

# Sunday Evening News

Week 15 (2018-04-23 / 04-29)

Selected and edited by **BGF** Jany

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Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter, zwei Themen beherrschten diese Woche die Medien.

- a) Die Haltung Deutschlands bei der Abstimmung im Berufungsausschuss für die Erneuerung der Zulassung der Zuckerrübe H7-1
- b) Das Verbot dreier Neonicotinoide in der EU, um das Insektensterben, insbesondere von Bienen einzudämmen.

**Zuckerrübe H7-1:** Im SCoPAFF hatte Deutschland für die Wiedezulassung der gv-Zuckerrübe gestimmt, aber es wurde wie gehabt damals keine qualifizierte Mehrheit erreicht. Die deutschen Medien haben daraufhin gegen die Erneuerung der Zulassung Stimmung gemacht und Deutschland sollte sich – wie vor dem Regierungswechsel – sich der Stimme enthalten.

**Berufungsausschuss Zuckerrübe H7-1**, wie gehabt keine qualifizierte Mehrheit, aber Deutschland stimmte dafür / *Appeal Committee sugar beet H7-1, as usually no qualified majority, but Germany was in favour (13 MS in favour, 12 MS against, 3 MS abstention)*

Auf meiner Webseite habe ich Dauer der Zulassungsverfahren für gv-Pflanzen zusammengestellt. Die aktuellen Weiterentwicklungen / „Fortschritte“ wird tabellarisch noch aufgenommen, d.h. die Gegebenheiten nach 31.12.2017.

<https://www.biotech-gm-food.com/pflanzen/antraege-zulassung-gentech-pflanzen>

Karin Bensch, ARD-Korrespondentin in Brüssel: **Gentechnik: EU-Importzulassung ist umstritten**

<https://www.ndr.de/nachrichten/Gentechnik-EU-Importzulassung-ist-umstritten,gentechnik230.html>

Bensch K. und Plaß C.: **Gentechnik durch die Hintertür**

[http://www.deutschlandfunk.de/europa-gentechnik-durch-die-hintertuer.1773.de.html?dram:article\\_id=416262](http://www.deutschlandfunk.de/europa-gentechnik-durch-die-hintertuer.1773.de.html?dram:article_id=416262)

<https://www.br.de/nachrichten/immer-mehr-gentechnik-produkte-in-europa-100.html>

## Neonicotinoide

Erik Hecht: **EU verbietet bienengefährdende Wirkstoffe**

<http://www.faz.net/aktuell/wirtschaft/eu-verbietet-bienengefaehrdende-neonicotinoide-15562127.html>

Merlot J. – Spiegel online: **Neonikotinoide** Das Verbot ist richtig, retten wird es die Bienen nicht

<http://www.spiegel.de/wissenschaft/natur/neonikotinoide-das-verbot-ist-richtig-wird-die-bienen-aber-nicht-retten-a-1204674.html>

The Guardian: **EU agrees total ban on bee-harming pesticides**

<https://www.theguardian.com/environment/2018/apr/27/eu-agrees-total-ban-on-bee-harming-pesticides>

## EuGH – new breeding techniques - interpretation

**ESA: POSITION PAPER ON THE OPINION OF ADVOCATE GENERAL BOBEK DELIVERED ON 18 JANUARY 2018 IN CASE C-528/16**

In December 2014, 9 French NGOs initiated legal proceedings against an Article of the French Environmental Code, which implements the EU GMO Directive. They argued that plant varieties in rapeseed and sunflower resulting from traditional or new forms of mutagenesis constitute ‘new hidden GMOs’ and as such need to be regulated as GMOs. The French Conseil d’Etat referred four preliminary questions to the European Court of Justice (ECJ), essentially to ascertain whether organisms resulting from traditional and new forms of mutagenesis should be subject to the GMO legislation. One year later, in October 2017, the ECJ convened in a grand chamber hearing, and on 18 January 2018 Advocate General Bobek delivered his Opinion in the case. *European Seed* met with Geert Glas, a lawyer from Allen & Overy, who published a legal article on the Court Case in [Bioscience Law Review](#) last year. Geert Glas, Partner at Allen & Overy (Belgium) LLP was asked by the European Seed Sector to provide a legal view on the opinion of the Advocate General.

[📄 position paper on advocate general bobek opinion c-528-16 final.pdf](#)

<https://www.euroseeds.eu/position-paper-opinion-advocate-general-bobek-delivered-18-january-2018-case-c-52816>

**ESA: So, What Did The Advocate General Bobek Say Exactly?  
A legal analysis of case number C-528/16 on mutagenesis in plants**

<http://european-seed.com/advocate-general-bobek-say-exactly/>

**VKM-EFSA: Summary Report of Joint VKM and EFSA Symposium** on risk assessment and risk management cooperation on environmental protection goals

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/sp.efsa.2018.EN-1405>

Shroff R. – lifegate

**Industrial agriculture isn't feeding the world, only agroecology can**

<https://www.lifegate.com/people/lifestyle/agroecology-fao-navdanya-international>

Frédéric Simon | EURACTIV.com: **EFSA boss: EU food law overhaul 'a big step towards transparency'**

<https://www.euractiv.com/section/agriculture-food/interview/efsa-boss-eu-food-law-overhaul-a-big-step-towards-transparency/>

Sara Lewis S.: **MEPs split on EFSA publishing confidential studies**

<https://iegpolicy.agribusinessintelligence.informa.com/PL216218/MEPs-split-on-EFSA-publishing-confidential-studies>

For further press releases and media reports: <https://www.biotech-gm-food.com/presse>

## Scientific papers

Varshney R.K., Singh V.K., Kumar A., Powell W., and Mark E Sorrells M.E. (2018): **Can genomics deliver climate-change ready crops?** *Curr Opin Plant Biol* ,

<https://doi.org/10.1016/j.pbi.2018.03.007>

Development of climate resilient crops with accelerating genetic gains in crops will require integration of different disciplines/technologies, to see the impact in the farmer's field. In this review, we summarize how we are utilizing our germplasm collections to identify superior alleles/haplotypes through NGS based sequencing approaches and how genomics-enabled technologies together with precise phenotyping are being used in crop breeding. Pre-breeding and genomics-assisted breeding approaches are contributing to the more efficient development of climate-resilient crops. It is anticipated that the integration of several disciplines/ technologies will result in the delivery of climate change ready crops in less time.

Etienne J., Stefania Chirico S., McEntaggart K., Papoutsis S., and Erik Millstone E. (2018): **EU Insights – Consumer perceptions of emerging risks in the food chain**

ICF ( in association with GfK)

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/sp.efsa.2018.EN-1394>

Wang G., Dong Y, Liu X., Yao G., Yang M. (2018): **The current status and development of insect-resistant genetically engineered poplar in China.** *Frontiers in Bioengineering and Biotechnology*

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 insectresistant 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. pdf-file available

Pray C., Huang J., Hu R. Deng H., Yang J. Morin X.K. (2018): **Prospects for cultivation of genetically engineered food crops in China**. *Global Food Security* 16, 133-137

Major food crops that contain genetically engineered (GE) traits cannot be legally grown in China, despite major investments in biotechnology research and despite government decisions that GE maize, [soybeans](#), and canola are safe to import and eat. The paper uses a political economy model to analyze why GE maize and GE rice have not been commercialized in China and whether they are like to be commercialized soon. This model draws on recently completed studies of consumers' and business managers' attitudes towards the safety and the profitability of GE rice and GE maize and on new publications of the potential economic impact of these crops. Consumer opposition and the absence of competitive GE traits from Chinese companies were two major factors constraining commercialization of GE food in the past. This paper predicts that GE maize is, however, likely to be commercialized in the near future due to recent developments in GE technology, the Chinese economy, and Chinese politics.

[https://www.researchgate.net/profile/Jikun\\_Huang/publication/323181979\\_Prospects\\_for\\_cultivation\\_of\\_genetically\\_engineered\\_food\\_crops\\_in\\_China/links/5aac7beda6fdcc1bc0b8db39/Prospects-for-cultivation-of-genetically-engineered-food-crops-in-China.pdf](https://www.researchgate.net/profile/Jikun_Huang/publication/323181979_Prospects_for_cultivation_of_genetically_engineered_food_crops_in_China/links/5aac7beda6fdcc1bc0b8db39/Prospects-for-cultivation-of-genetically-engineered-food-crops-in-China.pdf)

Sedeek K.E.M. (2018) **Plant Biotechnology Status in Egypt**. In: *The Handbook of Environmental Chemistry*. Springer, Berlin, Heidelberg DOI

[https://doi.org/10.1007/698\\_2017\\_196](https://doi.org/10.1007/698_2017_196)

Hunger and malnutrition are important factors that hinder the development of any country. Farmers have used traditional methods to solve the problem, but do not seem to succeed. However, plant biotechnology has potentials for improving crop productivity and ensuring food security. Also, it significantly shortens the time required for the production of new cultivars with desirable characteristics. Egypt hosts one of the oldest agricultural civilizations in the world (Craig, *The agriculture of Egypt*. Oxford University Press, Oxford, 1993). Despite this, it faces the risk of food insecurity due to the increasing rate of population and not using the modern technology to increase crop productivity. Therefore, Egypt started one of the most advanced plant biotechnology programs in Africa in 1990 and launched the Agricultural Genetic Engineering Research Institute (AGERI). AGERI is engaged in cutting-edge projects in the field of biotic and abiotic stress resistance, genome mapping, and bioinformatics. AGERI successfully engineered several crops which include wheat, cotton, maize, potato, cucumber, squash, melon, and tomato. These crops are in the pipeline of commercialization due to the governmental hesitation toward commercialization of genetically modified crops.

[https://link.springer.com/chapter/10.1007/698\\_2017\\_196](https://link.springer.com/chapter/10.1007/698_2017_196)

Vosman B., van't Westende W.P.C., Henken B., van Eekelen H.D.L.M., de Vos R.C.H. and Voorrips R.E. (2018): **Broad spectrum insect resistance and metabolites in close relatives of the cultivated tomato**. *Euphytica* 214, 46; DOI: [10.1007/s10681-018-2124-4](https://doi.org/10.1007/s10681-018-2124-4)

Wild relatives of tomato possess effective means to deal with several pests, among which are a variety of insects. Here we studied the presence of resistance components against *Trialeurodes vaporariorum*, *Myzus persicae*, *Frankliniella occidentalis*, and *Spodoptera exigua* in the *Lycopersicon* group of *Solanum* section *Lycopersicon* by means of bioassays and comprehensive metabolite profiling. Broad spectrum resistance was found in *Solanum galapagense* and a few accessions of *S. pimpinellifolium*. Resistance to the sap sucking insects may be based on the same mechanism, but different from the caterpillar resistance. Large and highly significant differences in the leaf metabolomes were found between *S. galapagense*, containing type IV trichomes, and its closest relative *S. cheesmaniae*, which lacks type IV trichomes. The most evident differences were the relatively high levels of different methylated forms of the flavonoid myricetin and many acyl sucrose structures in *S. galapagense*. Possible candidate genes regulating the production of these compounds were identified in the *Wf-1* QTL region of *S. galapagense*, which was previously shown to confer resistance to the whitefly *B. tabaci*. The broad spectrum insect resistance identified in *S. galapagense* will be very useful to increase resistance in cultivated tomato.

<https://link.springer.com/article/10.1007%2Fs10681-018-2124-4>

Samson Simon S., Otto M. & Engelhard M. (2018): **Synthetic gene drive: between continuity and novelty**. *EMBO reports* e45760 | DOI 10.15252/embr.201845760

Crucial differences between gene drive and genetically modified organisms require an adapted risk assessment for their use

<http://embr.embopress.org/content/early/2018/04/12/embr.201845760>

have a look also to:

<http://journals.sagepub.com/doi/full/10.1177/1535676018755117>

Robert King, Neil Andrew Brown, Martin Urban, Kim E. Hammond-Kosack. **Inter-genome comparison of the Quorn fungus *Fusarium venenatum* and the closely related plant infecting pathogen *Fusarium graminearum***. *BMC Genomics*, 2018; 19 (1),269 DOI:

[10.1186/s12864-018-4612-2](https://doi.org/10.1186/s12864-018-4612-2)

Background: The soil dwelling saprotrophic non-pathogenic fungus *Fusarium venenatum*, routinely used in the commercial fermentation industry, is phylogenetically closely related to the globally important cereal and non-cereal infecting pathogen *F. graminearum*. This study aimed to sequence, assemble and annotate the *F. venenatum* (strain A3/5) genome, and compare this genome with *F. graminearum*.

Results: Using shotgun sequencing, a 38,660,329 bp *F. venenatum* genome was assembled into four chromosomes, and a 78,618 bp mitochondrial genome. In comparison to *F. graminearum*, the predicted gene count of 13,946 was slightly lower. The *F. venenatum* centromeres were found to be 25% smaller compared to *F. graminearum*. Chromosome length was 2.8% greater in *F. venenatum*, primarily due to an increased abundance of repetitive elements and transposons, but not transposon diversity. On chromosome 3 a major sequence rearrangement was found, but its overall gene content was relatively unchanged. Unlike homothallic *F. graminearum*, heterothallic *F. venenatum* possessed the *MAT1-1* type locus, but lacked the *MAT1-2* locus. The *F. venenatum* genome has the type A trichothecene mycotoxin *TRI5* cluster, whereas *F. graminearum* has type B. From the *F. venenatum* gene set, 786 predicted proteins were species-specific versus NCBI. The annotated *F. venenatum* genome was predicted to possess more genes coding for hydrolytic enzymes and species-specific genes involved in the breakdown of polysaccharides than *F. graminearum*. Comparison of the two genomes reduced the previously defined *F. graminearum*-specific gene set from 741 to 692 genes. A comparison of the *F. graminearum* versus *F. venenatum* proteomes identified 15 putative secondary metabolite gene clusters (SMC), 109 secreted proteins and 38 candidate effectors not found in *F. venenatum*. Five of the 15 *F. graminearum*-specific SMCs that were either absent or highly divergent in the *F. venenatum* genome showed increased in planta expression. In addition, two predicted *F. graminearum* transcription factors previously shown to be required for fungal virulence on wheat plants were absent or exhibited high sequence divergence.

Conclusions: This study identifies differences between the *F. venenatum* and *F. graminearum* genomes that may contribute to contrasting lifestyles, and highlights the repertoire of *F. graminearum*-specific candidate genes and SMCs potentially required for pathogenesis.

<https://bmcbgenomics.biomedcentral.com/articles/10.1186/s12864-018-4612-2>

Yilmaz A., Peretz M., Aharony A., Sagi I. & Benvenisty N. (2018): **Defining essential genes for human pluripotent stem cells by CRISPR-Cas9 screening in haploid cells.** *Nature Cell Biology* 20, 610-619. DOI: [10.1038/s41556-018-0088-1](https://doi.org/10.1038/s41556-018-0088-1)

The maintenance of pluripotency requires coordinated expression of a set of essential genes. Using our recently established haploid human pluripotent stem cells (hPSCs), we generated a genome-wide loss-of-function library targeting 18,166 protein-coding genes to define the essential genes in hPSCs. With this we could allude to an intrinsic bias of essentiality across cellular compartments, uncover two opposing roles for tumour suppressor genes and link autosomal-recessive disorders with growth-retardation phenotypes to early embryogenesis. hPSC-enriched essential genes mainly encode transcription factors and proteins related to cell-cycle and DNA-repair, revealing that a quarter of the nuclear factors are essential for normal growth. Our screen also led to the identification of growth-restricting genes whose loss of function provides a growth advantage to hPSCs, highlighting the role of the P53-mTOR pathway in this context. Overall, we have constructed an atlas of essential and growth-restricting genes in hPSCs, revealing key aspects of cellular essentiality and providing a reference for future studies on human pluripotency.

<https://www.nature.com/articles/s41556-018-0088-1>

and Hebrew University of Jerusalem

Scientists generate an atlas of the human genome using stem cells

<https://phys.org/news/2018-04-scientists-atlas-human-genome-stem.html#iCp>

Gifford D.R., Furió V., Papkou A., Vogwill T., Oliver A. & MacLean R.C. (2018). **Identifying and exploiting genes that potentiate the evolution of antibiotic resistance.** *Nature Ecology & Evolution* (2018). [nature.com/articles/doi:10.1038/s41559-018-0547-x](https://doi.org/10.1038/s41559-018-0547-x)

There is an urgent need to develop novel approaches for predicting and preventing the evolution of antibiotic resistance. Here, we show that the ability to evolve de novo resistance to a clinically important  $\beta$ -lactam antibiotic, ceftazidime, varies drastically across the genus *Pseudomonas*. This variation arises because strains possessing the *ampR* global transcriptional regulator evolve resistance at a high rate. This does not arise because of mutations in *ampR*. Instead, this regulator potentiates evolution by allowing mutations in conserved peptidoglycan biosynthesis genes to induce high levels of  $\beta$ -lactamase expression. Crucially, blocking this evolutionary pathway by co-administering ceftazidime with the  $\beta$ -lactamase inhibitor avibactam can be used to eliminate pathogenic *P. aeruginosa* populations before they can evolve resistance. In summary, our study shows that identifying potentiator genes that act as evolutionary catalysts can be used to both predict and prevent the evolution of antibiotic resistance.

<https://www.nature.com/articles/s41559-018-0547-x>

University of Oxford

Scientists identify genetic catalysts that speed up evolution of antibiotic resistance

<https://phys.org/news/2018-04-scientists-genetic-catalysts-evolution-antibiotic.html#jCp>

Velasco E., Wang S., Sanet M., Fernández-Vázquez J., Jové D., Valledor E.G., O'Halloran T.V., & Balsalobre C. (2018): **A new role for Zinc limitation in bacterial pathogenicity: modulation of  $\alpha$ -hemolysin from uropathogenic *Escherichia coli*.** *Scientific Reports* (2018). DOI: [10.1038/s41598-018-24964-1](https://doi.org/10.1038/s41598-018-24964-1)

Metal limitation is a common situation during infection and can have profound effects on the pathogen's success. In this report, we examine the role of zinc limitation in the expression of a virulence factor in uropathogenic *Escherichia coli*. The pyelonephritis isolate J96 carries two hlyCABD operons that encode the RTX toxin  $\alpha$ -hemolysin. While the coding regions of both operons are largely conserved, the upstream sequences, including the promoters, are unrelated. We show here that the two hlyCABD operons are differently regulated. The hlyII operon is efficiently silenced in the presence of zinc and highly expressed when zinc is limited. In contrast, the hlyI operon does not respond to zinc limitation. Genetic studies reveal that zinc-responsive regulation of the hlyII operon is controlled by the Zur metallo regulatory protein. A Zur binding site was identified in the promoter sequence of the hlyII operon, and we observe direct binding of Zur to this promoter region. Moreover, we find that Zur regulation of the hly II operon modulates the ability of *E. coli* J96 to induce a cytotoxic response in host cell lines in culture. Our report constitutes the first description of the involvement of the zinc-sensing protein Zur in directly modulating the expression of a virulence factor in bacteria

<https://www.nature.com/articles/s41598-018-24964-1.pdf>

University of Barcelona

Zinc is able to modulate *Escherichia coli* bacteria's virulence, study finds

<https://phys.org/news/2018-04-zinc-modulate-escherichia-coli-bacteria.html#jCp>

De Barro P.J., Murphy B., Cassie C. Jansen C.C., Murray J. (2011): **The proposed release of the yellow fever mosquito, *Aedes aegypti* containing a naturally occurring strain of *Wolbachia pipientis*, a question of regulatory responsibility.** *J. Verbr. Lebensm.* 6 (S1), 33-40; DOI 10.1007/s00003-011-0671-x

In 2010 a proposal to release the yellow fever mosquito, *Aedes aegypti*, containing an intracellular symbiotic bacterium, *Wolbachia*, as a means of reducing the severity of outbreaks of dengue fever was lodged in Australia. The mosquito was infected with *Wolbachia* through embryonic microinjection. This proposal uncovered a gap in the regulatory process normally used to assess the release of species into Australia. Firstly, while the association between the mosquito and the bacterium was new, both species naturally occurred in Australia and so legislation governing the introduction of new species into Australia was ruled not relevant. Secondly, the infection of the mosquito with *Wolbachia* did not involve gene technology and so was not subject to legislation governing the approval of genetically modified organisms. The solution came through the decision to use existing legislation to regulate *Wolbachia* as a veterinary chemical product. This was a good outcome as it overcame the barrier that a lack of regulatory oversight may have posed to field trials taking place. Furthermore, the approach taken demonstrated a very high level of scrutiny with regulatory frameworks. An acceptable regulatory solution has been found, but the novelty of the science is such that the appropriateness of the regulatory process now needs to be reviewed to ensure that it is no more onerous for both the proponents and the regulators than it needs to be.

<https://link.springer.com/article/10.1007%2Fs00003-011-0671-x>

Sudhakar N., Shanmugam H., Sekar Kumaran S., Coelho A., Nunes R. and Isabel S. Carvalho I.S. (2018): Chapter 4 – **Omics Approaches in Fungal Biotechnology: Industrial and Medical Point of View.** *Omics Technologies and Bio-Engineering 2*, 53-70, Towards Improving Quality of Life; <https://doi.org/10.1016/B978-0-12-815870-8.00004-8>

Fungi are of excellent value nutritionally, and of great importance to vegetarians. Edible mushrooms are excellent sources of protein, have low-fat content, and are free of cholesterol. Most of these are hydrolytic in nature, being employed in different food processing industries as well as in refinement of fodder quality. Edible filamentous fungi producing enzymes present an added advantage for their use in food and feed. In fungi, laccase is present in ascomycetes, deuteromycetes, and basidiomycetes, and is particularly abundant in many white-rot fungi that degrade lignin. Laccases have been subject of intensive research in the last decades due to their broad substrate specificity. In the recent years, their uses span from the textile to the pulp and paper industries, and food applications to bioremediation processes.

<https://www.sciencedirect.com/science/article/pii/B9780128158708000048>

Kuddus M. (2018): **Cold-active enzymes in food biotechnology: An updated mini review.**

*Journal of Applied Biology & Biotechnology* Vol. 6(3), 58-63; DOI: 10.7324/JABB.2018.60310

Cold-active enzymes and their anticipated application in various industries including food industry attracted attention of worldwide scientific community. Cold-active enzymes, also known as psychrophilic enzymes,

possess high catalytic activity at low and moderate temperatures. Due to low-temperature activity, these enzymes utilize less energy in biochemical reactions and also stabilize fragile compounds in the reaction medium. The source of cold-active enzymes is basically psychrophilic/psychrotrophic microorganisms which are found in cold environments. In comparison to mesophilic and thermophilic enzymes, till date, very few cold-active enzymes are known and least explored so far in the food industry. This review contains latest development and innovation in cold-active enzymes along with their applications in food biotechnology. [http://jabonline.in/admin/php/uploads/276\\_pdf.pdf](http://jabonline.in/admin/php/uploads/276_pdf.pdf)

Rao Q., Jiang X., Li Y., Samiwala M., and Labuza T.P. (2018): **Can Glycation Reduce Food Allergenicity?** *J. Agric. Food Chem.* XXX XXX XXX DOI: 10.1021/acs.jafc.8b00660

As a naturally occurring reaction during food processing, glycation, also known as non-enzymatic browning or Maillard reaction, can improve food protein physiochemical properties and functionality. In this perspective, three aspects of glycation (terminology confusion between glycation and glycosylation, its current application, and its impact on immunoreactivity) are elaborated. Overall, the immunoreactivity of glycated proteins may decrease, remain unchanged, or even increase after food glycation. Also, it should be noted that the effect of glycation on the immunoglobulin (Ig)E- or IgG-binding capacity of allergens do not necessarily and correctly predict the allergenicity of the glycated protein in the allergic patient population. <https://pubs.acs.org/doi/abs/10.1021/acs.jafc.8b00660>

### **27th IGC International Grains Conference**

The 27th IGC International Grains Conference takes place on 19 - 20 June 2018 at the Queen Elizabeth II Centre, London. Now extended to a second day, the event offers enhanced opportunities to derive invaluable market insight and connect with other prominent industry professionals.

<https://www.igc.int/en/conference/programme.aspx>

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