

Sunday Evening News

Week 15 (2018-04-09 / 04-15)

Selected and edited by **BGF** Jany

Sehr geehrte Kollegen und Kolleginnen, liebe Freunde und Mitstreiter,

das neue Grundsatzprogramm der Partei Bündnis90/Die Grünen und ihr Überdenken der grundsätzlichen Ablehnung der Grünen Gentechnik sowie der Vorschlag EU-Kommission zu mehr Transparenz bei der Sicherheitsbewertung von Organismen und Lebensmitteln bildeten diese Woche den Schwerpunkt der Berichterstattung in den Medien.

Ersteres ist sicher lohnenswert, aber es allerdings bei dieser Partei gelingt, bleibt abzuwarten.

Der Kommissionsentwurf enthält einige richtige Ansätze, aber falls er so umgesetzt wird, bedeutet dies eine Schwächung der EFSA und einen größeren politischen Einfluss auf die EFSA und auf die Ergebnisse ihrer Stellungnahmen.

Dear all,

The planned new political basic program of green party Bündnis 90/Die Grünen and their rethinking of a fundamental rejection of GMOs (genetical engineering) and the EU Commission's proposal for more transparency in the safety assessment of organisms and foods were the focus of media this week.

The former is certainly commendable, but it remains to be seen at this party and their members, respectively.

The Commission's proposal contains some correct approaches, but if so implemented, it will weaken EFSA and will have a greater political impact on EFSA and the outcome of its opinions.

Bündnis90/Die Grünen – Green Party

Spiegel-online: **Grünen-Spitze will "vierte Phase" der Partei einläuten**

Die Grünen schreiben ein neues Programm, den Startschuss geben die Vorsitzenden: Annalena Baerbock und Robert Habeck wollen eine neue Ära einleiten - und stellen dafür auch alte Überzeugungen infrage.

Einen ganzen Absatz widmen sie auch der **Wissenschaft**. Der ist überraschend und neu: Die Vorsitzenden wollen ihre Position zum Einsatz der **Gentechnik** in der Landwirtschaft hinterfragen. Man müsse sich überlegen, ob neue Technologien nicht auch helfen könnten, die Versorgung mit Nahrungsmitteln gerade dort zu garantieren, wo Klimawandel für immer weniger Regen Sorge. Man wolle auch über den Einsatz von Gentechnik zur Bekämpfung von Krankheiten eine "offene und faire" Debatte führen.

Für die Grünen eine radikale Überlegung, weit von ihren sonst sehr konservativen Positionen beim Thema Gentechnik entfernt.

<http://www.spiegel.de/politik/deutschland/robert-habeck-und-annalena-baerbock-laeuten-neue-phase-der-gruenen-ein-a-1201885.html>

EU-Commission

Grefe C. – Zeit-online: **Die EU hat ein bisschen was aus Glyphosat gelernt**

Vertrauen bilden nach dem Glyphosat-Drama: Die Bewertung von Unkrautvernichtern oder genverändertem Saatgut wird transparenter. Ohne Bürgerdruck wäre das nicht passiert.

Die EFSA soll zwar ihre wissenschaftliche Unabhängigkeit bewahren, aber künftig durch Vertreterinnen und Vertreter der Mitgliedsstaaten in ihrer Geschäftsleitung stärker politisch kontrolliert werden.

<http://www.zeit.de/wissen/umwelt/2018-04/risikobewertung-glyphosat-eu-kommission-landwirtschaft-bayer-monsanto/komplettansicht>

Kelly E.: **EU wants to be more open on industry influence in food safety cases**

Proposal follows public concern over reapproval of controversial weedkiller glyphosate

The European Commission has set out a plan to boost transparency around industry-led studies on food safety, in a move to avoid controversy such as that which followed the approval of the controversial weedkiller glyphosate last year.

<https://sciencebusiness.net/news/eu-wants-be-more-open-industry-influence-food-safety-cases>

European Commission – Press release

Commission acts to boost trust in scientific studies on food safety

http://europa.eu/rapid/press-release_IP-18-2941_en.htm

European Commission – Fact Sheet

Commission's proposal on transparency and sustainability of the EU risk assessment model in the food chain

http://europa.eu/rapid/press-release_MEMO-18-2942_en.htm

Proposal for a REGULATION OF THE EUROPEAN PARLIAMENT AND OF THE COUNCIL on the transparency and sustainability of the EU risk assessment in the food chain amending Regulation (EC) No 178/2002 [on general food law], Directive 2001/18/EC [on the deliberate release into the environment of GMOs], Regulation (EC) No 1829/2003 [on GM food and feed], Regulation (EC) No 1831/2003 [on feed additives], Regulation (EC) No 2065/2003 [on smoke flavourings], Regulation (EC) No 1935/2004 [on food contact materials], Regulation (EC) No 1331/2008 [on the common authorisation procedure for food additives, food enzymes and food flavourings], Regulation (EC) No 1107/2009 [on plant protection products] and Regulation (EU) No 2015/2283 [on novel foods]

https://ec.europa.eu/food/sites/food/files/gfl_transparency_comm_proposal_20180410_en.pdf

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

Scientific papers:

The economics and politics of GM food labeling

edited by Jill McCluskey and Justus Wesseler

Labelling of food products is widely used and covers a wide range of food attributes. Some labels are mandatory, and some are voluntary. Food producers, processors, and retailers use them either to comply with mandatory food standards or for voluntary product differentiation. The use of food labels is not costless and has implications on the distribution of benefits and costs along the food supply chain. One controversial food labeling policies is the labeling of genetically modified organisms (GMOs). The European Union (EU) among others has a mandatory GMO labeling policy for food products, while the United States passed a law in 2016 that will go into effect in the near future. Voluntary labeling standards for GMO-free food products have been simultaneously developed by the private sector. Lately, GMO-free labeling of food products in the European Union and the United States has increased. The standards are not homogeneous across countries and food products, which can cause disruption in national and international food supply chains.

This special issue addresses GM food labeling policies by the private and public sector from an economic perspective. Important issues addressed include: The potential economic consequences of the mandatory labeling of GMO food products in the United States, the European Union, and other regions for the food supply chain and final food consumers; and drivers and economic implications of GMO-free labeling on the food supply chain in the European Union, the United States and other regions.

This special issue provides an authoritative review of current thinking and debates on GM labeling and discusses the implications for food policies

<https://www.sciencedirect.com/science/article/pii/S0306919218301027>

Papers of the special issue:

McCluskey Wesseler Winfree: [The economics and politics of GM food labeling: An introduction to the special issue.](#)

Zilberman Kaplan Gordon: [The political economy of labeling](#)

Bovay Alston: [GMO food labels in the United States: Economic implications of the new law](#)

Castellari Soregaroli Venus Wesseler: [Food processor and retailer non-GMO standards in the US and EU and the driving role of regulations](#)

Kalaitzandonakes Lusk Magnier: [The price of non-genetically modified \(non-GM\) food](#)

Dolgoplova Roosen: [Competitive niche in milk pricing: Analyzing price dynamics of GMO-free, organic, and conventional milk in Germany during 2009–2010](#)

Venus Drabik Wesseler: [The role of a German multi-stakeholder standard for livestock products derived from non-GMO feed](#)

Ghozzi Platoni Tillie Soregaroli: [TCE determinants and governance forms in the EU “non-GMO” soybean supply chain](#)

Lusk McFadden Wilson: [Do consumers care how a genetically engineered food was created or who created it?](#)

Delmond McCluskey Yormirzoev Rogova: [Russian consumer willingness to pay for genetically modified food](#)

For reprints - pdf-files, please contact colleague Justus Wesseler (Justus.wesseler@wur.nl)

Pechar E., Bernauer T, Mayer F. (2018): Beyond Political Ideology: The Impact of Attitudes Towards Government and Corporations on Trust in Science

Understanding public distrust of science is both theoretically and practically important. While previous research has focused on the association between political ideology and trust in science, it is at best an inconsistent predictor. This study demonstrates that two dimensions of political ideology—attitudes towards governments and corporations—can more precisely predict trust in science across issues. Using a survey in the United States and Germany on the science of climate change and genetically modified foods, we find that an individual’s trust in science varies across issues and that attitudes towards government and corporations are important predictors of this trust.

<http://journals.sagepub.com/doi/pdf/10.1177/1075547018763970>

Herman R. A., Fast B. J., Mathesius C. and Delaney B. (2018): Isoline use in crop composition studies with genetically modified crops under EFSA guidance. Regulatory Toxicology and Pharmacology 95 (2018) 204–206, <https://doi.org/10.1016/j.vrtph.2018.03.022>

The European [Food Safety](#) Authority (EFSA) oversees the safety evaluation of genetically modified (GM) crops in the European Union. EFSA requires inclusion of commercial non-GM reference lines and a non-GM isoline in crop composition studies with GM crops. Reference lines are used to construct equivalence limits for each compositional analyte. Results for the GM line are compared with these equivalence limits to assess compositional equivalence between the GM crop and the non-GM crop. If compositional equivalence cannot be concluded from this comparison, then results for the non-GM isoline can be used to determine if this finding is likely the result of the background non-GM genetics of the GM crop. If this latter comparison is not sufficient to assess the compositional safety of the GM crop, then a biological-relevance assessment for the analytes in question can be completed taking into account the greater body of knowledge of composition for the crop and diets. Thus, the isoline is a useful comparator but not required to assess the compositional safety of the GM crop, and therefore, unavoidable [genotype](#) differences between the isoline and GM line should not be grounds for rejection of compositional studies where the biological relevance of potential non-equivalence is addressed. https://ac.els-cdn.com/S0273230018300953/1-s2.0-S0273230018300953-main.pdf?_tid=6323f23c-6e97-4d21-b4b6-3fe1a63d50&acdnat=1523264120_149c1b0ca39ff173395dd560b1808047

Vezzani S. The International Regulatory Framework for the Use of GMOs and Products Thereof as Food Aid. European Journal of Risk Regulation 9 (2018), 120–136; doi:10.1017/err.2017.58

https://www.cambridge.org/core/services/aop-cambridge-core/content/view/26A0D1E88E47C0DE168DD25EC6652D0A/S1867299X17000587a.pdf/international_regulatory_framework_for_the_use_of_gmos_and_products_thereof_as_food_aid.pdf

Mark Lynas

Seeds of Science - Why We Got It So Wrong On GMOs

<https://www.bloomsbury.com/uk/seeds-of-science-9781472946959/>

<http://www.marklynas.org/2018/04/5-april-2018-seeds-of-science-published-in-the-uk/>

Raybould A and Macdonald P (2018): Policy-Led Comparative Environmental Risk Assessment of Genetically Modified Crops: Testing for Increased Risk Rather Than Profiling Phenotypes Leads to Predictable and Transparent Decision-Making. Front. Bioeng. Biotechnol. 6: 43. doi: 10.3389/fbioe.2018.00043

We describe two contrasting methods of comparative environmental risk assessment for genetically modified (GM) crops. Both are science-based, in the sense that they use science to help make decisions, but they differ in the relationship between science and policy. Policy-led comparative risk assessment begins by defining what would be regarded as unacceptable changes when the use a particular GM crop replaces an accepted use of another crop. Hypotheses that these changes will not occur are tested using existing or new data, and corroboration or falsification of the hypotheses is used to inform decision-making. Science-led comparative risk

assessment, on the other hand, tends to test null hypotheses of no difference between a GM crop and a comparator. The variables that are compared may have little or no relevance to any previously stated policy objective and hence decision-making tends to be *ad hoc* in response to possibly spurious statistical significance. We argue that policy-led comparative risk assessment is the far more effective method. With this in mind, we caution that phenotypic profiling of GM crops, particularly with omics methods, is potentially detrimental to risk assessment.

<https://www.frontiersin.org/articles/10.3389/fbioe.2018.00043/full>

Laura E. Dixon L.E. et al. (2018): *TEOSINTE BRANCHED1* Regulates Inflorescence Architecture and Development in Bread Wheat (*Triticum aestivum* L.) Plant Cell; DOI:

<https://doi.org/10.1105/tpc.17.00961>

The flowers of major cereals are arranged on reproductive branches known as spikelets, which group together to form an inflorescence. Diversity for inflorescence architecture has been exploited during domestication to increase crop yields, and genetic variation for this trait has potential to further boost grain production. Multiple genes that regulate inflorescence architecture have been identified by studying alleles that modify gene activity or dosage; however, little is known in wheat. Here, we show *TEOSINTE BRANCHED1* (*TB1*) regulates inflorescence architecture in bread wheat (*Triticum aestivum* L.) by investigating lines that display a form of inflorescence branching known as 'paired spikelets'. We show that *TB1* interacts with *FLOWERING LOCUS T1*, and that increased dosage of *TB1* alters inflorescence architecture and growth rate in a process that includes reduced expression of meristem identity genes, with allelic diversity for *TB1* found to associate genetically with paired spikelet development in modern cultivars. We propose *TB1* coordinates formation of axillary spikelets during the vegetative to floral transition, and that alleles known to modify dosage or function of *TB1* could help increase wheat yields.

<http://www.plantcell.org/content/plantcell/early/2018/02/14/tpc.17.00961.full.pdf>

Camargo A.M., Andow D.A., Castañera P.1 & Farinós G.P. (2018): **First detection of a *Sesamia nonagrioides* resistance allele to Bt maize in Europe.** Scientific Reports 8:3977 | DOI:10.1038/s41598-018-21943-4

The Ebro Valley (Spain) is the only hotspot area in Europe where resistance evolution of target pests to Cry1Ab protein is most likely, owing to the high and regular adoption of Bt maize (>60%). The high-dose/refuge (HDR) strategy was implemented to delay resistance evolution, and to be effective it requires the frequency of resistance alleles to be very low (<0.001). An F2 screen was performed in 2016 to estimate the frequency of resistance alleles in *Sesamia nonagrioides* from this area and to evaluate if the HDR strategy is still working effectively. Out of the 137 isofemale lines screened on Cry1Ab maize leaf tissue, molted larvae and extensive feeding were observed for two consecutive generations in one line, indicating this line carried a resistance allele. The frequency of resistance alleles in 2016 was 0.0036 (CI 95% 0.0004–0.0100), higher but not statistically different from the value obtained in 2004–2005. Resistance does not seem to be evolving faster than predicted by a *S. nonagrioides* resistance evolution model, but the frequency of resistance is now triple the value recommended for an effective implementation of the HDR strategy. Owing to this, complementary measures should be considered to further delay resistance evolution in the Ebro Valley.

<https://www.nature.com/articles/s41598-018-21943-4>

Zhang C.-J et al. (2018): **Evaluation of maximum potential gene flow from herbicide resistant *Brassica napus* to its male sterile relatives under open and wind pollination conditions.** Science of the Total Environment 634 (2018) 821–830;

<https://doi.org/10.1016/j.scitotenv.2018.03.390>

Pollen-mediated gene flow (PMGF) from genetically modified (GM) *Brassica napus* to its wild relatives by wind and insects is a major ecological concern in agricultural ecosystems. This study conducted is to estimate maximum potential gene flow and differentiate between wind- and bee-mediated gene flows from herbicide resistant (HR) *B. napus* to its closely-related male sterile (MS) relatives, *B. napus*, *B. juncea* and *Raphanus sativus*. Various markers, including pods formation in MS plants, herbicide resistance, and SSR markers, were used to identify the hybrids. Our results revealed the following: 1) maximum potential gene flow (a maximum % of the progeny of pollen recipient confirmed hybrid) to MS *B. napus* ranged from 32.48 to 0.30% and from 14.69 to 0.26% at 2–128m from HR *B. napus* under open and wind pollination conditions, respectively, and to MS *B. juncea* ranged from 21.95 to 0.24% and from 6.16 to 0.16%, respectively; 2) estimates of honeybee-mediated gene flow decreased with increasing distance from HR *B. napus* and ranged from 17.78 to 0.03% at 2–128 m for MS *B. napus* and from 15.33 to 0.08% for MS *B. juncea*; 3) a small-scale donor plots would strongly favour insect overwind pollination; 4) no gene flow occurred from HR *B. napus* to MS *R. sativus*. Our approach and findings are helpful in understanding the relative contribution of wind and bees to gene flow and useful for estimating maximum potential gene flow and managing environmental risks associated with gene flow

<https://www.sciencedirect.com/science/article/pii/S0048969718311501> pdf-file available

Colombo S.M., Campbell L.G., Murphy E.J., Sara L. Martin S.L. and Arts M.T. (2018): **Potential for novel production of omega-3 long-chain fatty acids by genetically engineered oilseed plants to alter terrestrial ecosystem dynamics**. *Agricultural Systems* 164, 31-37 ; <https://doi.org/10.1016/j.agsy.2018.03.004>

Two bioactive omega-3, long-chain, fatty acids (EPA and DHA), found in algal and fish oils, can now be produced in genetically engineered (GE) terrestrial oilseed crops. These fatty acids are involved in key physiological functions in invertebrates and vertebrates. They are known to be synthesized by primary producers in aquatic ecosystems, but not by terrestrial crop plants. Thus, the production of EPA and DHA by GE seed oil crops represents a fundamental shift in the accessibility of bioactive fatty acids to terrestrial consumers; one that may change their physiology and survival thereby altering ecological interactions among terrestrial organisms. Here we discuss the potential ecological and evolutionary consequences of the novel production of EPA and DHA by GE oilseed crops.

<https://www.sciencedirect.com/science/article/pii/S0308521X17306650?via%3Dihub> pdf-file available

Sadhu M. J. et al.: **Highly parallel genome variant engineering with CRISPR–Cas9**. *Nature Genetics* 50, 510–514 (2018) [nature.com/articles/doi:10.1038/s41588-018-0087-y](https://www.nature.com/articles/doi:10.1038/s41588-018-0087-y)

Understanding the functional effects of DNA sequence variants is of critical importance for studies of basic biology, evolution, and medical genetics; however, measuring these effects in a high-throughput manner is a major challenge. One promising avenue is precise editing with the CRISPR–Cas9 system, which allows for generation of DNA double-strand breaks (DSBs) at genomic sites matching the targeting sequence of a guide RNA (gRNA). Recent studies have used CRISPR libraries to generate many frameshift mutations genome wide through faulty repair of CRISPR-directed breaks by nonhomologous end joining (NHEJ)¹. Here, we developed a CRISPR-library-based approach for highly efficient and precise genome-wide variant engineering. We used our method to examine the functional consequences of premature-termination codons (PTCs) at different locations within all annotated essential genes in yeast. We found that most PTCs were highly deleterious unless they occurred close to the 3' end of the gene and did not affect an annotated protein domain. Unexpectedly, we discovered that some putatively essential genes are dispensable, whereas others have large dispensable regions. This approach can be used to profile the effects of large classes of variants in a high-throughput manner.

<https://www.nature.com/articles/s41588-018-0087-y>

and

University of California, Los Angeles

Scientists tweak CRISPR to speed up genomic editing

<https://phys.org/news/2018-04-scientists-tweak-crispr-genomic.html#jCp>

Conrado C., de Faria Catarina T., Esteban P. & Raposo António R. (2017): **Allergen Management as a Key Issue in Food Safety**

<https://www.taylorfrancis.com/books/e/9781498762885/chapters/10.1201%2F9781315153414-6>

In [Food Safety and Protection](#) editors: V Ravishankar Rai, Jamuna A Bai

<https://www.taylorfrancis.com/books/e/9781498762885>

Yuan, J "Allergenicity Assessment of Genetically Engineered (GE) Crops, GE Food Ingredients, and Non-Thermal Processed Soy Products" (2017). *ETD collection for University of Nebraska - Lincoln*. AAI10683589.

<https://digitalcommons.unl.edu/dissertations/AAI10683589>

Raveendran S. et al. (2018): **Applications of Microbial Enzymes in Food Industry**. *Food Technol. Biotechnol.* 56 (1) 16-30 (2018)

The use of enzymes or microorganisms in food preparations is an age-old process. With the advancement of technology, novel enzymes with wide range of applications and specificity have been developed and new application areas are still being explored. Micro-organisms such as bacteria, yeast and fungi and their enzymes are widely used in several food preparations for improving the taste and texture and they offer huge economic benefits to industries. Microbial enzymes are the preferred source to plants or animals due to several advantages such as easy, cost-effective and consistent production. The present review discusses the recent advancement in enzyme technology for food industries. A comprehensive list of enzymes used in food processing, the microbial source of these enzymes and the wide range of their application are discussed.

<http://ir.niist.res.in:8080/jspui/bitstream/123456789/3024/1/Applications%20of%20Microbial%20Enzymes%20-%20Sindhu%20R%20-%20Food%20technology%20and%20biotechnology.pdf>

Jackson Peter J. et al.: **Genome evolution across 1,011 *Saccharomyces cerevisiae* isolates**, *Nature* (2018) [doi:10.1038/s41586-018-0030-5](https://doi.org/10.1038/s41586-018-0030-5)

Large-scale population genomic surveys are essential to explore the phenotypic diversity of natural populations. Here we report the whole-genome sequencing and phenotyping of 1,011 *Saccharomyces cerevisiae* isolates, which together provide an accurate evolutionary picture of the genomic variants that shape the species-wide phenotypic landscape of this yeast. Genomic analyses support a single 'out-of-China' origin for this species, followed by several independent domestication events. Although domesticated isolates exhibit high variation in ploidy, aneuploidy and genome content, genome evolution in wild isolates is mainly driven by the accumulation of single nucleotide polymorphisms. A common feature is the extensive loss of heterozygosity, which represents an essential source of inter-individual variation in this mainly asexual species. Most of the single nucleotide polymorphisms, including experimentally identified functional polymorphisms, are present at very low frequencies. The largest numbers of variants identified by genome-wide association are copy-number changes, which have a greater phenotypic effect than do single nucleotide polymorphisms. This resource will guide future population genomics and genotype–phenotype studies in this classic model system. <https://www.nature.com/articles/s41586-018-0030-5.pdf>

and

Bob Yirka, Phys.org

Team creates detailed map of genetic evolution of *Saccharomyces cerevisiae*

<https://phys.org/news/2018-04-team-genetic-evolution-saccharomyces-cerevisiae.html#iCp>

Jagannathan M., Cummings R., Yukiko M Yamashita Y.M. (2018): **A conserved function for pericentromeric satellite DNA**. *eLife*, 7 DOI: [10.7554/eLife.34122](https://doi.org/10.7554/eLife.34122)

A universal and unquestioned characteristic of eukaryotic cells is that the genome is divided into multiple chromosomes and encapsulated in a single nucleus. However, the underlying mechanism to ensure such a configuration is unknown. Here we provide evidence that pericentromeric satellite DNA, which is often regarded as junk, is a critical constituent of the chromosome, allowing the packaging of all chromosomes into a single nucleus. We show that the multi AT-hook satellite DNA binding proteins, *D. melanogaster* D1 and mouse HMGA1, play an evolutionarily conserved role in bundling pericentromeric satellite DNA from heterologous chromosomes into 'chromocenters', a cytological association of pericentromeric heterochromatin. Defective chromocenter formation leads to micronuclei formation due to budding from the interphase nucleus, DNA damage and cell death. We propose that chromocenter and satellite DNA serves a fundamental role in encapsulating the full complement of the genome within a single nucleus, the universal characteristic of eukaryotic cells.

<https://elifesciences.org/articles/34122>

Purcell C.M., Seetharam A.S., Snodgrass O., Ortega-García S., Hyde J.R. and Severin J.A. (2018): **Insights into teleost sex determination from the *Seriola dorsalis* genome assembly**. *BMC Genomics* 19,31; . DOI: [10.1186/s12864-017-4403-1](https://doi.org/10.1186/s12864-017-4403-1)

Background: The assembly and annotation of a genome is a valuable resource for a species, with applications ranging from conservation genomics to gene discovery. Genomic resource development is especially important for species in culture, such as the California Yellowtail (*Seriola dorsalis*), the likely candidate for the establishment of commercial offshore aquaculture production in southern California. Genomic resource development for this species will improve the understanding of sex and other phenotypic traits, and allow for rapid increases in genetic improvement for and economic gain in culture production.

Results: We describe the assembly and annotation of the *S. dorsalis* genome, and present resequencing data from 45 male and 45 female wild-caught *S. dorsalis* used to identify a sex-determining region and marker in this species. The genome assembly captured approximately 93% of the total 685 MB genome with an average coverage depth of 180x. Using the assembled genome, resequencing data from the 90 fish were aligned to place boundaries on the sex-determining region. Sex-specific markers were developed based on a female-specific, 61 nucleotide deletion identified in that region. We hypothesize that Estradiol 17-beta-dehydrogenase is the putative sex-determining gene and propose a plausible genetic mechanism for ZW sex determination in *S. dorsalis* involving a female-specific deletion of a transcription factor binding motif that may be targeted by Sox3.

Conclusions: Understanding the mechanism of sex determination and development of assays to determine sex is critical both for management of wild fisheries and for development of efficient and sustainable aquaculture practices. In addition, this genome assembly for *S. dorsalis* will be a substantial resource for a variety of future research applications.

<https://bmcbgenomics.biomedcentral.com/track/pdf/10.1186/s12864-017-4403-1>

and

University of Texas at Austin

How to catch a fish genome with big data

<https://phys.org/news/2018-04-fish-genome-big.html#iCp>

Sajiki K. et al. (2018): **Genetic defects in SAPK signalling, chromatin regulation, vesicle transport and CoA-related lipid metabolism are rescued by rapamycin in fission yeast.**

Open Biology (2018). DOI: [10.1098/rsob.170261](https://doi.org/10.1098/rsob.170261)

Rapamycin inhibits TOR (target of rapamycin) kinase, and is being used clinically to treat various diseases ranging from cancers to fibrodysplasia ossificans progressiva. To understand rapamycin mechanisms of action more comprehensively, 1014 temperature-sensitive (ts) fission yeast (*Schizosaccharomyces pombe*) mutants were screened in order to isolate strains in which the ts phenotype was rescued by rapamycin. Rapamycin-rescued 45 strains, among which 12 genes responsible for temperature sensitivity were identified. These genes are involved in stress-activated protein kinase (SAPK) signalling, chromatin regulation, vesicle transport, and CoA- and mevalonate-related lipid metabolism. Subsequent metabolome analyses revealed that rapamycin upregulated stress-responsive metabolites, while it downregulated purine biosynthesis intermediates and nucleotide derivatives. Rapamycin alleviated abnormalities in cell growth and cell division caused by *sty1* mutants ($\Delta sty1$) of SAPK. Notably, in $\Delta sty1$, rapamycin reduced greater than 75% of overproduced metabolites (greater than 2x WT), like purine biosynthesis intermediates and nucleotide derivatives, to WT levels. This suggests that these compounds may be the points at which the SAPK/TOR balance regulates continuous cell proliferation. Rapamycin might be therapeutically useful for specific defects of these gene functions.

<http://rsob.royalsocietypublishing.org/content/royopenbio/8/3/170261.full.pdf>

and

Okinawa Institute of Science and Technology

Rapamycin resolves genetic defects in yeast

<https://phys.org/news/2018-04-rapamycin-genetic-defects-yeast.html#iCp>

Nghe P., Kogenaru M., Tans S. J. (2018): **Sign epistasis caused by hierarchy within signaling cascades.** Nature Communications 9, article number:1451; DOI: [10.1038/s41467-018-03644-8](https://doi.org/10.1038/s41467-018-03644-8)

Sign epistasis is a central evolutionary constraint, but its causal factors remain difficult to predict. Here we use the notion of parameterised optima to explain epistasis within a signalling cascade, and test these predictions in *Escherichia coli*. We show that sign epistasis arises from the benefit of tuning phenotypic parameters of cascade genes with respect to each other, rather than from their complex and incompletely known genetic bases. Specifically, sign epistasis requires only that the optimal phenotypic parameters of one gene depend on the phenotypic parameters of another, independent of other details, such as activating or repressing nature, position within the cascade, intra-genic pleiotropy or genotype. Mutational effects change sign more readily in downstream genes, indicating that optimising downstream genes is more constrained. The findings show that sign epistasis results from the inherent upstream-downstream hierarchy between signalling cascade genes, and can be addressed without exhaustive genotypic mapping.

<https://www.nature.com/articles/s41467-018-03644-8.pdf>

and

AMOLF

New method predicts evolution

<https://phys.org/news/2018-04-method-evolution.html#iCp>

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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