

Sunday Evening News

Week 23 (2018-06-04 / 06-10)

Selected and edited by **BGF** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,

Schwerpunkt der nationalen und internationalen Pressemeldungen war diese Woche die erfolgreiche Übernahme von Monsanto durch Bayer und das Streichen des Namens „Monsanto“.

Auf das Interview von **Sam Bloch** mit Klaas Martens möchte ich besonders hinweisen. Ähnlich wie Niggli ist Martens der Meinung, dass die neuen Züchtungstechniken auch für den biologischen Landbau von Bedeutung sind und genutzt werden sollten.

Dear all

This week, the focus of the national and international press releases was the successful takeover of Monsanto by Bayer and the cancellation of the name "Monsanto".

I would like to point out the interview of **Sam Bloch** with Klaas Martens. Similar to Niggli, Martens is convinced that the new breeding techniques are also important for organic farming and these techniques should be also applied.

Press releases – media reports

AFP: **Bayer completes \$63-billion Monsanto takeover**

<https://economictimes.indiatimes.com/news/international/business/bayer-completes-63-billion-monsanto-takeover/articleshow/64496273.cms>

Zoë Schlanger: **Monsanto is about to disappear. Everything will stay exactly the same**

<https://qz.com/1297749/the-end-of-the-monsanto-brand-bayer-pharmaceuticals-is-dropping-the-name-monsanto/>

Kurier: **Der Gentechnik-Teufel wird umgetauft**

Bayer übernimmt Monsanto. Der Name des US-Agrarkonzerns verschwindet. Die Nachfrage nach Nahrungsmitteln steigt.

<https://kurier.at/wirtschaft/der-gentechnik-teufel-wird-umgetauft/400046225>

manager-magazin: **Abschluss des 62-Milliarden-Deals am 7. Juni Bayer ist bei Monsanto-Kauf am Ziel - und streicht den Namen**

<http://www.manager-magazin.de/unternehmen/industrie/bayer-kapitalerhoehung-soll-uebernahme-von-monsanto-finanzieren-helfen-a-1210987.html>

Sam Bloch: At CRISPRcon, an organic luminary embraces gene editing. Will the industry follow?

Klaas Martens's unexpected support for gene-edited crops raises questions about how to define "GMOs" as technology rapidly changes.

<https://newfoodeconomy.org/klaas-martens-organic-gene-editing-crispr-gmo/>

Joan Conrow: **European studies disprove Seralini's GMO maize tumor claims**

<https://allianceforscience.cornell.edu/blog/2018/06/european-studies-disprove-seralinis-gmo-maize-tumor-claims/>

Bob Dobi: **Was The World's Largest Study Of GMOs Just Russian Propaganda?**

A Russian group launched a \$25 million study of genetically modified organisms. Then it disappeared.

https://www.buzzfeed.com/danvervano/factor-gmo-fake-science-russia?utm_term=.ysAEpLPKq#.fqKWM1DXp

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

Scientific papers

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

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 analyse 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>

Bradford, K.; Carter, N.; Eriksson, D.; Grabau, E.; Hood, E.; Parrott, W.; Wolt, J. D. (2018): **Regulatory Barriers to the Development of Innovative Agricultural Biotechnology by Small Businesses and Universities.** Issue Paper - Council for Agricultural Science and Technology 2018 No.59 pp.20 pp.

Since the early 1980s, American taxpayers have invested heavily in public, university, and small business developers of crops and foods improved using biotechnology. Yet the return on this investment, in terms of new, improved genetically engineered (GE) crops, is disappointingly thin. Although the U.S. Department of Agriculture, universities, and small businesses have developed dozens of GE crops - with improved traits ranging from healthier and less allergenic to safer and more environmentally sustainable - and carried many through safety and premarket testing, almost all have been denied commercial release mainly because of U.S. regulatory obstacles that disproportionately penalize public, academic, and smaller private breeding entities. In theory, scientifically sound regulations serve the public good by assuring a reasonable degree of product safety while not unduly stifling innovation. In a scientifically rigorous, risk-based safety assessment, the degree of regulatory scrutiny is commensurate with the degree of identified risk posed by the product in question. In reality, however, our current regulations are not based on product risk, but on spurious, undocumented risks posed by the process of genetic engineering. These regulations impose scrutiny well beyond that imposed on non-GE products posing similar risks. As well, the unnecessarily onerous and expensive regulations discourage and stifle innovation, especially in small businesses and universities. This report analyses the current U.S. regulatory system for GE crops, compares it with those of major trading partners, and considers various aspects of agricultural biotechnology regulation, including labeling and scientifically sound alternatives to the unnecessarily restrictive current regulatory system to allow the benefits of safe agricultural biotechnology products from small business and universities to accrue to farmers, consumers, and the environment.

<http://www.cast-science.org/download.cfm?PublicationID=284920&File=50B78D421EFE0C72E0EAC9323C30E73A.cfusion>

Gao Y.-J., Zhu H.-J., Chen Y., Li Y.-H., Peng Y.-F., and Chen X.-P.: (2018): **Safety Assessment of Bacillus thuringiensis Insecticidal Proteins Cry1C and Cry2A with a Zebrafish Embryotoxicity Test.** J. Agric. Food Chem. 66, 4336–4344, DOI: [10.1021/acs.jafc.8b01070](https://doi.org/10.1021/acs.jafc.8b01070)

As a result of the large-scale planting of transgenic *Bacillus thuringiensis* (Bt) crops, fish would be exposed to freely soluble Bt insecticidal protein(s) that are released from Bt crop tissues into adjacent bodies of water or by way of direct feeding on deposited plant material. To assess the safety of two Bt proteins Cry1C and Cry2A to fish, we used zebrafish as a representative species and exposed their embryos to 0.1, 1, and 10 mg/L of the two Cry proteins until 132 h post-fertilization and then several developmental, biochemical, and molecular parameters were evaluated. Chlorpyrifos (CPF), a known toxicant to aquatic organisms, was used as a positive control. Although CPF exposure resulted in significant developmental, biochemical, and molecular changes in the zebrafish embryos, there were almost no significant differences after Cry1C or Cry2A exposure. Thus, we conclude that zebrafish embryos are not sensitive to Cry1C and Cry2A insecticidal proteins at test concentrations.

Ranjbar M.K.N. et al. (2018): **Consequences of resistance evolution in a Cas9-based sex-conversion suppression gene drive for insect pest management.** PNAS 201713825; <https://doi.org/10.1073/pnas.171382511>

The use of a site-specific homing-based gene drive for insect pest control has long been discussed, but the easy design of such systems has become possible only with the recent establishment of CRISPR/Cas9 technology. In this respect, novel targets for insect pest management are provided by new discoveries regarding sex determination. Here, we present a model for a suppression gene drive designed to cause an all-male population collapse in an agricultural pest insect. To evaluate the molecular details of such a sex-conversion-based suppression gene drive experimentally, we implemented this strategy in *Drosophila melanogaster* to serve as a safe model organism. We generated a Cas9-based homing gene-drive element targeting the transformer gene and showed its high efficiency for sex conversion from females to males. However, non-homologous end joining increased the rate of mutagenesis at the target site, which resulted in the emergence of drive-resistant alleles and therefore curbed the gene drive. This confirms previous studies that simple homing CRISPR/Cas9 gene-drive designs will be ineffective. Nevertheless, by performing population dynamics simulations using the parameters we obtained in *D. melanogaster* and by adjusting the model for the agricultural pest *Ceratitis capitata*, we were able to identify adequate modifications that could be successfully applied for the management of wild Mediterranean fruit fly populations using our proposed sex-conversion-based suppression gene-drive strategy.

<http://jmarshall.berkeley.edu/KaramiNejadRanjbar2018PNAS.pdf>

Jacobs J. et al. (2018): **The transcription factor Grainy head primes epithelial enhancers for spatiotemporal activation by displacing nucleosomes**, *Nature Genetics* (2018). DOI: [10.1038/s41588-018-0140-x](https://doi.org/10.1038/s41588-018-0140-x)

Transcriptional enhancers function as docking platforms for combinations of transcription factors (TFs) to control gene expression. How enhancer sequences determine nucleosome occupancy, TF recruitment and transcriptional activation in vivo remains unclear. Using ATAC-seq across a panel of *Drosophila* inbred strains, we found that SNPs affecting binding sites of the TF Grainy head (Grh) causally determine the accessibility of epithelial enhancers. We show that deletion and ectopic expression of Grh cause loss and gain of DNA accessibility, respectively. However, although Grh binding is necessary for enhancer accessibility, it is insufficient to activate enhancers. Finally, we show that human Grh homologs—GRHL1, GRHL2 and GRHL3—function similarly. We conclude that Grh binding is necessary and sufficient for the opening of epithelial enhancers but not for their activation. Our data support a model positing that complex spatiotemporal expression patterns are controlled by regulatory hierarchies in which pioneer factors, such as Grh, establish tissue-specific accessible chromatin landscapes upon which other factors can act.

VIB (the Flanders Institute for Biotechnology)

<https://www.nature.com/articles/s41588-018-0140-x>

and

Grainyhead, a master regulator that controls DNA access

<https://phys.org/news/2018-06-grainyhead-master-dna-access.html#jCp>

Pandeya D. et al. (2018): **Selective fertilization with phosphite allows unhindered growth of cotton plants expressing the *ptxD* gene while suppressing weeds**. PNAS 201804862; <https://doi.org/10.1073/pnas.1804862115>

Weeds, which have been the bane of agriculture since the beginning of civilization, are managed manually, mechanically, and, more recently, by chemicals. However, chemical control options are rapidly shrinking due to the recent rise in the number of herbicide-resistant weeds in crop fields, with few alternatives on the horizon. Therefore, there is an urgent need for alternative weed suppression systems to sustain crop productivity while reducing our dependence on herbicides and tillage. Such a development will also allay some of the negative perceptions associated with the use of herbicide-resistance genes and heavy dependence on herbicides.

Transgenic plants expressing the bacterial *phosphite dehydrogenase* (*ptxD*) gene gain an ability to convert phosphite (Phi) into orthophosphate [Pi, the metabolizable form of phosphorus (P)]. Such plants allow for a selective fertilization scheme, based on Phi as the sole source of P for the crop, while offering an effective alternative for suppressing weed growth. Here, we show that, when P is supplied in the form of Phi, *ptxD*-expressing cotton (*Gossypium hirsutum* L.) plants outcompete, in both artificial substrates and natural soils from agricultural fields, three different monocot and dicot weed species intentionally introduced in the experiments, as well as weeds naturally present in the tested soils. Importantly, the *ptxD*/Phi system proved highly efficacious in inhibiting the growth of glyphosate-resistant Palmer amaranth. With over 250 weed species resistant to currently available herbicides, *ptxD*-transgenic plants fertilized with Phi could provide an effective alternative to suppressing the growth of these weeds while providing adequate nutrition to the crop.

<http://www.pnas.org/content/early/2018/05/30/1804862115>

Strauss B S. (2018): **Why Is DNA Double Stranded? The Discovery of DNA Excision Repair Mechanisms**. *Genetics* 209 (2), 357-366; <https://doi.org/10.1534/genetics.118.300958>

The persistence of hereditary traits over many generations testifies to the stability of the genetic material. Although the Watson–Crick structure for DNA provided a simple and elegant mechanism for replication, some

elementary calculations implied that mistakes due to tautomeric shifts would introduce too many errors to permit this stability. It seemed evident that some additional mechanism(s) to correct such errors must be required. This essay traces the early development of our understanding of such mechanisms. Their key feature is the cutting out of a section of the strand of DNA in which the errors or damage resided, and its replacement by a localized synthesis using the undamaged strand as a template. To the surprise of some of the founders of molecular biology, this understanding derives in large part from studies in radiation biology, a field then considered by many to be irrelevant to studies of gene structure and function. Furthermore, genetic studies suggesting mechanisms of mismatch correction were ignored for almost a decade by biochemists unacquainted or uneasy with the power of such analysis. The collective body of results shows that the double-stranded structure of DNA is critical not only for replication but also as a scaffold for the correction of errors and the removal of damage to DNA. As additional discoveries were made, it became clear that the mechanisms for the repair of damage were involved not only in maintaining the stability of the genetic material but also in a variety of biological phenomena for increasing diversity, from genetic recombination to the immune response.

http://www.genetics.org/content/209/2/357?lrscl=a86fead2-dc16-49d8-9587-8208a5128e47&utm_source=linkedin%20elevator&utm_medium=social%20media

Jeffrey A. Evans J.A., Williams A., Hager A.G., Mirsky S.B., Tranel P.J. and Davis A.S. (2018): **Confronting herbicide resistance with cooperative management.** Pest Management Science, <https://doi.org/10.1002/ps.5105>

BACKGROUND: Resistance of pathogens and pests to antibiotics and pesticides worldwide is rapidly reaching critical levels. The common-pool-resource nature of this problem (i.e., whereby the susceptibility to treatment of target organisms is a shared resource) has been largely overlooked. Using herbicide-resistant weeds as a model system, we developed a discrete-time landscape-scale simulation to investigate how aggregating herbicide management strategies at different spatial scales from individual farms to larger cooperative structures affects the evolution of glyphosate resistance in common waterhemp (*Amaranthus tuberculatus*). RESULTS: Our findings indicate that high-efficacy herbicide management strategies practiced at the farm scale are insufficient to slow resistance evolution in *A. tuberculatus*. When best practices were aggregated at large spatial scales, resistance evolution was hindered; conversely, when poor management practices were aggregated, resistance was exacerbated. Tank mixture-based strategies were more effective than rotation-based strategies in most circumstances, while applying glyphosate alone resulted in the poorest outcomes. CONCLUSIONS: Our findings highlight the importance of landscape-scale cooperative management for confronting common-pool-resource resistance problems in weeds and other analogous systems.

<https://onlinelibrary.wiley.com/doi/abs/10.1002/ps.5105>

Mischko W. et al, **Modular biomanufacturing for a sustainable production of terpenoid-based insect deterrents,** *Green Chemistry* 11,(2018). DOI: 10.1039/C8GC00434J

Synthetic agricultural insecticides are toxic to many species and accumulate in the environment. Therefore, the development of target-specific and biodegradable insecticides and deterrents is in demand. This study describes an improved and sustainable process for the green production of a biological insect repellent based on the diterpene cembratriene-ol (CBT-ol). This compound is a natural part of the tobacco (*Nicotiana sp.*) plant's defense against insects and thus minimizes damage to the environment. The study reports a new recombinant (*E. coli*) CBT-ol production and purification system. Efficient production was achieved by ribosomal binding site combinatorics using the BioBrick assembly system. These methods generated a metabolically balanced microbial system capable of generating $78.9 \pm 2.4 \text{ mg L}^{-1}$ CBT-ol in a 50 L bioreactor. Fermentations were entirely carried out on enzymatically generated wheat bran hydrolysate, representing a waste fraction of the grain milling process. The application of this complex and cost-efficient cultivation medium enabled an ecologically and economically sensible production of this high-value insect deterrent. Moreover, an ecologically favorable downstream processing protocol was established, combining adsorptive CBT-ol capture and centrifugal partition chromatography (CPC) followed by HPLC-based isomer separation. This is the first report using CPC to recover recombinant-generated, bioactive terpenes. The methodology enabled 95% CBT-ol recovery and purification in a single CPC step with significantly reduced solvent consumption in comparison to conventional chromatographic methods. *In vivo* and *in vitro* bioactivity studies confirmed the insecticide characteristics but also indicated that CBT-ol shows other bioactivities specifically targeting Gram-positive bacteria.

<http://pubs.rsc.org/en/Content/ArticleLanding/2018/GC/C8GC00434J#!divAbstract>

and

Technical University Munich

Biodegradable crop protection products without risks or side effects

<https://phys.org/news/2018-06-biodegradable-crop-products-side-effects.html#jCp>

Blasiak R, Jouffray J-B., Wabnitz C.C.C., Sundström E. and Österblom H. (2018): **Corporate control and global governance of marine genetic resources,** *Science Advances* 4 (6), eaar5237, DOI: 10.1126/sciadv.aar5237

Who owns ocean biodiversity? This is an increasingly relevant question, given the legal uncertainties associated with the use of genetic resources from areas beyond national jurisdiction, which cover half of the Earth's surface. We accessed 38 million records of genetic sequences associated with patents and created a database of 12,998 sequences extracted from 862 marine species. We identified >1600 sequences from 91 species associated with deep-sea and hydrothermal vent systems, reflecting commercial interest in organisms from remote ocean areas, as well as a capacity to collect and use the genes of such species. A single corporation registered 47% of all marine sequences included in gene patents, exceeding the combined share of 220 other companies (37%). Universities and their commercialization partners registered 12%. Actors located or headquartered in 10 countries registered 98% of all patent sequences, and 165 countries were unrepresented. Our findings highlight the importance of inclusive participation by all states in international negotiations and the urgency of clarifying the legal regime around access and benefit sharing of marine genetic resources. We identify a need for greater transparency regarding species provenance, transfer of patent ownership, and activities of corporations with a disproportionate influence over the patenting of marine biodiversity. We suggest that identifying these key actors is a critical step toward encouraging innovation, fostering greater equity, and promoting better ocean stewardship.

<http://advances.sciencemag.org/content/4/6/eaar5237>

Darvishi, F., Ariana, M., Marella, E.R. Borodinal I. (2018): **Advances in synthetic biology of oleaginous yeast *Yarrowia lipolytica* for producing non-native chemicals.** Appl Microbiol Biotechnol (2018). <https://doi.org/10.1007/s00253-018-9099-x>;

Oleaginous yeast *Yarrowia lipolytica* is an important industrial host for the production of enzymes, oils, fragrances, surfactants, cosmetics, and pharmaceuticals. More recently, improved synthetic biology tools have allowed more extensive engineering of this yeast species, which lead to the production of non-native metabolites. In this review, we summarize the recent advances of genome editing tools for *Y. lipolytica*, including the application of CRISPR/Cas9 system and discuss case studies, where *Y. lipolytica* was engineered to produce various non-native chemicals: short-chain fatty alcohols and alkanes as biofuels, polyunsaturated fatty acids for nutritional and pharmaceutical applications, polyhydroxyalkanoates and dicarboxylic acids as precursors for biodegradable plastics, carotenoid-type pigments for food and feed, and campesterol as a precursor for steroid drugs.

<https://link.springer.com/article/10.1007/s00253-018-9099-x>

Wikoff D.S. and Gary W Miller G.W. (2018): **Systematic Reviews in Toxicology: Toxicological Sciences** 163 (2), 335–337, <https://doi.org/10.1093/toxsci/kfy109>

Nieto C.H.D., Granero A.M., Zon M.A., Fernández H. (2018): **Sterigmatocystin: A mycotoxin to be seriously considered (Review)** Food and Chemical Toxicology 118, 460-470 ;

<https://doi.org/10.1016/j.fct.2018.05.057>

Sterigmatocystin is a carcinogenic compound that affects several species of crops and several species of experimental animals. The sterigmatocystin biosynthetic pathway is the best known and most studied. The International Agency for Research on Cancer classifies sterigmatocystin in the Group 2B. Three groups of analytical methods to determine sterigmatocystin in food can be found: chromatographic, ELISA immunoassays and chemical sensors. In addition, sterigmatocystin is a precursor of aflatoxin B₁ in those cases where cereals and/or food are contaminated with fungi capable of producing aflatoxins. Chemical structures of sterigmatocystin and aflatoxin B₁ are similar. These mycotoxins are pathogens of animals and cereals, producing a major economic impact on biotechnology and agricultural and food industries. This review summarizes different aspects related to sterigmatocystin such as its biosynthesis, toxicological studies and analytical methods for its determination.

<https://www.sciencedirect.com/science/article/pii/S0278691518303570>

Khan M.S. and Joyia F.A. (2018): **Biotechnology and GM Crops.** Developing Sustainable Agriculture in Pakistan, Chapter 19

https://www.researchgate.net/profile/Muhammad_Sarwar_Khan2/publication/325286061_Biotechnology_and_GM_Crops/links/5b03f32c0f7e9be94bdb23d2/Biotechnology-and-GM-Crops.pdf

Sandall, Leah, "AGRI 115: Biotechnology – Food, Health and Environment, A Peer Review of Teaching Project Benchmark Portfolio" (2018). UNL Faculty Course Portfolios . 104.

<https://digitalcommons.unl.edu/cgi/viewcontent.cgi?article=1105&context=prtunl>

Swings T. et al. (2018): **CRISPR-FRT targets shared sites in a knock-out collection for off-the-shelf genome editing,** *Nature Communications* 9, Article number: 2231 (2018); DOI:

[10.1038/s41467-018-04651-5](https://doi.org/10.1038/s41467-018-04651-5)

CRISPR advances genome engineering by directing endonuclease sequence specificity with a guide RNA molecule (gRNA). For precisely targeting a gene for modification, each genetic construct requires a unique gRNA. By generating a gRNA against the flippase recognition target (FRT) site, a common genetic element

shared by multiple genetic collections, CRISPR-FRT circumvents this design constraint to provide a broad platform for fast, scarless, off-the-shelf genome engineering.

<https://www.nature.com/articles/s41467-018-04651-5>
<https://www.nature.com/articles/s41467-018-04651-5.pdf>

Baylor College of Medicine

Gene editing just got easier

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

Hernández-Terán A., Wegier A., Benítez M., Lira R. and Ana E. Escalante A.E. (2017): **Domesticated, Genetically Engineered, and Wild Plant Relatives Exhibit Unintended Phenotypic Differences: A Comparative Meta-Analysis Profiling Rice, Canola, Maize, Sunflower, and Pumpkin.** *Front. Plant Sci.*, - <https://doi.org/10.3389/fpls.2017.02030>
<https://www.frontiersin.org/articles/10.3389/fpls.2017.02030/full#B24>

Krimsky, S. & Gillam, C. (2018): **Roundup litigation discovery documents: implications for public health and journal ethics** *J Public Health Pol* (2018). <https://doi.org/10.1057/s41271-018-0134-z>

This paper reviews the court-released discovery documents obtained from litigation against Monsanto over its herbicide Roundup and through Freedom of Information Act requests (requests to regulatory agencies and public universities in the United States). We sought evidence of corporate malfeasance and undisclosed conflicts of interest with respect to issues of scientific integrity. The findings include evidence of ghost writing, interference in journal publication, and undue influence of a federal regulatory agency.

<https://link.springer.com/article/10.1057%2Fs41271-018-0134-z>

European Chemicals Agency (ECHA) and European Food Safety Authority (EFSA) with support from the Joint Research Centre (JRC). **Guidance for the identification of endocrine disruptors in the context of Regulations (EU) No 528/2012 and (EC) No 1107/2009** (Pre-publication version; June 2018)

https://www.efsa.europa.eu/sites/default/files/scientific_output/5311.pdf

Tagungen – Conferences

BIOFLAVOUR 2018 - Biotechnology of Flavours, Fragrances and Functional Ingredients
18 – 21 September 2018 DECHEMA-Haus, Frankfurt am Main
<http://dechema.de/en/bioflavour2018.html>

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. 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.

This file is saved at <https://www.biotech-gm-food.com/sunday-evening-news/> as well as at <https://www.wgg-ev.de/infos/wgg-nachrichten/>

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