

# Sunday Evening News

Week 04 (2018-01-22 / 01-28)

Selected and edited by **BGF** Jany

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Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,

Aus terminlichen Gründen erhalten Sie die Sunday Evening News bereits am Sonntagmorgen. Ich hoffe es ist auch etwas Interessantes für Sie dabei. Für die Pressemeldungen brauchen Sie nicht bis Sonntag warten. Die ausgewählten tagesaktuellen deutsch- und englischsprachigen finden Sie stets auf <https://www.biotech-gm-food.com/presse>.

*Dear all*

Due to scheduling reasons, you will receive the Sunday Evening News on Sunday morning. I hope you will find there something interesting also for you. You do not need to wait until Sunday for the press releases. You will always find the selected ones in German and English languages at <https://www.biotech-gm-food.com/press>.

## Media reports – press releases

Max Rauner

### Genfood – besser als sein Ruf?

Auf der Suche nach ein paar Körnchen Wahrheit im absurden Kampf um den Golden Reis  
Reader's Digest Februar-Heft 2, 66-74 (2018) **lesenswert!**

Im Wortlaut sehr ähnlicher Artikel

Max Rauner- zeit-online

### Sind Sie auch ... gegen Genfood?

Und wissen Sie eigentlich noch genau, warum? Folgen Sie unserem Autor Max Rauner auf der Suche nach ein paar Körnchen Wahrheit im absurden Kampf um den Goldenen Reis.

<http://www.zeit.de/zeit-wissen/2017/04/genetechnik-genfood-pflanzen-ernaehrung-gesundheit>

## EU Reporter Correspondent: EFSA: Risk assessments in EU food sector – Commission launches public consultation on transparency

<https://www.eureporter.co/health/2018/01/23/risk-assessments-in-eufoodsector-commission-launches-public-consultation-on-transparency/>

## Commission: Public Consultation on the transparency and sustainability of the EU risk assessment in the food chain

[https://ec.europa.eu/info/consultations/public-consultation-transparency-and-sustainability-eu-risk-assessment-food-chain\\_en](https://ec.europa.eu/info/consultations/public-consultation-transparency-and-sustainability-eu-risk-assessment-food-chain_en)

## Vogel G. – Science: A new Merkel-led government could be good news for German science

<http://www.sciencemag.org/news/2018/01/new-merkel-led-government-could-be-good-news-german-science>

## Spiegel-online: Glyphosat-Streit "Es hat keine Verschwörung gegeben"

Proteste, eine Klage, jetzt auch noch ein Sonderausschuss im EU-Parlament: Glyphosat ist ein Reizthema. Bernhard Url, Chef der EU-Lebensmittelbehörde Efsa, rechtfertigt die Nutzung des Unkrautvernichters.

<http://www.spiegel.de/gesundheit/ernaehrung/glyphosat-streit-efsa-chef-bernhard-url-es-gab-keine-verschwoerung-a-1189134.html>

## Url B. (2018): Don't attack science agencies for political gain

Eroding trust in regulatory agencies will not improve democratic accountability, warns Bernhard Url Nature 553, 381

<https://www.nature.com/articles/d41586-018-01071-9>

## Porterfield A. – Genetic Literacy Project: IARC cancer agency mounts PR effort as probe of possible corruption grows

[https://geneticliteracyproject.org/2018/01/17/iarc-cancer-agency-pr-effort-probe-possible-corruption/?mc\\_cid=9d958e1c10&mc\\_eid=fcbe812b3b](https://geneticliteracyproject.org/2018/01/17/iarc-cancer-agency-pr-effort-probe-possible-corruption/?mc_cid=9d958e1c10&mc_eid=fcbe812b3b)

### In connection with ECJ AG Bobek:

#### ml – transcript : **CRISPR-Organismen: Mal GVO, mal nicht**

Mit neuartigen molekularen Werkzeugen entwickelte Organismen fallen nicht unbedingt unter die strenge EU-Regulierung von gentechnisch veränderten Organismen (GVO), so ein offizielles Vorabentscheidungsverfahren des Europäischen Gerichtshofes.

<https://transkript.de/news/crispr-organismen-mal-gvo-mal-nicht.html>

#### **BÖLW: BÖLW fordert klare europäische Regelungen und warnt vor nationalen Alleingängen**

<https://www.fruchtportal.de/artikel/bolw-fordert-klare-europaische-regelungen-und-warnt-vor-nationalen-alleingangen/031978>

#### Jaffe G.: **European Union Opinion on Gene Editing: Insightful or Missed Opportunity?**

Conclusion: Overall, the Advocate General's opinion clarifies the scope of the EU's GMO directive and how to interpret the exemption for mutagenesis techniques. However, the key question of how that directive applies to new molecular gene-edited products, if at all, remains unanswered, at least until the ECJ weighs in.

<https://cspinet.org/news/european-union-opinion-gene-editing-insightful-or-missed-opportunity-20180125>

### **Publications: Mutagenesis and gene engineering**

Robiński J. und Wasmer M. (2018): **Produkte gezielter Mutagenese sind keine GVOs gemäß Art. 3 i.V.m. Anhang I B der Richtlinie 2001/18/EG.** Journal of Consumer Protection and Food Safety. <https://doi.org/10.1007/s00003-017-1147-4>.

Die Europäische Richtlinie 2001/18/EG regelt die Freisetzung gentechnisch veränderter Organismen (GVO). Züchtungen mittels Mutagenese sind gemäß Art. 3 i.V.m. Anhang I B von der Richtlinie ausgenommen. Gilt diese Ausnahme nur für Produkte chemischer und strahleninduzierter Mutagenese oder auch für neue biotechnologische Verfahren gezielter Mutagenese? Unserer Analyse gemäß sind durch Mutagenese gewonnene Organismen von allen Regelungen der Richtlinie ausgenommen und fallen auch nicht in den Anwendungsbereich der Legaldefinition des Begriffs des genetisch veränderten Organismus im Sinne der Richtlinie. Der Begriff Mutagenese ist zudem dynamisch auszulegen, nach dessen naturwissenschaftlicher Bedeutung, welche auch gezielte Mutagenese umfasst. Dies bedeutet, dass Produkte gezielter Mutagenese keine GVOs im Sinne der Richtlinie sind.

<https://link.springer.com/article/10.1007%2Fs00003-017-1147-4> pdf-file available

#### Kathleen L. Heffernan K. L. and Herring R.J (2018): **The End of the GMO? Genome Editing, Gene Drives and New Frontiers of Plant Technology.** Review of Agrarian Studies

Improvements to agriculture will constitute one of the world's greatest challenges in the coming century. Political and social controversies, as well as complications of plant breeding, intellectual property, and regulation, have compromised the promised impact of genetically engineered – typically transgenic – crops designated as “GMOs.” Genome editing is a new suite of molecular tools for assisting biologists identify genes that control agronomic traits such as drought tolerance and pest resistance, as well as to elucidate how expression of these genes is intertwined within the functional framework of the cell. This technology has recently gained momentum for its ability to accelerate the crop breeding process in an unprecedented fashion and expand the range of crop varieties with improved precision and lower costs. This review explains the basic concepts and provides examples of how genome editing could help address the United Nation's Sustainable Development Goals with respect to food, agriculture, and medicine. It concludes with a discussion of the potential social impact of genome editing and gene drive. These effects are contingent on the resolution of novel ethical and regulatory challenges that add new layers of complexity to societal questions of appropriate technology, in agriculture and beyond. We expect these questions to replace the irresolvable GMO debate. [http://www.ras.org.in/the\\_end\\_of\\_the\\_gmo\\_genome\\_editing\\_gene\\_drives\\_and\\_new\\_frontiers\\_of\\_plant\\_technology#A-title1](http://www.ras.org.in/the_end_of_the_gmo_genome_editing_gene_drives_and_new_frontiers_of_plant_technology#A-title1)

#### CIMMYT (2017): **Position Statement on Novel Genome Editing Technologies in Crops**

<http://www.cimmyt.org/wp-content/uploads/2016/04/CIMMYT-Position-Statement-on-Novel-Genome-Editing-Technologies-17Dec2017.pdf>

#### Spök A. et al (2018): **Inclusive development and prioritization of review questions in a highly controversial field of regulatory science.** *Environ Evid* (2018) 7:1;

<https://doi.org/10.1186/s13750-017-0113-z>

How to best assess potential health, environmental and other impacts of genetically modified organisms (GMOs) and how to interpret the resulting evidence base have been long-standing controversial issues in the EU. As a response, transparency and inclusiveness became a major focus of regulatory science activities in the GMO impact area. Nevertheless, nearly three decades of controversies resulted in a heavily polarized policy environment, calling for further efforts. Against this backdrop the EU funded project GRACE explored the value of evidence synthesis approaches for GMO impact assessment and developed an evidence synthesis framework with a strong emphasis on openness, stakeholder engagement, transparency, and responsiveness to tackle regulatory science challenges. This framework was tested and implemented in the course of 14 systematic reviews or maps conducted on selected review questions spanning potential health, environmental, and socioeconomic impacts of GMOs. An inclusive development and prioritisation of review questions is of key importance in evidence synthesis as it helps to provide a better link between stakeholder demands and concerns and policy relevant outcomes. This paper, therefore, places a particular focus on the stakeholder involvement strategy developed and experiences gathered during this particular step in the course of the GRACE project. Based on this experience, possible lessons for future engagement exercises in highly controversial fields of regulatory science are discussed.

<https://environmentalevidencejournal.biomedcentral.com/articles/10.1186/s13750-017-0113-z>

**please pay attention to:**

New Research Topic in *Frontiers Plant Science*

**Plant Genome Editing – Policies and Governance**

The homepage of the Research Topic can be found by following this link:

<https://www.frontiersin.org/research-topics/7596/plant-genome-editing---policies-and-governance>

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Niu L. et al. (2018): **Transgenic Bt cotton expressing Cry1Ac/Cry2Ab or Cry1Ac/EPSPS does not affect the plant bug *Adelphocoris suturalis* or the pollinating beetle *Haptoncus luteolus***. *Environmental Pollution* 234 (2018) 788e793,  
<https://doi.org/10.1016/j.envpol.2017.11.047>

The widespread cultivation of transgenic Bt cotton makes assessing the potential effects of this recombinant crop on non-target organisms a priority. However, the effect of Bt cotton on many insects is currently virtually unknown. The plant bug *Adelphocoris suturalis* is now a major pest of cotton in southern China and the beetle *Haptoncus luteolus* is one of the most ancient cotton pollinators. We conducted laboratory experiments to evaluate the toxicity of the Bt cotton varieties ZMSJ, which expresses the toxins Cry1Ac and Cry2Ab, and ZMKCKC, which expresses Cry1Ac and EPSPS, on adult *A. suturalis* and *H. luteolus*. No significant increase in the mortality of either species was detected after feeding on Bt cotton leaves or pollen for 7 days. Trace amounts of Cry1Ac and Cry2Ab proteins could be detected in both species but in vitro binding experiments found no evidence of Cry1Ac and Cry2Ab binding proteins. These results demonstrate that feeding on the leaves or pollen of these two Bt cotton varieties has no toxic effects on adult *A. suturalis* or *H. luteolus*.

<https://www.sciencedirect.com/science/article/pii/S0269749117329275?via%3Dihub>

Keng-Lou James Hung, Jennifer M. Kingston, Matthias Albrecht, David A. Holway, Joshua R. Kohn. **"The worldwide importance of honey bees as pollinators in natural habitats."** *Proc Royal Soc B* 285: 20172140. Published: 10-January-2018. DOI: 10.1098/rspb.2017.2140

The western honey bee (*Apis mellifera*) is the most frequent floral visitor of crops worldwide, but quantitative knowledge of its role as a pollinator outside of managed habitats is largely lacking. Here we use a global dataset of 80 published plant–pollinator interaction networks as well as pollinator effectiveness measures from 34 plant species to assess the importance of *A. mellifera* in natural habitats. *Apis mellifera* is the most frequent floral visitor in natural habitats worldwide, averaging 13% of floral visits across all networks (range 0–85%), with 5% of plant species recorded as being exclusively visited by *A. mellifera*. For 33% of the networks and 49% of plant species, however, *A. mellifera* visitation was never observed, illustrating that many flowering plant taxa and assemblages remain dependent on non-*A. mellifera* visitors for pollination. *Apis mellifera* visitation was higher in warmer, less variable climates and on mainland rather than island sites, but did not differ between its native and introduced ranges. With respect to single-visit pollination effectiveness, *A. mellifera* did not differ from the average non-*A. mellifera* floral visitor, though it was generally less effective than the most effective non-*A. mellifera* visitor. Our results argue for a deeper understanding of how *A. mellifera*, and potential future changes in its range and abundance, shape the ecology, evolution, and conservation of plants, pollinators, and their interactions in natural habitats.

<http://rspb.royalsocietypublishing.org/content/285/1870/20172140>

Koller T., Brunner S., Herren G., Hurni S. and Keller B. (2018): **Pyramiding of transgenic Pm3 alleles in wheat results in improved powdery mildew resistance in the field.** *Theoretical and Applied Genetics* (2018). DOI: [10.1007/s00122-017-3043-9](https://doi.org/10.1007/s00122-017-3043-9)

Allelic Pm3 resistance genes of wheat confer race-specific resistance to powdery mildew (*Blumeria graminis* f. sp. *tritici*, Bgt) and encode nucleotide-binding domain, leucine-rich repeat (NLR) receptors. Transgenic wheat lines overexpressing alleles Pm3a, b, c, d, f, and g have previously been generated by transformation of cultivar Bobwhite and tested in field trials, revealing varying degrees of powdery mildew resistance conferred by the transgenes. Here, we tested four transgenic lines each carrying two pyramided Pm3 alleles, which were generated by crossbreeding of lines transformed with single Pm3 alleles. All four allele-pyramided lines showed strongly improved powdery mildew resistance in the field compared to their parental lines. The improved resistance results from the two effects of enhanced total transgene expression levels and allele-specificity combinations. In contrast to leaf segment tests on greenhouse-grown seedlings, no allelic suppression was observed in the field. Plant development and yield scores of the pyramided lines were similar to the mean scores of the corresponding parental lines, and thus, the allele pyramiding did not cause any negative effects. On the contrary, in pyramided line, Pm3b × Pm3f normal plant development was restored compared to the delayed development and reduced seed set of parental line Pm3f. Allele-specific RT qPCR revealed additive transgene expression levels of the two Pm3 alleles in the pyramided lines. A positive correlation between total transgene expression level and powdery mildew field resistance was observed. In summary, allele pyramiding of Pm3 transgenes proved to be successful in enhancing powdery mildew field resistance. <https://link.springer.com/content/pdf/10.1007%2Fs00122-017-3043-9.pdf>

and PLOS: Combination of resistance genes offers better protection for wheat against powdery mildew

<https://phys.org/news/2018-01-combination-resistance-genes-wheat-powdery.html#jCp>

Barbado C., Córdoba-Cañero D, Ariza R.R., and Teresa Roldán-Arjona T. (2018): **Non-enzymatic release of N7-methylguanine channels repair of abasic sites into an AP-endonuclease independent pathway in Arabidopsis.** *Proc Natl Acad Sci*,115: 201719497. doi: 10.1073/pnas.1719497115.

Abasic (apurinic/aprimidinic, AP) sites in DNA arise from spontaneous base loss or by enzymatic removal during base excision repair. It is commonly accepted that both classes of AP site have analogous biochemical properties and are equivalent substrates for AP endonucleases and AP lyases, although the relative roles of these two types of enzymes are not well understood. We provide here genetic and biochemical evidence that, in *Arabidopsis*, AP sites generated by spontaneous loss of N7-methylguanine (N7-meG) are exclusively repaired through an AP endonuclease-independent pathway initiated by FPG, a bifunctional DNA glycosylase with AP lyase activity. Abasic site incision catalyzed by FPG generates a single-nucleotide gap with a 3'-phosphate terminus that is processed by the DNA 3'-phosphatase ZDP before repair is completed. We further show that the major AP endonuclease in *Arabidopsis* (ARP) incises AP sites generated by enzymatic N7-meG excision but, unexpectedly, not those resulting from spontaneous N7-meG loss. These findings, which reveal previously undetected differences between products of enzymatic and nonenzymatic base release, may shed light on the evolution and biological roles of AP endonucleases and AP lyases.

<https://www.ncbi.nlm.nih.gov/pubmed/29339505>

and

Researchers disprove one of the most widespread assumptions among geneticists regarding DNA

<https://phys.org/news/2018-01-widespread-assumptions-geneticists-dna.html#jCp>

Peng Wang P. et al. (2017): **Thermo-triggered Release of CRISPR-Cas9 System by Lipid-Encapsulated Gold Nanoparticles for Tumor Therapy,** *Angewandte Chemie International Edition* . DOI: [10.1002/anie.201708689](https://doi.org/10.1002/anie.201708689)

CRISPR/Cas9 system is a powerful toolbox for gene editing. However, the low delivery efficiency is still a big hurdle impeding its applications. Herein, we report a strategy to deliver Cas9-sgPlk-1 plasmids (CP) by a multifunctional vehicle for tumor therapy. We condensed CPs on TAT peptide-modified Au nanoparticles (AuNPs/CP, ACP) via electrostatic interactions, and coated lipids (DOTAP, DOPE, cholesterol, PEG2000-DSPE) on the ACP to form lipid-encapsulated, AuNPs-condensed CP (LACP). LACP can enter tumor cells and release CP into the cytosol by laser-triggered thermo-effects of the AuNPs; the CP can enter nuclei by TAT guidance, enabling effective knock-outs of target gene (*Plk-1*) of tumor (melanoma) and inhibition of the tumor both in vitro and in vivo. This AuNPs-condensed, lipid-encapsulated, and laser-controlled delivery system provides a versatile method for high efficiency CRISPR/Cas9 delivery and targeted gene editing for treatment of a wide spectrum of diseases.

<http://onlinelibrary.wiley.com/doi/10.1002/anie.201708689/abstract;jsessionid=286053F8F5D9F09DB884EBCD0F83D194.f04t01?systemMessage=Please+be+advised+that+we+experienced+an+unexpected+issue+that+occurred+on+Saturday+and+Sunday+January+20th+and+21>

[st+that+caused+the+site+to+be+down+for+an+extended+period+of+time+and+affected+the+ability+of+users+to+access+content+on+Wiley+Online+Library.+This+issue+has+now+been+fully+resolved.+We+apologize+for+any+inconvenience+this+may+have+caused+and+are+working+to+ensure+that+we+can+alert+you+immediately+of+any+unplanned+periods+of+downtime+or+disruption+in+the+future.](#)

and

Thermo-triggered release of a genome-editing machinery by modified gold nanoparticles for tumor therapy  
<https://phys.org/news/2018-01-thermo-triggered-genome-editing-machinery-gold-nanoparticles.html#Cp>

Sociale M., Wulf A.-L., Breiden B., Klee, K., Thielisch M., Eckardt F., Sellin J., Bülow M.-H., Löbber S., Weinstock N., Voelzmann A., Schultze J., Sandhoff K. und Bauer R. (2018):  
**Ceramide Synthase Schlank Is a Transcriptional Regulator Adapting Gene Expression to Energy Requirements**; Cell Reports 22, S. 1–12, DOI: 10.1016/j.celrep.2017.12.090

Maintenance of metabolic homeostasis requires adaption of gene regulation to the cellular energy state via transcriptional regulators. Here, we identify a role of ceramide synthase (CerS) Schlank, a multiple transmembrane protein containing a catalytic lag1p motif and a homeodomain, which is poorly studied in CerSs, as a transcriptional regulator. ChIP experiments show that it binds promoter regions of lipases *lipase3* and *magro* via its homeodomain. Mutation of nuclear localization site 2 (NLS2) within the homeodomain leads to loss of DNA binding and deregulated gene expression, and NLS2 mutants can no longer adjust the transcriptional response to changing lipid levels. This mechanism is conserved in mammalian CerS2 and emphasizes the importance of the CerS protein rather than ceramide synthesis. This study demonstrates a double role of CerS Schlank as an enzyme and a transcriptional regulator, sensing lipid levels and transducing the information to the level of gene expression.

[http://www.cell.com/cell-reports/abstract/S2211-1247\(17\)31927-7](http://www.cell.com/cell-reports/abstract/S2211-1247(17)31927-7)

pdf-file: [http://www.cell.com/cell-reports/pdf/S2211-1247\(17\)31927-7.pdf](http://www.cell.com/cell-reports/pdf/S2211-1247(17)31927-7.pdf)

Nowoshilow S. et al. (2018): **The axolotl genome and the evolution of key tissue formation regulators**. Nature, doi: [10.1038/nature25458](https://doi.org/10.1038/nature25458).

Salamanders serve as important tetrapod models for developmental, regeneration and evolutionary studies. An extensive molecular toolkit makes the Mexican axolotl (*Ambystoma mexicanum*) a key representative salamander for molecular investigations. Here we report the sequencing and assembly of the 32-gigabase-pair axolotl genome using an approach that combined long-read sequencing, optical mapping and development of a new genome assembler (MARVEL). We observed a size expansion of introns and intergenic regions, largely attributable to multiplication of long terminal repeat retroelements. We provide evidence that intron size in developmental genes is under constraint and that species-restricted genes may contribute to limb regeneration. The axolotl genome assembly does not contain the essential developmental gene *Pax3*. However, mutation of the axolotl *Pax3* paralogue *Pax7* resulted in an axolotl phenotype that was similar to those seen in *Pax3*<sup>-/-</sup> and *Pax7*<sup>-/-</sup> mutant mice. The axolotl genome provides a rich biological resource for developmental and evolutionary studies.

<https://www.nature.com/articles/nature25458>

pdf-file: <https://www.nature.com/articles/nature25458.pdf>

Markus Alexander Grohme M. A. et al. (2018): **Schmidtea mediterranea and the evolution of core cellular mechanisms**. Nature; 24 January, 2018 (DOI: 10.1038/nature25473)

The planarian *Schmidtea mediterranea* is an important model for stem cell research and regeneration, but adequate genome resources for this species have been lacking. Here we report a highly contiguous genome assembly of *S. mediterranea*, using long-read sequencing and a *de novo* assembler (MARVEL) enhanced for low-complexity reads. The *S. mediterranea* genome is highly polymorphic and repetitive, and harbours a novel class of giant retroelements. Furthermore, the genome assembly lacks a number of highly conserved genes, including critical components of the mitotic spindle assembly checkpoint, but planarians maintain checkpoint function. Our genome assembly provides a key model system resource that will be useful for studying regeneration and the evolutionary plasticity of core cell biological mechanisms.

<https://www.nature.com/articles/nature25473>

pdf-file: <https://www.nature.com/articles/nature25473.pdf>

Byrne RP, Martiniano R, Cassidy LM, Carrigan M, Hellenthal G, Hardiman O, et al. (2018) Insular Celtic population structure and genomic footprints of migration. *PLoS Genet* 14(1): e1007152. [doi.org/10.1371/journal.pgen.1007152](https://doi.org/10.1371/journal.pgen.1007152)

Previous studies of the genetic landscape of Ireland have suggested homogeneity, with population substructure undetectable using single-marker methods. Here we have harnessed the haplotype-based method fineSTRUCTURE in an Irish genome-wide SNP dataset, identifying 23 discrete genetic clusters which segregate with geographical provenance. Cluster diversity is pronounced in the west of Ireland but reduced in the east where older structure has been eroded by historical migrations. Accordingly, when populations from the neighbouring island of Britain are included, a west-east cline of Celtic-British ancestry is revealed along with a

particularly striking correlation between haplotypes and geography across both islands. A strong relationship is revealed between subsets of Northern Irish and Scottish populations, where discordant genetic and geographic affinities reflect major migrations in recent centuries. Additionally, Irish genetic proximity of all Scottish samples likely reflects older strata of communication across the narrowest inter-island crossing. Using GLOBETROTTER we detected Irish admixture signals from Britain and Europe and estimated dates for events consistent with the historical migrations of the Norse-Vikings, the Anglo-Normans and the British Plantations. The influence of the former is greater than previously estimated from Y chromosome haplotypes. In all, we paint a new picture of the genetic landscape of Ireland, revealing structure which should be considered in the design of studies examining rare genetic variation and its association with traits.

<http://journals.plos.org/plosgenetics/article/file?id=10.1371/journal.pgen.1007152&type=printable>  
and

<https://phys.org/news/2018-01-historical-migrations-left-genetic-footprints.html#jCp>

Ledford H. (2018) **The lost art of looking at plants** - Advances in genomics and imaging are reviving a fading discipline. *Nature* 553, 396-398

<https://www.nature.com/articles/d41586-018-01075-5>

Janiak M.C., Chaney M.E, and Tosi A.J. (2017): **Evolution of Acidic Mammalian Chitinase Genes (CHIA) Is Related to Body Mass and Insectivory in Primates**. *Molecular Biology and Evolution*. msx312, <https://doi.org/10.1093/molbev/msx312>

Insects are an important food resource for many primates, but the chitinous exoskeletons of arthropods have long been considered to be indigestible by the digestive enzymes of most mammals. However, recently mice and insectivorous bats were found to produce the enzyme acidic mammalian chitinase (AMCase) to digest insect exoskeletons. Here, we report on the gene *CHIA* and its paralogs, which encode AMCase, in a comparative sample of nonhuman primates. Our results show that early primates likely had three *CHIA* genes, suggesting that insects were an important component of the ancestral primate diet. With some exceptions, most extant primate species retain only one functional *CHIA* paralog. The exceptions include two colobine species, in which all *CHIA* genes have premature stop codons, and several New World monkey species that retain two functional genes. The most insectivorous species in our sample also have the largest number of functional *CHIA* genes. *Tupaia chinensis* and *Otolemur garnettii* retain three functional *CHIA* paralogs, whereas *Tarsius syrichta* has a total of five, two of which may be duplications specific to the tarsier lineage. Selection analyses indicate that *CHIA* genes are under more intense selection in species with higher insect consumption, as well as in smaller-bodied species (<500 g), providing molecular support for Kay's Threshold, a well-established component of primatological theory which proposes that only small primates can be primarily insectivorous. These findings suggest that primates, like mice and insectivorous bats, may use the enzyme AMCase to digest the chitin in insect exoskeletons, providing potentially significant nutritional benefits.

<https://academic.oup.com/mbe/advance-article/doi/10.1093/molbev/msx312/4693806>

and

Study says humans can digest bugs, assuming they want to

<https://phys.org/news/2018-01-humans-digest-bugs-assuming.html#jCp>

Manuel Delgado-Baquerizo M. et al. (2018): **A global atlas of the dominant bacteria found in soil**. *Science* 359, Issue 6373, 320-325 DOI: 10.1126/science.aap9516

The immense diversity of soil bacterial communities has stymied efforts to characterize individual taxa and document their global distributions. We analyzed soils from 237 locations across six continents and found that only 2% of bacterial phylotypes (~500 phylotypes) consistently accounted for almost half of the soil bacterial communities worldwide. Despite the overwhelming diversity of bacterial communities, relatively few bacterial taxa are abundant in soils globally. We clustered these dominant taxa into ecological groups to build the first global atlas of soil bacterial taxa. Our study narrows down the immense number of bacterial taxa to a "most wanted" list that will be fruitful targets for genomic and cultivation-based efforts aimed at improving our understanding of soil microbes and their contributions to ecosystem functioning.

<http://science.sciencemag.org/content/359/6373/320>

Doron S. et al., **"Systematic discovery of antiphage defense systems in the microbial pangenome,"** *Science* (2018). *Science* eaar4120; [science.sciencemag.org/cgi/doi/10.1126/science.aar4120](https://science.sciencemag.org/cgi/doi/10.1126/science.aar4120)

The arms race between bacteria and phages led to the development of sophisticated antiphage defense systems, including CRISPR-Cas and restriction-modification systems. Evidence suggests that unknown defense systems are located in "defense islands" in microbial genomes. We comprehensively characterized the bacterial defensive arsenal by examining gene families that are clustered next to known defense genes in prokaryotic genomes. Candidate defense systems were systematically engineered and validated in model bacteria for their antiphage activities. We report nine previously unknown antiphage systems and one antiplasmid system that are widespread in microbes and strongly protect against foreign invaders. These include systems that adopted components of the bacterial flagella and condensin complexes. Our data also

suggest a common, ancient ancestry of innate immunity components shared between animals, plants, and bacteria.

<http://science.sciencemag.org/content/early/2018/01/25/science.aar4120>

De Santis E. et al. Antimicrobial peptide capsids of de novo design, *Nature Communications* (2017). DOI: [10.1038/s41467-017-02475-3](https://doi.org/10.1038/s41467-017-02475-3)

The spread of bacterial resistance to antibiotics poses the need for antimicrobial discovery. With traditional search paradigms being exhausted, approaches that are altogether different from antibiotics may offer promising and creative solutions. Here, we introduce a de novo peptide topology that—by emulating the virus architecture—assembles into discrete antimicrobial capsids. Using the combination of high-resolution and real-time imaging, we demonstrate that these artificial capsids assemble as 20-nm hollow shells that attack bacterial membranes and upon landing on phospholipid bilayers instantaneously (seconds) convert into rapidly expanding pores causing membrane lysis (minutes). The designed capsids show broad antimicrobial activities, thus executing one primary function—they destroy bacteria on contact

<https://www.nature.com/articles/s41467-017-02475-3>

pdf-file: <https://www.nature.com/articles/s41467-017-02475-3.pdf>

and

Synthetic virus to tackle antimicrobial resistance

<https://phys.org/news/2018-01-synthetic-virus-tackle-antimicrobial-resistance.html>

#### **EFSA:**

**New uncertainty approach to make advice ‘more transparent and robust’**

<http://www.efsa.europa.eu/en/press/news/180124-0>

#### **Ankündigung:**

Ministerium für Ländlichen Raum und Verbraucherschutz Baden-Württemberg  
Informations- und Diskussionsveranstaltung mit Minister Hauck zu “Neuen  
Züchtungsmethoden – Grundsätzliches, Nutzpflanzen, Nutztiere“

Stuttgart Innenministerium Raum E001 Willy-Brandt-Straße 41

9. April 2018, 14:00 – 18:00

Auskünfte: [astrid.fleischer@mlr.bwl.de](mailto:astrid.fleischer@mlr.bwl.de)

Wie immer wird für Hinweise und der Zusendung von Publikationen und sonstigen Informationen gedankt. Pdf-files 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). Sie finden hier 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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