

# Sunday Evening News

Week 25 (2018-06-18 / 06-24)

Selected and edited by **BGF** Jany

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Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,

Dear all,

Currently, genetic engineering plays almost no role in the German-speaking media. That's fine, but everyone is waiting for the ECJ judgment on the new breeding techniques. Then we will see what happens! Perhaps the most incredible news was sent out by the party AfD

## **Volker Schnurrbusch (AfD): Chancen der Genom-Editierung nutzbar machen**

<https://www.openpr.de/news/1008311/Volker-Schnurrbusch-AfD-Chancen-der-Genom-Editierung-nutzbar-machen.html>

and the most interesting one is probably about the virus-resistant pigs.

## **BBC : Gene-edited farm animals are on their way**

<https://www.stlucianewsonline.com/gene-edited-farm-animals-are-on-their-way/>

please have a look on the paper of Burkard C. et al. (below)

## **other press releases or media reports**

University of Edinburgh: **Gene-edited pigs are resistant to billion-dollar virus**

<https://www.sciencedaily.com/releases/2018/06/180620150139.htm>

Val Giddings

## **Gene Editing, GMOs, and Fear-Based Marketing**

<https://itif.org/publications/2018/06/18/gene-editing-gmos-and-fear-based-marketing>

John Horgan: **Sorgen über das Ende der Wissenschaft – und der Menschheit**

<https://www.spektrum.de/news/geht-die-menschheit-und-die-wissenschaft-unter-interview-mit-martin-rees/1572718>

Bastiaan T Rutjens

## **What makes people distrust science? Surprisingly, not politics**

<https://www.stopfake.org/en/what-makes-people-distrust-science-surprisingly-not-politics/>

more press releases at <https://www.biotech-gm-food.com/presse>

## **Scientific papers**

Gerhard Flachowsky (2018): **Influence of Feed From Genetically Modified Plants on the Composition and Quality of Foods of Animal Origin**. Chapter 5 : Genetically Engineered Foods <http://dx.doi.org/10.1016/B978-0-12-811519-0.00005-4>

Plant breeding can be considered as the starting point for the human food chain. Bioengineering methods have been introduced as breeding techniques over the past 20 years. The global commercial cultivation of genetically modified plants (GMPs) increased from 1.7 million ha in 1996 to ~180 million ha in 2015, with maize, soybean, cotton, and rapeseed being the most important GMPs during this time. In addition to producing high and stable plant yields, GMPs have also been bred to be resistant to insects or as plant production aids (GMPs of the 1st generation were produced without substantial changes in the composition and nutritive value). Later, GMPs were bred to enhance the composition (e.g., biofortification, GMPs of the second-generation were bred with nutrition in mind). Many feeding studies have been performed in laboratory animals and food-producing animals using GMPs or coproducts from GMPs (i.e., soybean meal, cotton seed meal, and rapeseed cake). Studies using food-producing animals have enabled researchers to analyze animal health and welfare, follow the integration of transgenic DNA and newly expressed proteins, and analyze the influence of GMPs on the composition and quality of foods of animal origin (i.e., milk, eggs, meat, and fish). Feeds from the first-generation GMPs did not significantly influence the composition and quality of foods of animal origin. In addition, there was no scientific evidence to suggest that recombinant DNA and newly expressed proteins had off-target chemical and physiological effects in animals. Therefore, first-generation GMP feeds can be considered as equivalents to their isogenic counterparts. Second-generation GMP feeds (with output traits) may influence the composition and quality of animal feeds, especially the fatty acid

composition. Minerals and vitamins from biofortified plants can be stored in some animal organs or may be excreted in milk or eggs. A lower content of undesirable substances may improve the feed value of GMPs. <https://www.sciencedirect.com/science/article/pii/B9780128115190000054> pdf-file available

Guest Editors: Peadar G. Lawlor, Michelle M. Epstein and Gijs A. Kleter, **“Is it possible to monitor livestock for feed-related impacts on animal health?”** (Outcomes of the EU FP7-funded MARLON project), *Food and Chemical Toxicology*, vol. 117 (July 2018), pp. 1-88. <https://www.sciencedirect.com/journal/food-and-chemical-toxicology/vol/117>

Burkard C., Opriessnig T., Mileham A.J., Stadejek T., Ait-Ali T., Lilloco S.G., Whitelaw C.B., Archibald A.L. (2018): **Pigs lacking the scavenger receptor cysteine-rich domain 5 of CD163 are resistant to PRRSV-1 infection..** *Journal of Virology*, 2018; JVI.00415-18 DOI: [10.1128/JVI.00415-18](https://doi.org/10.1128/JVI.00415-18)

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) has a narrow host cell tropism, limited to cells of the monocyte/macrophage lineage. CD163 protein is expressed at high levels on the surface of specific macrophage types and a soluble form is circulating in blood. CD163 has been described as a fusion receptor for PRRSV, with the scavenger receptor cysteine-rich domain 5 (SRCR5) region having been shown to be the interaction site for the virus.

As reported earlier, we have generated pigs in which Exon 7 of the CD163 gene has been deleted using CRISPR/Cas9 editing in pig zygotes. These pigs express CD163 protein lacking SRCR5 ( $\Delta$ SRCR5 CD163) and show no adverse effects when maintained under standard husbandry conditions. The  $\Delta$ SRCR5 CD163 was not only detected on the surface of macrophage subsets, but the secreted, soluble protein can also be detected in the serum of the edited pigs, as shown here by porcine soluble CD163-specific ELISA. Previous results showed that primary macrophage cells from  $\Delta$ SRCR5 CD163 animals are resistant to PRRSV-1, subtypes 1, 2, and 3, as well as PRRSV-2 infection *in vitro*. Here,  $\Delta$ SRCR5 pigs were challenged with a highly virulent PRRSV-1, subtype 2 strain. In contrast to the wildtype control group,  $\Delta$ SRCR5 pigs showed no signs of infection and no viremia or antibody response indicative of a productive infection. Histopathological analysis of lung and lymph node tissue showed no presence of virus replicating cells in either tissue. This shows that  $\Delta$ SRCR5 pigs are fully resistant to infection by the virus.

<http://jvi.asm.org/content/early/2018/05/31/JVI.00415-18>

Duensing N., Sprink T., Parrott W.A., Fedorova A., Lema M.A., Wolt J.D. and Detlef Bartsch D. (2018): **Novel features and considerations for ERA and regulation of crops produced by genome editing.** *Front. Bioeng. Biotechnol.*, <https://doi.org/10.3389/fbioe.2018.00079>

Novel features and considerations for ERA and regulation of crops produced by genome editing  
Genome editing describes a variety of molecular biology applications enabling targeted and precise alterations of the genomes of plants, animals and microorganisms. These rapidly developing techniques are likely to revolutionize the breeding of new crop varieties. Since genome editing can lead to the development of plants that could also have come into existence naturally or by conventional breeding techniques, there are strong arguments that these cases should not be classified as genetically modified organisms (GMOs) and be regulated no differently from conventionally bred crops. If a specific regulation would be regarded necessary, the application of genome editing for crop development may challenge risk assessment and post-market monitoring. In the session “Plant genome editing—any novel features to consider for ERA and regulation?” held at the 14th ISBGMO, scientists from various disciplines as well as regulators, risk assessors and potential users of the new technologies were brought together for a knowledge-based discussion to identify knowledge gaps and analyze scenarios for the introduction of genome-edited crops into the environment. It was aimed to enable an open exchange forum on the regulatory approaches, ethical aspects and decision-making considerations.

<https://www.frontiersin.org/articles/10.3389/fbioe.2018.00079/full>

Geoffrey Henry Siwo G.H. (2018): **The Global State of Genome Editing** biorxiv:doi: <https://doi.org/10.1101/341198>

Genome editing technologies hold great promise in fundamental biomedical research, development of treatments for animal and plant diseases, and engineering biological organisms for food and industrial applications. Therefore, a global understanding of the growth of the field is needed to identify challenges, opportunities and biases that could shape the impact of the technology. To address this, the study presented performs automated literature mining of scientific publications on genome editing in the past year to infer research trends in 2 key genome editing technologies- CRISPR/Cas systems and TALENs. The study finds that genome editing research is disproportionately distributed between and within countries, with researchers in the US and China accounting for 50% of authors in the field whereas countries across Africa are underrepresented. Furthermore, genome editing research is also disproportionately being explored on diseases such as cancer, Duchene Muscular Dystrophy, sickle cell disease and malaria. Gender biases are also evident in genome editing research with considerably fewer women as principal investigators. The results of this study

suggest that automated mining of scientific literature could enhance tracking global trends that could help identify biases in research as a means to mitigate future inequalities and tap the full potential of the technology

<https://www.biorxiv.org/content/early/2018/06/11/341198.full.pdf+html>

Haque E. et al. (2018): **Application of CRISPR/Cas9 Genome Editing Technology for the Improvement of Crops Cultivated in Tropical Climates: Recent Progress, Prospects, and Challenges.** Front. Plant Sci., <https://doi.org/10.3389/fpls.2018.00617>

The world population is expected to increase from 7.3 to 9.7 billion by 2050. Pest outbreak and increased abiotic stresses due to climate change pose a high risk to tropical crop production. Although conventional breeding techniques have significantly increased crop production and yield, new approaches are required to further improve crop production in order to meet the global growing demand for food. The Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/Cas9 (CRISPR-associated protein9) genome editing technology has shown great promise for quickly addressing emerging challenges in agriculture. It can be used to precisely modify genome sequence of any organism including plants to achieve the desired trait. Compared to other genome editing tools such as zinc finger nucleases (ZFNs) and transcriptional activator-like effector nucleases (TALENs), CRISPR/Cas9 is faster, cheaper, precise and highly efficient in editing genomes even at the multiplex level. Application of CRISPR/Cas9 technology in editing the plant genome is emerging rapidly. The CRISPR/Cas9 is becoming a user-friendly tool for development of non-transgenic genome edited crop plants to counteract harmful effects from climate change and ensure future food security of increasing population in tropical countries. This review updates current knowledge and potentials of CRISPR/Cas9 for improvement of crops cultivated in tropical climates to gain resiliency against emerging pests and abiotic stresses.

[https://www.frontiersin.org/articles/10.3389/fpls.2018.00617/full?utm\\_source=S-TWT&utm\\_medium=SNET&utm\\_campaign=ECO\\_FPLS\\_XXXXXXX\\_auto-dlvrit%0A](https://www.frontiersin.org/articles/10.3389/fpls.2018.00617/full?utm_source=S-TWT&utm_medium=SNET&utm_campaign=ECO_FPLS_XXXXXXX_auto-dlvrit%0A)

Kofsky J., Hengyou Zhang H. and Song B.-H. (2018): **The untapped genetic reservoir: The past, current, and future applications of the wild soybean (Glycine soja)** Front. Plant Sci. | doi: 10.3389/fpls.2018.00949

There is a considerable demand for crop improvement, especially considering the increasing growth of world population, continuing climatic fluctuations, and rapidly evolving plant pests and pathogens. Crop wild relatives hold great potential in providing beneficial alleles for crop improvement. Wild soybean, *Glycine soja* (Siebold & Zucc.), the wild ancestor to the domesticated soybean (*Glycine max* (L.) Merr.), harbors a high level of genetic variation. Research on *G. soja* has been largely devoted to understanding the domestication history of the soybean, while little effort has been made to explore its genetic diversity for crop improvement. High genomic diversity and expanded traits make *G. soja* populations an excellent source for soybean improvement. This review summarizes recent successful research examples of applying wild soybeans in dissecting the genetic basis of various traits, with a focus on abiotic/biotic stress tolerance and resistance. We also discuss the limitations of using *G. soja*. Perspective future research is proposed, including the application of advanced biotechnology and emerging genomic data to further utilize the wild soybean to counterbalance the rising demand for superior crops. We proposed there is an urgent need for international collaboration on germplasm collection, resource sharing, and conservation. We hope to use the wild soybean as an example to promote the exploration and use of wild resources for crop improvement in order to meet future food requirements.

<https://www.frontiersin.org/articles/10.3389/fpls.2018.00949/abstract>

Prasanna HS, Swami DV, Bhagya HP, Bhavishya and Shivakumar SN (2018): **Botanicals: Potential plant protection chemicals: A review** International Journal of Chemical Studies 2018 6 (3): 217-222

The medicinal and aromatic plants are traditionally used in pest and disease control from time immemorial. The MAPs extracts/botanicals are easy to prepare and use, locally available, eco friendly, biodegradable, do not persist in soil and water and less or no toxic to vertebrates (fishes, birds and mammals). As upon regular using of synthetic PPCs the appearance of resistant strains is observed i.e., > 500 insect and mite species are resistant to one or more insecticides (World Resources Institute, 1994). So the application of double and triple rates of synthetic PPCs has to be used to maintain control. These synthetic PPCs also cause environmental hazards. As the persistency of synthetic PPCs is more and they have long degradation periods it can accumulate in the food chain and also results in the generation of high and acute toxicities. These synthetic PPCs also causes carcinogenicity, mutagenity, hormonal imbalance, spermatotoxicity etc... and interfere in human health issues. The estimation done by World Health Organization (WHO) says that 2 lakh people/year are killed worldwide due to pesticide poisoning. The synthetic PPCs have very less selectivity so that they kill both beneficial and harmful organisms. These synthetic PPCs also results in groundwater contamination & secondary pest outbreaks. So in order to avoid these problems use of MAPs is one of the necessary step in pest and disease management. The active ingredients of medicinal plants are N containing compounds (Alkaloids, glycosides etc.) and aromatic plants are essential oils. These EOs are complex mixture of terpenoids (C 10

& C 15) & and aromatic phenols and their oxides, ethers, alcohols, esters, aldehydes and ketones. These were used Flavour and fragrances, condiment or spice, medicines, antimicrobial/insecticidal agents, insect repellent or protect stored products. Also as fumigant and contact insecticidal activities. Botanicals can be used as fumigant in stored pest & soil born pathogens. These botanicals also has anti fungal, anti bacterial & anti viral activities and can be used to control the diseases. The drawback of botanicals is Poor availability of raw material and the efficacy v/s synthetic pesticides is very low. So technology validated & commercial formulation should be available, along with these many other MAPs should be explored and efficacy of botanicals should be improves through biotechnology & nanotechnology.

[https://www.researchgate.net/profile/Prasanna\\_H\\_S3/publication/325718539\\_Botanicals\\_Potential\\_plant\\_protection\\_chemicals\\_A\\_review/links/5b1fc475aca272277fa7f27a/Botanicals-Potential-plant-protection-chemicals-A-review.pdf](https://www.researchgate.net/profile/Prasanna_H_S3/publication/325718539_Botanicals_Potential_plant_protection_chemicals_A_review/links/5b1fc475aca272277fa7f27a/Botanicals-Potential-plant-protection-chemicals-A-review.pdf)

Lenaerts B, de Mey Y, Demont M (2018): **Global impact of accelerated plant breeding: Evidence from a meta-analysis on rice breeding.** PLoS ONE 13(6): e0199016.;

<https://doi.org/10.1371/journal.pone.0199016>

Rice breeders in Asia and elsewhere in the world have long overlooked trying to shorten the time it takes to develop new varieties. Plant breeders have proposed a technique called Rapid Generation Advance (RGA) as a way to accelerate the results of public rice breeding programs. However, little is known about RGA's potential impact. Here, we present the first results of a global impact study of RGA. More specifically, we calculated the multiplier effects of RGA on the research benefits generated by conventional rice breeding programs and applied them to a meta-analysis of selected impact studies in the literature. These insights are a first crucial step in developing a targeted approach for disseminating RGA technology among rice breeders to accelerate the impact of their public rice breeding programs around the world. We show that the additional benefits due to time savings are considerable and offer some insights into the economics of breeding. Our results confirm that the adoption of accelerated breeding would lead to substantial advantages to rice breeding programs and the earlier variety release leads to significant economic benefits to society. This can be important to policy makers when reshaping their public breeding methods and optimising their return on research investments in breeding.

<http://journals.plos.org/plosone/article/file?id=10.1371/journal.pone.0199016&type=printable>

Adenle, A. A., Morris, E. J., Murphy, D. J., Phillips, P. W. B., Trigo, E., Kearns, P., Li, Y.-H., Quemada, H., Falck-Zepeda, J. and Komen, J. (2018): **Rationalizing governance of genetically modified products in developing countries** Nature Biotechnology 36 (2),137-139

<http://dx.doi.org/10.1038/nbt.4069>

<https://www.nature.com/articles/nbt.4069>

<http://www.ask-force.org/web/Developing/Adenle-Rationalizing-governance-GM-products-developing-contries-2018.pdf>

Placide R, Patrick K. and Bellancille U. (2018): **Is quantitative genetics still necessary in this age of genomics?** African Journal of Agricultural Research 13(24), 1227-1232, DOI: 10.5897/AJAR2017.12746

<http://www.academicjournals.org/journal/AJAR/article-full-text-pdf/C3540FA57414>

Kurihara Y., Makita Y., Kawashima M., Fujita T., Iwasaki S., Matsui M. (2018): **Transcripts from downstream alternative transcription start sites evade uORF-mediated inhibition of gene expression in Arabidopsis**, *Proceedings of the National Academy of Sciences* (2018).

[DOI: 10.1073/pnas.1804971115](https://doi.org/10.1073/pnas.1804971115)

Plants adapt to alterations in light conditions by controlling their gene expression profiles. Expression of light-inducible genes is transcriptionally induced by transcription factors such as HY5. However, few detailed analyses have been carried out on the control of transcription start sites (TSSs). Of the various wave-lengths of light, it is blue light (BL) that regulates physiological responses such as hypocotyl elongation and flowering time. To understand how gene expression is controlled not only by transcript abundance but also by TSS selection, we examined genome-wide TSS profiles in Arabidopsis seedlings after exposure to BL irradiation following initial growth in the dark. Thousands of genes use multiple TSSs, and some transcripts have upstream ORFs (uORFs) that take precedence over the main ORF (mORF) encoding proteins. The uORFs often function as translation inhibitors of the mORF or as triggers of nonsense-mediated mRNA decay (NMD). Transcription from TSSs located downstream of the uORFs in 220 genes is enhanced by BL exposure. This type of regulation is found in HY5 and HYH, major regulators of light-dependent gene expression. Translation efficiencies of the genes showing enhanced usage of these TSSs increased upon BL exposure. We also show that transcripts from TSSs upstream of uORFs in 45 of the 220 genes, including HY5, accumulated in a mutant of NMD. These results suggest that BL controls gene expression not only by enhancing transcriptions but also by choosing the TSS, and

transcripts from downstream TSSs evade uORF-mediated inhibition to ensure high expression of light-regulated genes.

<http://www.pnas.org/content/pnas/early/2018/06/13/1804971115.full.pdf>

and RIKEN

**Blue gene regulation helps plants respond properly to light**

<https://phys.org/news/2018-06-blue-gene-properly.html#jCp>

Foo M., Gherman I., Zhang P., Bates D.C., Denby K. J. (2018): **A Framework for Engineering Stress Resilient Plants Using Genetic Feedback Control and Regulatory Network Rewiring**, *ACS Synthetic Biology* (2018). *ACS Synth. Biol.*, 7 (6), 1553–1564; DOI: [10.1021/acssynbio.8b00037](https://doi.org/10.1021/acssynbio.8b00037)

Crop disease leads to significant waste worldwide, both pre- and postharvest, with subsequent economic and sustainability consequences. Disease outcome is determined both by the plants' response to the pathogen and by the ability of the pathogen to suppress defense responses and manipulate the plant to enhance colonization. The defense response of a plant is characterized by significant transcriptional reprogramming mediated by underlying gene regulatory networks, and components of these networks are often targeted by attacking pathogens. Here, using gene expression data from *Botrytis cinerea*-infected *Arabidopsis* plants, we develop a systematic approach for mitigating the effects of pathogen-induced network perturbations, using the tools of synthetic biology. We employ network inference and system identification techniques to build an accurate model of an *Arabidopsis* defense subnetwork that contains key genes determining susceptibility of the plant to the pathogen attack. Once validated against time-series data, we use this model to design and test perturbation mitigation strategies based on the use of genetic feedback control. We show how a synthetic feedback controller can be designed to attenuate the effect of external perturbations on the transcription factor CHE in our subnetwork. We investigate and compare two approaches for implementing such a controller biologically—direct implementation of the genetic feedback controller, and rewiring the regulatory regions of multiple genes—to achieve the network motif required to implement the controller. Our results highlight the potential of combining feedback control theory with synthetic biology for engineering plants with enhanced resilience to environmental stress.

<https://pubs.acs.org/doi/10.1021/acssynbio.8b00037>

University of Warwick

**Rewiring plant defence genes to reduce crop waste**

<https://phys.org/news/2018-06-rewiring-defence-genes-crop.html#jCp>

Carter B., Bishop B., Ho K.K., Huang R., Jia W., Zhang H., Pascuzzi P.E., Deal R., Ogas J. (2018): **The Chromatin Remodelers PKL and PIE1 Act in an Epigenetic Pathway that Determines H3K27me3 Homeostasis in Arabidopsis**. *The Plant Cell*; DOI:

<https://doi.org/10.1105/tpc.17.00867>

Selective, tissue-specific gene expression is facilitated by the epigenetic modification H3K27me3 (trimethylation of lysine 27 on histone H3) in plants and animals. Much remains to be learned about how H3K27me3-enriched chromatin states are constructed and maintained. Here we identify a genetic interaction in *Arabidopsis thaliana* between the chromodomain helicase DNA-binding chromatin remodeler PICKLE (PKL), which promotes H3K27me3 enrichment, and the SWR1-family remodeler PHOTOPERIOD INDEPENDENT EARLY FLOWERING 1 (PIE1), which incorporates the histone variant H2A.Z. Chromatin immunoprecipitation-sequencing and RNA-sequencing reveal that PKL, PIE1, and the H3K27 methyltransferase CURLY LEAF act in a common gene expression pathway and are required for H3K27me3 levels genome-wide. Additionally, H3K27me3-enriched genes are largely a subset of H2A.Z-enriched genes, further supporting the functional linkage between these marks. We also found that recombinant PKL acts as a prenucleosome maturation factor, indicating that it promotes retention of H3K27me3. These data support the existence of an epigenetic pathway in which PIE1 promotes H2A.Z, which in turn promotes H3K27me3 deposition. After deposition, PKL promotes retention of H3K27me3 after DNA replication and/or transcription. Our analyses thus reveal roles for H2A.Z and ATP-dependent remodelers in construction and maintenance of H3K27me3-enriched chromatin in plants.

<http://www.plantcell.org/content/early/2018/05/25/tpc.17.00867>

Louloupi A., Ntini E., Conrad T., and Vang Ørom U.A. (2018): **Transient N-6-Methyladenosine Transcriptome Sequencing Reveals a Regulatory Role of m6A in Splicing Efficiency**, *Cell Reports* 23, 3429–3437. DOI: [10.1016/j.celrep.2018.05.077](https://doi.org/10.1016/j.celrep.2018.05.077)

Splicing efficiency varies among transcripts, and tight control of splicing kinetics is crucial for coordinated gene expression. N-6-methyladenosine (m6A) is the most abundant RNA modification and is involved in regulation of RNA biogenesis and function. The impact of m6A on regulation of RNA splicing kinetics is unknown. Here, we provide a time-resolved high-resolution assessment of m6A on nascent RNA transcripts and unveil its importance for the control of RNA splicing kinetics. We find that early co-transcriptional m6A deposition near splice junctions promotes fast splicing, while m6A modifications in introns are associated with long, slowly

processed introns and alternative splicing events. In conclusion, we show that early m6A deposition specifies the fate of transcripts regarding splicing kinetics and alternative splicing.

[https://www.cell.com/cell-reports/pdf/S2211-1247\(18\)30858-1.pdf](https://www.cell.com/cell-reports/pdf/S2211-1247(18)30858-1.pdf)

and Lisbeth Heilesen, Aarhus University

**Encrypted messages in biological processes**

<https://phys.org/news/2018-06-encrypted-messages-biological.html#jCp>

Lamichhane J.R., Osdaghi E., Behlau F., Köhl J., Jones J.B., Jean-Noël Aubertot J.-N. (2018): **Thirteen decades of anti-microbial copper compounds applied in agriculture. A review.**

*Agronomy for Sustainable Development* 38, 28 - DOI: 10.1007/s13593-018-0503-9

Since the initial use of Bordeaux mixture in 1885 for plant disease control, a large number of copper-based antimicrobial compounds (CBACs) have been developed and applied for crop protection. While these compounds have revolutionized crop protection in the 20th century, their continuous and frequent use has also raised concerns about the long-term sustainability of copper (Cu)-based crop protection system. Here, we review CBACs used in crop protection and highlight their benefits and risks, and potential for their improvement and opportunities for further research to develop alternatives to CBACs. The major findings are (i) the relatively high toxicity to plant pathogens, low cost, low mammalian toxicity of the fixed Cu compounds, and their chemical stability and prolonged residual effects are major benefits of these compounds; (ii) phytotoxicity, development of copper-resistant strains, soil accumulation and negative effects on soil biota as well as on food quality parameters are key disadvantages of CBACs. (iii) regulatory pressure in agriculture worldwide to limit the use of CBACs has led to several restrictions, including that imposed by the regulation 473/2002 in the European Union; and (iv) mitigation strategies to limit the negative effects of CBACs include their optimized use, soil remediation and development and application of alternatives to CBACs for a sustainable crop protection. We conclude that recent research and policy efforts have led to the development of a number of alternatives to CBACs, which should be further intensified to ensure that growers have sufficient tools for the implementation of sustainable crop protection strategies.

<https://link.springer.com/article/10.1007/s13593-018-0503-9>

**EFSA: Conclusion on the peer review of the pesticide risk assessment of the active substance copper compounds copper(I), copper(II) variants namely copper hydroxide, copper oxychloride, tribasic copper sulfate, copper(I) oxide, Bordeaux mixture.** EFSA

*Journal* 2018;16(1):5152, 25 pp. <https://doi.org/10.2903/j.efsa.2018.5152>

The conclusions of the EFSA following the peer review of the initial risk assessments carried out by the competent authorities of the rapporteur Member State, France, and co-rapporteur Member State, Germany, for the pesticide active substance copper compounds are reported. The context of the peer review was that required by Commission Implementing Regulation (EU) No 844/2012. The conclusions were reached on the basis of the evaluation of the representative uses of copper compounds as a fungicide on grapes, tomatoes and cucurbits. The reliable end points appropriate for use in regulatory risk assessment are presented. Missing information identified as being required by the regulatory framework is listed. Concerns are identified.

Reminder

**OECD Conference on Genome Editing APPLICATIONS IN AGRICULTURE**

Implications for Health, Environment and Regulation

Paris, 28-29 June 2018

[https://issuu.com/oecd.publishing/docs/programme\\_web\\_version](https://issuu.com/oecd.publishing/docs/programme_web_version)

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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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