicide-tolerant crops were also included. A total of 64 peer reviewed studies have been published between 1994 and 2017. We also compiled 18 studies submitted to and examined by the US EPA between 1993 and 2002. Our analyses converge to the conclusion that the studied Cry proteins, RNAi or herbicide tolerance proteins do not negatively affect the survival of honey bees and have no potential sublethal effect in controlled laboratory conditions or in field/semifield trials. The risk of PI will mainly depend on their concentration in pollen and need to be assessed case by case.

<https://www.sciencedirect.com/science/article/pii/S0065229617300769?via%3Dihub>

Thompson H.M., Levine S.L., Doering J., Norman S., Manson P., Sutton P., von Mérey G. (2014): **Evaluating Exposure and Potential Effects on Honeybee Brood (*Apis mellifera*) Development Using Glyphosate as an Example**. *Integrated Environmental Assessment and Management* 10 (3), 463–470

This study aimed to develop an approach to evaluate potential effects of plant protection products on honeybee brood with colonies at realistic worst-case exposure rates. The approach comprised 2 stages. In the first stage, honeybee colonies were exposed to a commercial formulation of glyphosate applied to flowering *Phacelia tanacetifolia* with glyphosate residues quantified in relevant matrices (pollen and nectar) collected by foraging bees on days 1, 2, 3, 4, and 7 postapplication and glyphosate levels in larvae were measured on days 4 and 7. Glyphosate levels in pollen were approximately 10 times higher than in nectar and glyphosate demonstrated rapid decline in both matrices. Residue data along with foraging rates and food requirements of the colony were then used to set dose rates in the effects study. In the second stage, the toxicity of technical glyphosate to developing honeybee larvae and pupae, and residues in larvae, were then determined by feeding treated sucrose directly to honeybee colonies at dose rates that reflect worst-case exposure scenarios. There were no significant effects from glyphosate observed in brood survival, development, and mean pupal weight. Additionally, there were no biologically significant levels of adult mortality observed in any glyphosate treatment group. Significant effects were observed only in the fenoxycarb toxic reference group and included increased brood mortality and a decline in the numbers of bees and brood. Mean glyphosate residues in larvae were comparable at 4 days after spray application in the exposure study and also following dosing at a level calculated from the mean measured levels in pollen and nectar, showing the applicability and robustness of the approach for dose setting with honeybee brood studies. This study has developed a versatile and predictive approach for use in higher tier honeybee toxicity studies. It can be used to realistically quantify exposure of colonies to pesticides to allow the appropriate dose rates to be determined, based on realistic worst-case residues in pollen and nectar and estimated intake by the colony, as shown by the residue analysis. Previous studies have used the standard methodology developed primarily to identify pesticides with insect-growth disrupting properties of pesticide formulations, which are less reliant on identifying realistic exposure scenarios. However, this adaptation of the method can be used to determine dose–response effects of colony level exposure to pesticides with a wide range of properties. This approach would limit the number of replicated tunnel or field-scale studies that need to be undertaken to assess effects on honeybee brood and may be of particular benefit where residues in pollen and nectar are crop- and/or formulation-specific, such as systemic seed treatments and granular applications.

<https://setac.onlinelibrary.wiley.com/doi/epdf/10.1002/ieam.1529>

only for remining:

Mesnager R. and Antoniou M.N. (2017): **Facts and Fallacies in the Debate on Glyphosate Toxicity**. *Front. Public Health*, <https://doi.org/10.3389/fpubh.2017.00316>  
<https://www.frontiersin.org/articles/10.3389/fpubh.2017.00316/full>

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Bretting P.K. (2018): **2017 Frank Meyer Medal for Plant Genetic Resources Lecture: Stewards of Our Agricultural Future**. *Crop Science* (2018). DOI: [10.2135/cropsci2018.05.0334](https://doi.org/10.2135/cropsci2018.05.0334)

Humanity's survival depends on crops—the green line standing between us and calamity. To meet ever expanding human needs, crops must become increasingly more productive, mainly through genetic gains that exploit diverse plant genetic resources (PGR), the raw materials for crop breeding. For millennia, PGR have been conserved by individuals, communities, and organizations. These stewards of our agricultural future have been nearly as diverse as the PGR that they have conserved. Their invaluable roles in underpinning the security of global agriculture have largely been underappreciated. Furthermore, the challenges and complexity of successful PGR stewardship have been inadequately recognized. This paper pays tribute to these stewards' characteristic attributes and their contributions to PGR conservation and sustainable use. It describes the pervasive impacts of PGR on crop agriculture and explains how numerous factors have affected PGR stewardship capacities. Plant genetic resource stewardship involves many different components, which are typically conducted over extended timeframes. Sustained, adequate support for PGR maintenance, a key component, has been the exception rather than the rule. Past and present PGR stewardship successes and challenges furnish numerous lessons for meeting future demands. Such lessons include recognizing the importance to PGR stewardship of: dedicated and diverse PGR stewards, continual and persistent financial

support for PGR genebanks and their staffs, protecting crop wild relatives, and safeguarding genebank collections from extreme weather and introduced pests and pathogens. In the future, PGR stewardship might be conducted more frequently and more adequately by multi-institutional networks enabled by advances in information technology and artificial intelligence.

<https://dl.sciencesocieties.org/publications/cs/pdfs/0/0/cropsci2018.05.0334>

and

American Society of Agronomy

Plant genetic resources ensure ag's future

<https://phys.org/news/2018-09-genetic-resources-ag-future.html#jCp>

Wang G, Dong Y, Liu X, Yao G, Yu X and Yang M (2018) **The Current Status and Development of Insect-Resistant Genetically Engineered Poplar in China**. *Front. Plant Sci.* 9:1408. doi: 10.3389/fpls.2018.01408

Poplar is one of the main afforestation tree species in China, and the use of a single, or only a few, clones with low genetic diversity in poplar plantations has led to increasing problems with insect pests. The use of genetic engineering to cultivate insect-resistant poplar varieties has become a hot topic. Over the past 20 years, there have been remarkable achievements in this area. To date, nearly 22 insect-resistant poplar varieties have been created and approved for small-scale field testing, environmental release, or pilot-scale production. Here, we comprehensively review the development of insect resistant genetically modified (GM) poplars in China. This review mostly addresses issues surrounding the regulation and commercialization of Bt poplar in China, the various insecticidal genes used, the effects of transgenic poplars on insects, toxic protein expression, multigene transformation, the stability of insect resistance, and biosafety. The efficacy of GM poplars for pest control differed among different transgenic poplar clones, larval instars, and insect species. The Bt protein analysis revealed that the expression level of Cry3A was significantly higher than that of Cry1Ac. Temporal and spatial studies of Bt protein showed that its expression varied with the developmental stage and tissue. The inheritance and expression of the exogenous gene were reviewed in transgenic hybrid poplar progeny lines and grafted sections. Biosafety issues, in terms of transgene stability and the effects on soil microorganisms, natural enemies of insects, and arthropod communities are also discussed.

Zhang W. et al. (2018): **Multidecadal, county-level analysis of the effects of land use, Bt cotton, and weather on cotton pests in China**. *PNAS*

<http://www.pnas.org/content/early/2018/07/10/1721436115>

Long-term changes in land use, climate, and agricultural technologies may affect pest severity and management. The influences of these major drivers can only be identified by analyzing long-term data. This study examines panel data on land use, adoption of genetically modified *Bacillus thuringiensis* (Bt) insect-resistant cotton, weather, pest severity, and insecticide use on three major cotton pests for 51 counties in China during 1991–2015. Bt cotton had pervasive effects on the whole pest complex in cotton and its management. Adoption resulted in major reductions in insecticide use for bollworm control. The resulting restoration of aphid biological control decreased aphid severity. However, mirid bugs, which have few effective natural enemies in cotton, increased in severity with warming May and reduced insecticide spraying against bollworm. The effects of landscape on pest severity were pest specific. The severity of cotton aphid and mirid bugs decreased with higher land use diversity, but the severity of highly polyphagous cotton bollworm was unrelated to land use diversity. Shares of forest, water body, and unused land area were negatively associated with the severity of mirid bugs, whereas cotton bollworm responded positively to the shares of water body and unused land area. Farmers sprayed insecticides at mild infestation levels and responded aggressively to severe bollworm outbreaks. Findings support the usefulness of Bt-based plant resistance as a component of integrated pest management (IPM) but highlight the potential for unexpected outcomes resulting from agroecosystem feedback loops as well as the importance of climate

<http://www.pnas.org/content/pnas/early/2018/07/10/1721436115.full.pdf>

Mishra R, Joshi RK and Zhao K (2018) **Genome Editing in Rice: Recent Advances, Challenges, and Future Implications**. *Front. Plant Sci.* 9:1361. doi: 10.3389/fpls.2018.01361

Rice (*Oryza sativa* L.) is the major food source for more than three billion people of the world. In the last few decades, the classical, mutational, and molecular breeding approaches have brought about tremendous increase in rice productivity with the development of novel rice varieties. However, stagnation in rice yield has been reported in recent decade owing to several factors including the emergence of pests and phytopathogens, climate change, and other environmental issues posing great threat to global food security. There is an urgent need to produce more rice and associated cereals to satisfy the mammoth task of feeding a still growing population expected to reach 9.7 billion by 2050. Advances in genomics and emergence of multiple genome editing technologies through use of engineered site-specific nucleases (SSNs) have revolutionized the field of plant science and agriculture. Among them, the CRISPR/Cas9 system is the most advanced and widely accepted because of its simplicity, robustness, and high efficiency. The availability of huge genomic resources together with a small genome size makes rice more suitable and feasible for genetic manipulation. As such, rice has been increasingly used to test the efficiency of different types of genome editing technologies to study the functions of various genes and demonstrate their potential in genetic improvement. Recently developed approaches including CRISPR/Cpf1 system and base editors have evolved as more efficient and accurate genome editing tools which might accelerate the pace of crop improvement. In the present review, we focus on the genome editing strategies for rice improvement, thereby highlighting the

applications and advancements of CRISPR/Cas9 system. This review also sheds light on the role of CRISPR/Cpf1 and base editors in the field of genome editing highlighting major challenges and future implications of these tools in rice improvement.

**Biradar H, Karan R and Subudhi PK (2018): Transgene Pyramiding of Salt Responsive Protein 3-1 (SaSRP3-1) and SaVHAc1 From *Spartina alterniflora* L. Enhances Salt Tolerance in Rice.** *Front. Plant Sci.* 9: 1304; doi: 10.3389/fpls.2018.01304

The transgenic technology using a single gene has been widely used for crop improvement. But the transgenic pyramiding of multiple genes, a promising alternative especially for enhancing complexly inherited abiotic stress tolerance, has received little attention. Here, we developed and evaluated transgenic rice lines with a single Salt Responsive Protein 3-1 (SaSRP3-1) gene as well as pyramids with two-genes SaSRP3-1 and Vacuolar HC-ATPase subunit c1 (SaVHAc1) derived from a halophyte grass *Spartina alterniflora* L. for salt tolerance at seedling, vegetative, and reproductive stages. The overexpression of this novel gene SaSRP3-1 resulted in significantly better growth of *E. coli* with the recombinant plasmid under 600 mM NaCl stress condition compared with the control. During early seedling and vegetative stages, the single gene and pyramided transgenic rice plants showed enhanced tolerance to salt stress with minimal wilting and drying symptoms, improved shoot and root growth, and significantly higher chlorophyll content, relative water content, and KC/NaC ratio than the control plants. The salt stress screening during reproductive stage revealed that the transgenic plants with single gene and pyramids had better grain filling, whereas the pyramided plants showed significantly higher grain yield and higher grain weight compared to control plants. Our study demonstrated transgenic pyramiding as a viable approach to achieve higher level of salt tolerance in crop plants.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.01304/full>

**Santos-Vigil K.-I, Ilhuicatzí-Alvarado D., García-Hernández, A.L., Herrera-García J.S., Moreno-Fierros L. (2018): Study of the allergenic potential of *Bacillus thuringiensis* Cry1Ac toxin following intra-gastric administration in a murine model of food-allergy.** *International Immunopharmacology* 61 (2018) 185–196

Cry1Ac toxin, from *Bacillus thuringiensis*, is widely used as a biopesticide and expressed in genetically modified (GM) plants used for human and animal consumption. Since Cry1Ac is also immunogenic and able to activate macrophages, it is crucial to thoroughly evaluate the immunological effects elicited after intra-gastric administration. The allergenic potential of purified Cry1Ac was assessed and compared with that induced in a murine model of food-allergy to ovalbumin (OVA), in which animals are sensitized with the adjuvant Cholera toxin (CT). Mice were weekly intragastrically administered with: i) vehicle phosphate-buffered saline (PBS), ii) OVA, iii) OVA plus CT iv) Cry1Ac or v) OVA plus Cry 1Ac. Seven weeks after, mice were intragastrically challenged and allergic reactions along with diverse allergy related immunological parameters were evaluated at systemic and intestinal level. The groups immunized with, Cry1Ac, OVA/Cry1Ac or OVA/CT developed moderate allergic reactions, induced significant IgE response and increased frequencies of intestinal granulocytes, IgE+ eosinophils and IgE+ lymphocytes. These same groups also showed colonic lymphoid hyperplasia, notably in humans, this has been associated with food allergy and intestinal inflammation. Although the adjuvant and allergenic potential of CT were higher than the effects of Cry1Ac, the results show that applied intra-gastrically at 50 µg doses, Cry1Ac is immunogenic, moderately allergenic and able to provoke intestinal lymphoid hyperplasia. Moreover, Cry1Ac is also able to induce anaphylaxis, since when mice were intragastrically sensitized with increasing doses of Cry1Ac, with every dose tested, a significant drop in rectal temperature was recorded after intravenous challenge.

<https://www.ncbi.nlm.nih.gov/pubmed/29886072>

**Kyrou K. et al. (2018): A CRISPR–Cas9 gene drive targeting *doublesex* causes complete population suppression in caged *Anopheles gambiae* mosquitoes.** *nature biotechnology* advance online publication

<https://www.nature.com/articles/nbt.4245>, <https://www.nature.com/articles/nbt.4245.pdf>

**Lin Y, Hung C-Y, Bhattacharya C, Nichols S, Rahimuddin H, Kittur FS, Leung T and Xie J (2018): An Effective Way of Producing Fully Assembled Antibody in Transgenic Tobacco Plants by Linking Heavy and Light Chains via a Self-Cleaving 2A Peptide.** *Front. Plant Sci.* 9:1379. doi: 10.3389/fpls.2018.01379

Therapeutic monoclonal antibodies (mAbs) have evolved into an important class of effective medicine in treatment of various diseases. Since the antibody molecule consists of two identical heavy chains (HC) and two light chains (LC), each chain encoded by two different genes, their expressions at similar levels are critical for efficient assembly of functional recombinant mAbs. Although the plant-based expression system has been tested to produce fully assembled recombinant mAbs, coordinately expressing HC and LC at similar levels in a transgenic plant remains a challenge. A sequence coding for a foot-and-mouth disease virus (FMDV) 2A peptide has been successfully used to link two or more genes, which enable the translated polyprotein to be “self-cleaved” into individual protein in various genetically modified organisms. In the present study, we exploited the usage of F2A in Ebola virus monoclonal antibody (EBOV mAb) production. We found that transgenic tobacco plants carrying a transcription unit containing HC and LC linked by 2A not only produced similar levels of HC and LC but also rendered a higher yield of fully assembled EBOV mAb compared to those expressing HC and LC in two independent transcription units. Purified EBOV mAb bound to an Ebola epitope peptide with apparent K<sub>d</sub>-values of 90.13–149.2 nM, indicating its proper assembly and high affinity binding to Ebola

epitope peptide. To our knowledge, this is the first report showing mAb production by overexpressing a single transcription unit consisting of HC, LC and 2A in stable transformed tobacco plants.  
<https://www.frontiersin.org/articles/10.3389/fpls.2018.01379/full>

## Tagungen – Conferences - Meetings

### **Alles Fake? Wissenschaft im Zeitalter der vielen Wahrheiten**

Die Veranstaltung ist kostenfrei.

Anmeldung bis zum 08.11.2018 unter [www.bfr-akademie.de/deutsch/7-bfrstakeholderkonferenz](http://www.bfr-akademie.de/deutsch/7-bfrstakeholderkonferenz)  
[https://www.bfr-akademie.de/media/wysiwyg/2018/STK2018/7.Stakeholderkonferenz\\_Programmflyer.pdf](https://www.bfr-akademie.de/media/wysiwyg/2018/STK2018/7.Stakeholderkonferenz_Programmflyer.pdf)

### **Gute Gentechnik, böse Gentechnik? – Konferenz an der Uni Halle**

Konferenz mit Workshops: "Prämissen und Anspruchsgruppen der roten und grünen Genomeditierung" vom 10.10.2018 – 11.10.2018

[http://kluth.jura.uni-halle.de/bmbf\\_genomelection/konferenz/](http://kluth.jura.uni-halle.de/bmbf_genomelection/konferenz/)

### **International Conference on Uncertainty in Risk Analysis**

Challenges and Advances in Assessing, Managing and Communicating Uncertainty

February 20 – 22, 2019, Berlin

The conference is free of charge. Please register online on the website of the BfR Academy.

<https://www.bfr-akademie.de/english/events/uncertainty-conference.html>

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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](http://www.wgg-ev.de). Hier finden Sie weitere interessante Informationen.

*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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