

# Sunday Evening News No 263

Week 03 (2022-10-17 – 2022-23-01)

Selected and edited by **BGF** Jany

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Das Regierungsprogramm der Ampelkoalition lautet „Mehr Fortschritt wagen“. Im Koalitionsvertrag ist zwar nicht klar beschrieben, was unter „Fortschritt“ zu verstehen ist und wer was wagt. Allerdings scheint der Koalitionspartner, die Partei Bündnis 90/Die Grünen, im Bereich Landwirtschaft, Ernährung und neue Technologien ein etwas seltsames Verständnis von „Mehr Fortschritt wagen“ zu haben.

Das Landwirtschaftsministerium hat ein neues Forschungsprogramm ausgeschrieben:  
**BMEL macht den ökologischen Landbau zu seinem Leitbild für eine nachhaltige Landwirtschaft**

Zwei neue Bekanntmachungen in den Bereichen Pflanzenzüchtung und regionale Bio-Wertschöpfungsketten flankieren dieses Ziel.

<https://www.bmel.de/SharedDocs/Pressemitteilungen/DE/2022/05-oekolandbau-bekanntmachungen.html>

„Die neue Bundesregierung hat den ökologischen Landbau zu ihrem Leitbild für eine nachhaltige Landwirtschaft gemacht. Daher soll die Öko-Landbaufläche bis zum Jahr 2030 auf 30 Prozent ausgeweitet werden. Das **Bundesministerium für Ernährung und Landwirtschaft** flankiert das Flächenziel gleich zu Beginn der Legislaturperiode mit zwei neuen Bekanntmachungen. Gesucht werden innovative Forschungs- und Entwicklungsvorhaben im Bereich Pflanzenzüchtung und im Bereich regionale Bio-Wertschöpfungsketten.

Wichtige Zielsetzungen sind unter anderem eine Steigerung der Flächenerträge, die Verbesserung der Nährstoff- und Wassernutzungseffizienz und die Erhöhung der Stresstoleranz gegenüber biotischen und abiotischen Faktoren.

Daher können Projekte zur Züchtungsmethodik inklusive Phänotypisierung bzw. Verbesserung der Selektionseffizienz oder verbesserte Zuchtmethoden, nicht jedoch gentechnische Verfahren oder Verfahren der Genomeditierung, gefördert werden.

<https://www.bundesprogramm.de/aktuelles/bekanntmachungen>

[https://www.bundesprogramm.de/fileadmin/user\\_upload/BAz\\_AT\\_12.01.2022\\_B5.pdf](https://www.bundesprogramm.de/fileadmin/user_upload/BAz_AT_12.01.2022_B5.pdf)

## **Moderne fortschrittliche Verfahren werden nicht gefördert!**

Dies ist nichts Neues! Siehe auch das geplante und bereits ausgeschriebene Forschungsprogramm in Baden-Württemberg 2020 „Forschungsprogramm Genome Editing – mit Biotechnologie zu einer nachhaltigen Landwirtschaft“. Das Forschungsprogramm wurde durch Ministerpräsident W. Kretschmann auf Druck der grünen Partei gestoppt. (siehe <https://www.biotech-gm-food.com/gruene-frieren-forschungsprogramm-zu-genome-editing-ein>)

Die Ministerin S. Lemke hat sich bereits dezidiert gegen eine Änderung des Gentechnikgesetzes ausgesprochen und fordert, dass die neuen genomischen Techniken pauschal unter das Gentechnikrecht fallen müssen und sogar noch strenger reguliert werden müssen als die klassische Gentechnik.

**Neue Verfahren und Fortschritte in den Möglichkeiten genetischer Veränderungen werden ignoriert und nach Möglichkeit verhindert !**

## **Iser J.C.: Eine "Hausfreundschaft" für die Agrarwende**

Aufbruch statt gegenseitiger Blockade: Umwelt- und Agrarministerium wollen die Landwirtschaft gemeinsam neu ausrichten. Offen ist, wie die Agrarwende bezahlt werden soll.

[https://www.zeit.de/wirtschaft/2022-01/landwirtschaft-cem-oezdemir-steffi-lemke-agrarwende?utm\\_referrer=https%3A%2F%2Fwww.google.de%2F](https://www.zeit.de/wirtschaft/2022-01/landwirtschaft-cem-oezdemir-steffi-lemke-agrarwende?utm_referrer=https%3A%2F%2Fwww.google.de%2F)

Die enge Koordinierung und Zusammenarbeit sind grundsätzlich zu begrüßen. Sie wird letztlich auch Auswirkungen auf das Abstimmungsverhalten Deutschlands bei neuen und fortschrittlichen Technologien und Verfahren bei zulassungspflichtigen Erzeugnissen haben (Komitologieverfahren).

## **BMWi: Habeck und Lemke bekräftigen Kritik an Atomregeln in Taxonomie**

<https://www.bmwi.de/Redaktion/DE/Pressemitteilungen/2022/01/20220122-habeck-und-lemke-bekraeftigen-kritik-an-atomregeln-in-taxonomie.html>

Schwerpunkte der Berichterstattung waren diese Woche die Transplantation einer gentechnisch veränderten Schweineniere an einem hirntoten Patienten und die Entwicklungen zur Regulation von Genomeditierungsverfahren im vereinigten Königreich.

The government programme of the traffic light coalition is "Dare more progress". The coalition agreement does not clearly describe what is meant by "progress" and who dares to do what. However, the coalition partner, the party Alliance 90/The Greens party, seems to have a somewhat strange understanding of "dare more progress" in the field of agriculture, food and new technologies.

### **BMEL macht den ökologischen Landbau zu seinem Leitbild für eine nachhaltige Landwirtschaft**

Zwei neue Bekanntmachungen in den Bereichen Pflanzenzüchtung und regionale Bio-Wertschöpfungsketten flankieren dieses Ziel.

<https://www.bmel.de/SharedDocs/Pressemitteilungen/DE/2022/05-oekolandbau-bekanntmachungen.html>

### **BMEL makes organic farming its guiding principle for sustainable agriculture**

Two new announcements in the areas of plant breeding and regional organic value chains flank this goal.

The Ministry of Agriculture has announced a new research program:

“The new German government has made organic farming its guiding principle for sustainable agriculture. Therefore, the organic agricultural area is to be expanded to 30 percent by 2030. The Federal Ministry of Food and Agriculture is flanking the area target right at the beginning of the legislative period with two new announcements. It is looking for innovative research and development projects in the field of plant breeding and in the field of regional organic value chains.

Important objectives include increasing yields per hectare, improving nutrient and water use efficiency and increasing stress tolerance to biotic and abiotic factors.

Therefore, projects on breeding methodology including phenotyping or improving selection efficiency or improved breeding methods, **but not genetic engineering or genome editing methods, can be funded.**”

<https://www.bundesprogramm.de/aktuelles/bekanntmachungen>

[https://www.bundesprogramm.de/fileadmin/user\\_upload/BAnz\\_AT\\_12.01.2022\\_B5.pdf](https://www.bundesprogramm.de/fileadmin/user_upload/BAnz_AT_12.01.2022_B5.pdf)

### **Modern advanced methods are not promoted!**

This is nothing new! See also the planned and already announced research programme in Baden-Württemberg 2020 "Research Programme Genome Editing - with Biotechnology to Sustainable Agriculture". The research programme was stopped by Minister President W. Kretschmann under pressure from the Green Party. (see <https://www.biotech-gm-food.com/gruene-frieren-forschungsprogramm-zu-genome-editing-ein>)

Minister S. Lemke has already spoken out firmly against an amendment to the Genetic Engineering Act and demands that the new genomic techniques be subject across the board by the Genetic Engineering Act and be regulated even more strictly than classical genetic engineering.

### **New techniques and advances in the possibilities of genetic modification are ignored and, if possible, prevented!**

#### **Iser J.C.: Eine "Hausfreundschaft" für die Agrarwende**

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[https://www.zeit.de/wirtschaft/2022-01/landwirtschaft-cem-oezdemir-steffi-lemke-agrarwende?utm\\_referrer=https%3A%2F%2Fwww.google.de%2F](https://www.zeit.de/wirtschaft/2022-01/landwirtschaft-cem-oezdemir-steffi-lemke-agrarwende?utm_referrer=https%3A%2F%2Fwww.google.de%2F)

#### **Iser J.C.: A "house friendship" for the agricultural turnaround**

A new beginning instead of mutual blockade: the Ministry of the Environment and the Ministry of Agriculture want to realign agriculture together. It remains to be seen how the agricultural turnaround will be paid for.

The close coordination and cooperation are fundamentally to be welcomed. It will ultimately also have an impact on Germany's voting behaviour on new and advanced technologies and processes for products subject to authorisation (comitology procedure).

**BMWi: Habeck und Lemke bekräftigen Kritik an Atomregeln in Taxonomie**

<https://www.bmwi.de/Redaktion/DE/Pressemitteilungen/2022/01/20220122-habeck-und-lemke-bekraeftigen-kritik-an-atomregeln-in-taxonomie.html>

**BMWi: Habeck and Lemke reiterate criticism of nuclear rules in taxonomy**

This week's reporting focussed on the transplantation of a genetically modified pig kidney on a brain-dead patient and the developments on the regulation of genome editing procedures in the United Kingdom.

**Press Releases – Media Reports / Pressemeldungen und Medienberichte**

**Norero D.: GMO 25-year safety endorsement: 280 science institutions, more than 3,000 studies**

<https://geneticliteracyproject.org/2022/01/21/gmo-20-year-safety-endorsement-280-science-institutions-more-3000-studies/>

**Foote N.: Großbritannien will Vorreiter bei Gentechnikforschung werden**

<https://www.euractiv.de/section/landwirtschaft-und-ernahrung/news/grossbritannien-will-vorreiter-bei-gentechnikforschung-werden/>

**GOV.UK: New powers granted to research gene editing in plants**

<https://www.gov.uk/government/news/new-powers-granted-to-research-gene-editing-in-plants>

**Harvey F.: UK moves closer to allowing gene editing of crops by allowing more research**

<https://www.theguardian.com/science/2022/jan/20/uk-moves-closer-to-allowing-gene-editing-of-crops-by-allowing-more-research>

**A Bigger Conversation: FILLING IN THE BLANKS: WHAT DEFRA DIDN'T SAY**

[https://abiggerconversation.org/wp-content/uploads/2022/01/Filling-in-the-Blanks\\_Defra-Consultation\\_ABC\\_Jan2022.pdf](https://abiggerconversation.org/wp-content/uploads/2022/01/Filling-in-the-Blanks_Defra-Consultation_ABC_Jan2022.pdf)

**Dionglay C.: Japan's 3 genome-edited food products now in Japanese market**

<https://businessmirror.com.ph/2022/01/23/japans-3-genome-edited-food-products-now-in-japanese-market/>

**wissenschaft.de: Xenotransplantation von Schweinenieren**

<https://www.wissenschaft.de/gesundheits-medizin/xenotransplantation-von-schweinenieren/>

**Le Page M.: Genetically modified pig kidneys transplanted into a brain-dead person**

<https://www.newscientist.com/article/2305449-genetically-modified-pig-kidneys-transplanted-into-a-brain-dead-person/>

Only some selected press releases or media reports are listed here. The daily up-date of the press releases and media reports are [here](#): (January week 02)

**Publications – Publikationen**

Messmer, T., Klevernic, I., Furquim, C. et al. (2022): **A serum-free media formulation for cultured meat production supports bovine satellite cell differentiation in the absence of serum starvation**. *Nat Food* **3**, 74–85 (2022) | <https://doi.org/10.1038/s43016-021-00419-1>

Cultured meat production requires the robust differentiation of satellite cells into mature muscle fibres without the use of animal-derived components. Current protocols induce myogenic differentiation in vitro through serum starvation, that is, an abrupt reduction in serum concentration. Here we used RNA sequencing to investigate the transcriptomic remodelling of bovine satellite cells during myogenic differentiation induced by serum starvation. We characterized canonical myogenic gene expression, and identified surface receptors upregulated during the early phase of differentiation, including *IGF1R*, *TFRC* and *LPAR1*. Supplementation of ligands to these receptors enabled the formulation of a chemically defined media that induced differentiation in the absence of serum starvation and/or transgene expression. Serum-free myogenic differentiation was of similar extent to that induced by serum starvation, as evaluated by transcriptome analysis, protein expression and the presence of a functional contractile apparatus. Moreover, the serum-free differentiation media

supported the fabrication of three-dimensional bioartificial muscle constructs, demonstrating its suitability for cultured beef production.

<https://www.nature.com/articles/s43016-021-00419-1>

Porrett P.M., Orandi B.J., Kumar V., Houp J. et al. (2022): **First clinical-grade porcine kidney xenotransplant using a human decedent model.** American Journal of Transplantation |

<https://doi.org/10.1111/ajt.16930>

A radical solution is needed for the organ supply crisis, and the domestic pig is a promising organ source. In preparation for a clinical trial of xenotransplantation, we developed an *in vivo* pre-clinical human model to test safety and feasibility tenets established in animal models. After performance of a novel, prospective compatible crossmatch, we performed bilateral native nephrectomies in a human brain-dead decedent and subsequently transplanted two kidneys from a pig genetically engineered for human xenotransplantation. The decedent was hemodynamically stable through reperfusion, and vascular integrity was maintained despite the exposure of the xenografts to human blood pressure. No hyperacute rejection was observed, and the kidneys remained viable until termination 74 h later. No chimerism or transmission of porcine retroviruses was detected. Longitudinal biopsies revealed thrombotic microangiopathy that did not progress in severity, without evidence of cellular rejection or deposition of antibody or complement proteins. Although the xenografts produced variable amounts of urine, creatinine clearance did not recover. Whether renal recovery was impacted by the milieu of brain death and/or microvascular injury remains unknown. In summary, our study suggests that major barriers to human xenotransplantation have been surmounted and identifies where new knowledge is needed to optimize xenotransplantation outcomes in humans.

<https://onlinelibrary.wiley.com/doi/10.1111/ajt.16930>

<https://onlinelibrary.wiley.com/doi/epdf/10.1111/ajt.16930>

Jenkins, D., Dobert, R., Atanassova, A. et al. **Impacts of the regulatory environment for gene editing on delivering beneficial products.** *In Vitro Cell.Dev.Biol.-Plant* 57, 609–626 (2021).

<https://doi.org/10.1007/s11627-021-10201-4>

Various genome-editing technologies have been embraced by plant breeders across the world as promising tools for the improvement of different crops to deliver consumer benefits, improve agronomic performance, and increase sustainability. The uptake of genome-editing technologies in plant breeding greatly depends on how governments regulate its use. Some major agricultural production countries have already developed regulatory approaches that enable the application of genome editing for crop improvement, while other governments are in the early stages of formulating policy. Central to the discussion is the principle of “like products should be treated in like ways” and the subsequent utilization of exclusions and exemptions from the scope of GMO regulations for these products. In some countries, the outcomes of genome editing that could also have been achieved through conventional breeding have been defined as not needing GMO regulatory oversight. In this paper, we provide a short overview of plant breeding and the history of plant biotechnology policy development, the different classes of current regulatory systems and their use of exemptions and exclusions for genome-edited plants, and the potential benefits of such approaches as it relates to achieving societal goals.

<https://link.springer.com/article/10.1007/s11627-021-10201-4#citeas>

<https://link.springer.com/content/pdf/10.1007/s11627-021-10201-4.pdf>

Kim Y. et al. (2021): **EXPRESS: GMO Labeling Policy and Consumer Choice,** Journal of Marketing | DOI: 10.1177/00222429211064901

Most scientists claim that genetically modified organisms (GMOs) in foods are safe for human consumption and offer societal benefits such as better nutritional content. In contrast, many consumers remain skeptical about their safety. Against this backdrop of diverging views, the authors investigate the impact of different GMO labeling policy regimes on products consumers choose. Guided by the literature on negativity bias, structural alignment theory, and message presentation, and based on findings from four experiments, authors show that consumer demand for GM foods depends on the labeling regime policymakers adopt. Both absence-focused (“non-GMO”) and presence-focused (“contains GMO”) labeling regimes reduce the market share of GM foods, with the reduction being greater in the latter case. GMO labels reduce the importance consumers place on price and enhance their willingness-to-pay for non-GM products. Results indicate that specific label design choices policymakers implement (in the form of color and style) also affect consumer responses to GM labeling. Consumer attitudes toward GMOs moderate this effect – consumers with neutral attitudes toward GMOs are influenced most significantly by the label design.

<https://journals.sagepub.com/doi/10.1177/00222429211064901>

Waltz E. (2022): **GABA-enriched tomato is first CRISPR-edited food to enter market**

Sanatech Seed’s Sicilian Rouge CRISPR-edited ‘health-promoting’ tomatoes reach consumers and may open the market to more genome-edited fruit, vegetables and even fish.

Nature Biotechnology 40, 9-11 | <https://doi.org/10.1038/d41587-021-00026-2>

<https://www.nature.com/articles/d41587-021-00026-2>

Hüdig M., Laibach N., Hein A-C. (2022): **Genome Editing in Crop Plant Research—Alignment of Expectations and Current Developments.** *Plants*, 11(2), 212 |

<https://doi.org/10.3390/plants11020212>

The rapid development of genome editing and other new genomic techniques (NGT) has evoked manifold expectations on purposes of the application of these techniques to crop plants. In this study, we identify and align these expectations with current scientific development. We apply a semi-quantitative text analysis approach on political, economic, and scientific opinion papers to disentangle and extract expectations towards the application of NGT-based plants. Using the sustainable development goals (SDG) of the 2030 agenda as categories, we identify contributions to food security or adaptation to climatic changes as the most frequently mentioned expectations, accompanied by the notion of sustainable agriculture and food systems. We then link SDG with relevant plant traits and review existing research and commercial field trials for genome-edited crop plants. For a detailed analysis we pick as representative traits drought tolerance and resistance against fungal pathogens. Diverse genetic setscrews for both traits have been identified, modified, and tested under laboratory conditions, although there are only a few in the field. All in all, NGT-plants that can withstand more than one stressor or different environments are not documented in advanced development states. We further conclude that developing new plants with modified traits will not be sufficient to reach food security or adaptation to climatic changes in a short time frame. Further scientific development of sustainable agricultural systems will need to play an important role to tackle SDG challenges, as well.

<https://www.mdpi.com/2223-7747/11/2/212>

Ceccarelli S. and Grando S. (2022): **Evolutionary Plant Breeding as a Response to the Complexity of Climate Change.** *iScience* 23 (12), 101815

<https://www.sciencedirect.com/science/article/pii/S2589004220310129>

Brackett N.F., Pomés A. and Chapman M.D. (2022): **New Frontiers: Precise Editing of Allergen Genes Using CRISPR.** *Front. Allergy*, | <https://doi.org/10.3389/falgy.2021.821107>

Genome engineering with clustered regularly interspaced short palindromic repeats (CRISPR) technology offers the unique potential for unequivocally deleting allergen genes at the source. Compared to prior gene editing approaches, CRISPR boasts substantial improvements in editing efficiency, throughput, and precision. CRISPR has demonstrated success in several clinical applications such as sickle cell disease and  $\beta$ -thalassemia, and preliminary knockout studies of allergenic proteins using CRISPR editing show promise. Given the advantages of CRISPR, as well as specific DNA targets in the allergen genes, CRISPR gene editing is a viable approach for tackling allergy, which may lead to significant disease improvement. This review will highlight recent applications of CRISPR editing of allergens, particularly cat allergen Fel d 1, and will discuss the advantages and limitations of this approach compared to existing treatment options.

<https://www.frontiersin.org/articles/10.3389/falgy.2021.821107/full>

Kress W.J., Soltis D.E., Kersey P.J., Wegrzyn, J.L. Leebens-Mack J.H., Gostel M.R., Liu X., Soltis P.S. (2022): **Green plant genomes: What we know in an era of rapidly expanding opportunities.** *PNAS* 119 (4) e2115640118 | <https://doi.org/10.1073/pnas.2115640118>

Green plants play a fundamental role in ecosystems, human health, and agriculture. As de novo genomes are being generated for all known eukaryotic species as advocated by the Earth BioGenome Project, increasing genomic information on green land plants is essential. However, setting standards for the generation and storage of the complex set of genomes that characterize the green lineage of life is a major challenge for plant scientists. Such standards will need to accommodate the immense variation in green plant genome size, transposable element content, and structural complexity while enabling research into the molecular and evolutionary processes that have resulted in this enormous genomic variation. Here we provide an overview and assessment of the current state of knowledge of green plant genomes. To date fewer than 300 complete chromosome-scale genome assemblies representing fewer than 900 species have been generated across the estimated 450,000 to 500,000 species in the green plant clade. These genomes range in size from 12 Mb to 27.6 Gb and are biased toward agricultural crops with large branches of the green tree of life untouched by genomic-scale sequencing. Locating suitable tissue samples of most species of plants, especially those taxa from extreme environments, remains one of the biggest hurdles to increasing our genomic inventory. Furthermore, the annotation of plant genomes is at present undergoing intensive improvement. It is our hope that this fresh overview will help in the development of genomic quality standards for a cohesive and meaningful synthesis of green plant genomes as we scale up for the future.

<https://www.pnas.org/content/pnas/119/4/e2115640118.full.pdf>

Arbatli S., Weiss J., Egea-Cortines M. (2021): **Gene and Genome Editing with CRISPR/Cas Systems for Fruit and Vegetable Improvement.** In: Tang G., Teotia S., Tang X., Singh D. (eds) *RNA-Based Technologies for Functional Genomics in Plants. Concepts and Strategies in Plant Sciences.* Springer, Cham. [https://doi.org/10.1007/978-3-030-64994-4\\_11](https://doi.org/10.1007/978-3-030-64994-4_11)

Ever since the advent of agriculture, breeding new varieties has relied upon crosses between individuals from a single species, and since the early twentieth century with relatives or via mutagenesis. Two major problems have been found time and again. First, combining genomes to improve a character often times causes decreases in other traits as a result of genetic linkage. The second is that natural variation does not always comprise all the possibilities a genome may have in terms of allelic combinations suitable for further improving a set of characters. In the last twenty years a number of technologies have been developed allowing the perturbation of a single gene. Development of genome editing technologies includes zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs) and Clustered Regularly Interspaced Palindromic Repeats (CRISPR). Here we review current methodologies regarding to the use of gRNA targeted gene and

genome editing strategies by various CRISPR/Cas9 systems in agriculture. The molecular mechanism of DNA modification by CRISPR/Cas relies on guide RNA molecules comprising 20–25 DNA bases homologous to the target locus. This has opened the possibility of tackling single loci or multiple paralogs in a gene family. Importantly, complex genomes with polyploid structures such as wheat or camelina have been successfully engineered with single guides. This opens a new window of opportunities to engineer gene families, pathways and complex genomes that was unfeasible before the advent of CRISPR/Cas.  
[https://link.springer.com/chapter/10.1007%2F978-3-030-64994-4\\_11](https://link.springer.com/chapter/10.1007%2F978-3-030-64994-4_11)

Rizzo G., Monzon J.P., Tenorio F.A., Howard R., Cassman K.G., Grassini P. (2022): **Climate and agronomy, not genetics, underpin recent maize yield gains in favorable environments.** PNAS 119 (4) e2113629119 | <https://doi.org/10.1073/pnas.2113629119>

Quantitative understanding of factors driving yield increases of major food crops is essential for effective prioritization of research and development. Yet previous estimates had limitations in distinguishing among contributing factors such as changing climate and new agronomic and genetic technologies. Here, we distinguished the separate contribution of these factors to yield advance using an extensive database collected from the largest irrigated maize-production domain in the world located in Nebraska (United States) during the 2005-to-2018 period. We found that 48% of the yield gain was associated with a decadal climate trend, 39% with agronomic improvements, and, by difference, only 13% with improvement in genetic yield potential. The fact that these findings were so different from most previous studies, which gave much-greater weight to genetic yield potential improvement, gives urgency to the need to reevaluate contributions to yield advances for all major food crops to help guide future investments in research and development to achieve sustainable global food security. If genetic progress in yield potential is also slowing in other environments and crops, future crop-yield gains will increasingly rely on improved agronomic practices.  
<https://www.pnas.org/content/pnas/119/4/e2113629119.full.pdf>

Blaxter M., Archibald J.M., Childers A.K., Coddington J.A. et al. (2022): **Why sequence all eukaryotes?** PNAS 119 (4) e2115636118; <https://doi.org/10.1073/pnas.2115636118>

Life on Earth has evolved from initial simplicity to the astounding complexity we experience today. Bacteria and archaea have largely excelled in metabolic diversification, but eukaryotes additionally display abundant morphological innovation. How have these innovations come about and what constraints are there on the origins of novelty and the continuing maintenance of biodiversity on Earth? The history of life and the code for the working parts of cells and systems are written in the genome. The Earth BioGenome Project has proposed that the genomes of all extant, named eukaryotes—about 2 million species—should be sequenced to high quality to produce a digital library of life on Earth, beginning with strategic phylogenetic, ecological, and high-impact priorities. Here we discuss why we should sequence all eukaryotic species, not just a representative few scattered across the many branches of the tree of life. We suggest that many questions of evolutionary and ecological significance will only be addressable when whole-genome data representing divergences at all of the branchings in the tree of life or all species in natural ecosystems are available. We envisage that a genomic tree of life will foster understanding of the ongoing processes of speciation, adaptation, and organismal dependencies within entire ecosystems. These explorations will resolve long-standing problems in phylogenetics, evolution, ecology, conservation, agriculture, bioindustry, and medicine.  
<https://www.pnas.org/content/pnas/119/4/e2115636118.full.pdf>

Stephan, T., Burgess S.M., Cheng H., Danko C.G. et al. (2022): **Darwinian genomics and diversity in the tree of life.** PNAS 119 (4) e2115644119 | <https://doi.org/10.1073/pnas.2115644119>

Genomics encompasses the entire tree of life, both extinct and extant, and the evolutionary processes that shape this diversity. To date, genomic research has focused on humans, a small number of agricultural species, and established laboratory models. Fewer than 18,000 of ~2,000,000 eukaryotic species (<1%) have a representative genome sequence in GenBank, and only a fraction of these have ancillary information on genome structure, genetic variation, gene expression, epigenetic modifications, and population diversity. This imbalance reflects a perception that human studies are paramount in disease research. Yet understanding how genomes work, and how genetic variation shapes phenotypes, requires a broad view that embraces the vast diversity of life. We have the technology to collect massive and exquisitely detailed datasets about the world, but expertise is siloed into distinct fields. A new approach, integrating comparative genomics with cell and evolutionary biology, ecology, archaeology, anthropology, and conservation biology, is essential for understanding and protecting ourselves and our world. Here, we describe potential for scientific discovery when comparative genomics works in close collaboration with a broad range of fi  
<https://www.pnas.org/content/pnas/119/4/e2115644119.full.pdf>

Saleh D. et al. (2022): **Genome-wide evolutionary response of European oaks during the Anthropocene,** Evolution Letters | DOI: [10.1002/evl3.269](https://doi.org/10.1002/evl3.269)

The pace of tree microevolution during Anthropocene warming is largely unknown. We used a retrospective approach to monitor genomic changes in oak trees since the Little Ice Age (LIA). Allelic frequency changes were assessed from whole-genome pooled sequences for four age-structured cohorts of sessile oak (*Quercus petraea*) dating back to 1680, in each of three different oak forests in France. The genetic covariances of allelic frequency changes increased between successive time periods, highlighting genome-wide effects of linked selection. We found imprints of parallel linked selection in the three forests during the late LIA, and a shift of

selection during more recent time periods of the Anthropocene. The changes in allelic covariances within and between forests mirrored the documented changes in the occurrence of extreme events (droughts and frosts) over the last 300 years. The genomic regions with the highest covariances were enriched in genes involved in plant responses to pathogens and abiotic stresses (temperature and drought). These responses are consistent with the reported sequence of frost (or drought) and disease damage ultimately leading to the oak dieback after extreme events. They provide support for adaptive evolution of long-lived species during recent climatic changes. Although we acknowledge that other sources (e.g., gene flow, generation overlap) may have contributed to temporal covariances of allelic frequency changes, the consistent and correlated response across the three forests lends support to the existence of a systematic driving force such as natural selection.  
<https://onlinelibrary.wiley.com/doi/10.1002/evl3.269>  
<https://onlinelibrary.wiley.com/doi/epdf/10.1002/evl3.269>

Zhang M., Ma Y., Luo J., Jichao J. et al. (2022): **Transgenic insect-resistant Bt cotton expressing Cry1Ac/1Ab does not harm the insect predator *Geocoris pallidipennis*.**

Ecotoxicology and Environmental Safety 230, 113129 | <https://doi.org/10.1016/j.ecoenv.2021.113129>

The large-scale commercial cultivation of genetically modified (GM) cotton has brought significant economic and environmental benefits. However, GM crops must undergo strict environmental monitoring and long-term observation. An important natural enemy insect in cotton fields, *Geocoris pallidipennis*, can ingest the Bt protein expressed in GM cotton by feeding on herbivorous insects that feed on the cotton. However, the potential risk of GM cotton to *G. pallidipennis* is still unclear. We here evaluated the effects of Bt cotton expressing the Cry1Ac/1Ab protein on nymphs and adults *G. pallidipennis*. Cry1Ac protein was detected in the midgut of the cotton bollworm, *Helicoverpa armigera*, after it ingested Bt cotton, and in the midgut of *G. pallidipennis* nymphs and adults preying on Bt-fed *H. armigera*. However, the survival rate, growth, development, and fecundity of *G. pallidipennis* were not adversely affected. Furthermore, *G. pallidipennis* cadherins, and those genes related to detoxification, antioxidant activity, nutrient utilization, and immune function were not differentially expressed in response to Cry1Ac exposure. Finally, we showed that Cry1Ac could not bind to brush border membrane vesicles (BBMV) proteins in *G. pallidipennis* nymphs or adults. In summary, these results indicate that the potential negative effect of transgenic Cry1Ac/1Ab cotton on the insect predator *G. pallidipennis* is negligible.

<https://www.sciencedirect.com/science/article/pii/S0147651321012410>

Rosa L.P., Eimanifar A., Kimes A.G., Brooks S.A., Ellis J.A. (2021): **Attack of the dark clones the genetics of reproductive and color traits of South African honey bees (*Apis mellifera* spp.)** PLOS ONE | DOI: [10.1371/journal.pone.0260833](https://doi.org/10.1371/journal.pone.0260833)

The traits of two subspecies of western honey bees, *Apis mellifera scutellata* and *A.m. capensis*, endemic to the Republic of South Africa (RSA), are of biological and commercial relevance. Nevertheless, the genetic basis of important phenotypes found in these subspecies remains poorly understood. We performed a genome wide association study on three traits of biological relevance in 234 *A.m. capensis*, 73 *A.m. scutellata* and 158 hybrid individuals. Thirteen markers were significantly associated to at least one trait ( $P \leq 4.28 \times 10^{-6}$ ): one for ovariole number, four for scutellar plate and eight for tergite color. We discovered two possible causative variants associated to the respective phenotypes: a deletion in *GB46429* or *Ebony* (NC\_007070.3:g.14101325G>del) (R69Efs\*85) and a nonsense on *GB54634* (NC\_007076.3:g.4492792A>G;p.Tyr128\*) causing a premature stop, substantially shortening the predicted protein. The mutant genotypes are significantly associated to phenotypes in *A.m. capensis*. Loss-of-function of *Ebony* can cause accumulation of circulating dopamine, and increased dopamine levels correlate to ovary development in queenless workers and pheromone production. Allelic association ( $P = 1.824 \times 10^{-5}$ ) of NC\_007076.3:g.4492792A>G;p.Tyr128\* to ovariole number warrants further investigation into function and expression of the *GB54634* gene. Our results highlight genetic components of relevant production/conservation behavioral phenotypes in honey bees.

<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0260833>

Kordj, M., Salami, R., Bolouri, P. et al.(2022): **White biotechnology and the production of bio-products.** *Syst Microbiol and Biomanuf* | <https://doi.org/10.1007/s43393-022-00078-8>

White biotechnology uses enzymes and microorganisms to produce value-added chemicals from renewable sources. White biotechnology provides valuable components for the food, pharmaceutical, agricultural sectors as well as other industries. Metabolic diversity in fungi, yeast, and bacteria can be exploited to produce food additives and other industrial products. This is an interesting topic for those interested in screening and metabolic testing of microorganisms, industrial biotechnology, fermentation technology, and the biological products research community. The use of microbial-derived compounds has a long history in the food industry, and compounds such as flavorings, essential amino acids, poly-unsaturated fatty acids, organic acids, gelling, etc. can be obtained from microbial sources. Also, the role of microbes in human health and well-being cannot be ignored. Microbes produce primary metabolites such as vitamins, nucleotides, and amino acids, as well as secondary metabolites. These secondary metabolites are used to make many drugs. In agriculture, microbes are also used to make fertilizers and biological pesticides. This paper reviews the types of bio-products obtained through biotechnology and the barriers and challenges of white biotechnology.

<https://link.springer.com/content/pdf/10.1007/s43393-022-00078-8.pdf>

Ouyang H., Hong J., Malroy J., Zhu X. (2021): **An E. coli-Based Biosynthetic Platform Expands the Structural Diversity of Natural Benzoxazoles**, *ACS Synth. Biol.* 10 (9), 2151–2158 |

<https://doi.org/10.1021/acssynbio.1c00228>

Benzoxazoles are frequently found in synthetic pharmaceuticals and medicinally active natural products. To facilitate benzoxazole-based drug development, an eco-friendly and rapid platform for benzoxazole production is required. In this study, we have completed the biosynthesis of benzoxazoles in *E. coli* by coexpressing the minimal set of enzymes required for their biosynthesis. Moreover, by coupling this *E. coli*-based platform with precursor-directed biosynthesis, we have shown that the benzoxazole biosynthetic system is highly promiscuous in incorporating fluorine, chlorine, nitrile, picolinic, and alkyne functionalities into the scaffold. Our *E. coli*-based system thus paves the way for straightforward generation of novel benzoxazole analogues through future protein engineering and combinatorial biosynthesis.

<https://pubs.acs.org/doi/10.1021/acssynbio.1c00228>

**EFSA:**

CEP Panel (2022). Scientific Opinion on the safety evaluation of the food enzyme catalase from porcine liver. *EFSA Journal* 20(1): 7009, 10 pp.

<https://doi.org/10.2903/j.efsa.2022.7009>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2022.7009>

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