

2022: Sunday Evening News No 262

Week 02 (2022-10-01 – 2022-16-01)

Selected and edited by **BGF** Jany

Dear all,

Nächste Woche, am Donnerstag 20.01.2022 tagen der SCoPAFF (Sojabohne GMB 151) und der Berufungsausschuss (Baumwolle GHB 614) im Komitologieverfahren für die Zulassungen von gv-Pflanzen zum Import. Man darf gespannt sein, wie Deutschland hier abstimmen wird, da beide Ministerien, das Landwirtschafts- und das Umweltministerium, von den Grünen geführt werden. Die grüne Partei lehnt bekanntlich die Vermarktung von Produkten aus gv-Pflanzen ab.

Der BDI (Bundesverband der Deutschen Industrie) hat eine Zusammenstellung des Führungspersonals der Bundesregierung veröffentlicht. Die [► Broschüre](#) gibt einen guten Überblick.

Next week, on Thursday, January 20, 2022, the SCoPAFF (topic: soybean GMB 151) and the appeals committee (topic: cotton GHB 614) will meet in the comitology procedure for the approval of GM plants for import. It will be interesting to see how Germany will vote here, since both ministries, the Ministry of Agriculture and the Ministry of the Environment, are led by the Greens. As is well known, the Green Party rejects the marketing of products made from GM plants.

The BDI (Federal Association of German Industry) has published a summary of the federal government's management staff. The [► brochure](#) gives a good overview.(in German)

Die Transplantation eines gentechnisch veränderten Schweineherzens und die Ergebnisse aus der Publikation „**Mutation bias reflects natural selection in *Arabidopsis thaliana***“ der Gruppe um D. Weigel vom MPI-Tübingen beherrschten diese Woche die Medien.

The transplantation of a genetically modified pig heart and the results from the publication "**Mutation bias reflects natural selection in *Arabidopsis thaliana***" by the research group around D. Weigel from the MPI-Tübingen dominated the media this week.

Meetings – Conferences / Tagungen - Konferenzen

DBV: Digitaler Agrarpolitischer Jahresauftakt

18. Januar 2022, 18:30 Uhr bis 20:30 Uhr

<https://www.bauernverband.de/topartikel/digitaler-agrarpolitischer-jahresauftakt>

BfN: BfN-Zukunftsworkshop vom 15. - 16. März 2022

<https://www.bfn.de/veranstaltungen/bfn-zukunftsworkshop-vom-15-16-maerz-2022>

8th International Akademie Fresenius : **Feed Conference**

EU Green Deal and Animal Nutrition Strategies – What comes next?

28 and 29 March 2022 in Mainz/Germany and via Live Stream

<https://www.akademie-fresenius.de/veranstaltungen/detail/produkt/8th-international-akademie-fresenius-feed-conference/?L=354&cHash=e61420607d47c352d1d72e13308c17bb>

Press Releases – Media Reports / Pressemeldungen und Medienberichte

Baker H.: New study provides first evidence of non-random mutations in DNA

This goes against one of the key assumptions of the theory of evolution.

<https://www.livescience.com/non-random-dna-mutations>

Testbiotech: New findings on the evolution of plants

Research outcomes also concern the differences between New GE and conventional breeding

<https://www.testbiotech.org/en/news/new-findings-evolution-plants>

MPI – Weigel D.: Pflanzen vermeiden gefährliche Mutationen

<https://www.mpg.de/18127703/0111-entw-ein-schritt-voraus-wie-pflanzen-gefaehrliche-mutationen-vermeiden-151730-x?c=2191>

Fröndhoff B: „Es erzeugt den Puls, es erzeugt den Druck, es ist sein Herz“ – Erster Mensch bekommt Herz vom Schwein

<https://www.handelsblatt.com/technik/medizin/medizin-es-erzeugt-den-puls-es-erzeugt-den-druck-es-ist-sein-herz-erster-mensch-bekommt-herz-vom-schwein/27964546.html?ticket=ST-3082306-MiY0hZXLwqci37jQzfP3-ap3>

Lob-Hüdepohl: **Moraltheologe: Kein Einwand gegen Schweineherz-Transplantation**

<https://www.katholisch.de/artikel/32703-moraltheologe-kein-einwand-gegen-schweineherz-transplantation>

TAB-Arbeitsbericht Nr. 191: **Genome Editing am Menschen - Hoffnungen oder Hybris?**

<https://www.tab-beim-bundestag.de/news-2021-12-14-genome-editing-am-menschen-hoffnungen-oder-hybris.php>

VIP: **Applications submitted for new field trials with genome-edited maize**

<https://vib.be/news/applications-submitted-new-field-trials-genome-edited-maize>

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

Monroe, J.G., Srikant, T., Carbonell-Bejerano, P. et al. (2022): **Mutation bias reflects natural selection in *Arabidopsis thaliana***. Nature | <https://doi.org/10.1038/s41586-021-04269-6>

Since the first half of the twentieth century, evolutionary theory has been dominated by the idea that mutations occur randomly with respect to their consequences¹. Here we test this assumption with large surveys of de novo mutations in the plant *Arabidopsis thaliana*. In contrast to expectations, we find that mutations occur less often in functionally constrained regions of the genome—mutation frequency is reduced by half inside gene bodies and by two-thirds in essential genes. With independent genomic mutation datasets, including from the largest *Arabidopsis* mutation accumulation experiment conducted to date, we demonstrate that epigenomic and physical features explain over 90% of variance in the genome-wide pattern of mutation bias surrounding genes. Observed mutation frequencies around genes in turn accurately predict patterns of genetic polymorphisms in natural *Arabidopsis* accessions ($r = 0.96$). That mutation bias is the primary force behind patterns of sequence evolution around genes in natural accessions is supported by analyses of allele frequencies. Finally, we find that genes subject to stronger purifying selection have a lower mutation rate. We conclude that epigenome-associated mutation bias² reduces the occurrence of deleterious mutations in *Arabidopsis*, challenging the prevailing paradigm that mutation is a directionless force in evolution. <https://www.nature.com/articles/s41586-021-04269-6.pdf>

Reardon S.: **First pig-to-human heart transplant: what can scientists learn?**

Researchers hope that a person who has so far lived for a week with a genetically modified pig heart will provide a trove of data on the possibilities of xenotransplantation.

Nature | doi: <https://doi.org/10.1038/d41586-022-00111-9>
<https://www.nature.com/articles/d41586-022-00111-9>

Romanello M., McGushin A., Di Napoli C., Drummond P. et al.:(2021) **The 2021 report of the Lancet Countdown on health and climate change: code red for a healthy future**. The Lancet 398 (10311), 1619-1662, | [https://doi.org/10.1016/S0140-6736\(21\)01787-6](https://doi.org/10.1016/S0140-6736(21)01787-6)

The *Lancet* Countdown is an international collaboration that independently monitors the health consequences of a changing climate. Publishing updated, new, and improved indicators each year, the *Lancet* Countdown represents the consensus of leading researchers from 43 academic institutions and UN agencies. The 44 indicators of this report expose an unabated rise in the health impacts of climate change and the current health consequences of the delayed and inconsistent response of countries around the globe—providing a clear imperative for accelerated action that puts the health of people and planet above all else. [https://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(21\)01787-6/fulltext](https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(21)01787-6/fulltext)

Romanello M., van Daalen K., Anto J.N., Dasandi N. et al (2021): **Tracking progress on health and climate change in Europe**. The Lancet – Public Health 6 (11) e858-e865,

Left unabated, climate change will have catastrophic effects on the health of present and future generations. Such effects are already seen in Europe, through more frequent and severe extreme weather events, alterations to water and food systems, and changes in the environmental suitability for infectious diseases. As one of the largest current and historical contributors to greenhouse gases and the largest provider of financing for climate change mitigation and adaptation, Europe's response is crucial, for both human health and the planet. To ensure that health and wellbeing are protected in this response it is essential to build the capacity to understand, monitor, and quantify health impacts of climate change and the health co-benefits of accelerated action. Responding to this need, the *Lancet* Countdown in Europe is established as a transdisciplinary research collaboration for monitoring progress on health and climate change in Europe. With the wealth of data and academic expertise available in Europe, the collaboration will develop region-specific indicators to address the

main challenges and opportunities of Europe's response to climate change for health. The indicators produced by the collaboration will provide information to health and climate policy decision making, and will also contribute to the European Observatory on Climate and Health.

[https://www.thelancet.com/journals/lanpub/article/PIIS2468-2667\(21\)00207-3/fulltext](https://www.thelancet.com/journals/lanpub/article/PIIS2468-2667(21)00207-3/fulltext)

Kortetmäki T.: (2022): **Agriculture and Climate Change - Ethical Considerations**

[https://www.ekah.admin.ch/inhalte/ekah-dateien/dokumentation/publikationen/Buchreihe Beiträege zu Ethik und Biotechnologie/Buch 15 Inhalt Agriculture and Climate Change.pdf](https://www.ekah.admin.ch/inhalte/ekah-dateien/dokumentation/publikationen/Buchreihe%20Beitraege%20zu%20Ethik%20und%20Biotechnologie/Buch%2015%20Inhalt%20Agriculture%20and%20Climate%20Change.pdf)

Banakar R, Schubert M, Kurgan G, Rai KM et al. (2022): **Efficiency, Specificity and Temperature Sensitivity of Cas9 and Cas12a RNPs for DNA free Genome Editing in Plants.**

Front. Genome Ed. 3:760820. | <https://doi.org/10.3389/fgeed.2021.760820>

Delivery of genome editing reagents using CRISPR-Cas ribonucleoproteins (RNPs) transfection offers several advantages over plasmid DNA-based delivery methods, including reduced off-target editing effects, mitigation of random integration of non-native DNA fragments, independence of vector constructions, and less regulatory restrictions. Compared to the use in animal systems, RNP-mediated genome editing is still at the early development stage in plants. In this study, we established an efficient and simplified protoplast-based genome editing platform for CRISPR-Cas RNP delivery, and then evaluated the efficiency, specificity, and temperature sensitivity of six Cas9 and Cas12a proteins. Our results demonstrated that Cas9 and Cas12a RNP delivery resulted in genome editing frequencies (8.7–41.2%) at various temperature conditions, 22°C, 26°C, and 37°C, with no significant temperature sensitivity. LbCas12a often exhibited the highest activities, while AsCas12a demonstrated higher sequence specificity. The high activities of CRISPR-Cas RNPs at 22° and 26°C, the temperature preferred by plant transformation and tissue culture, led to high mutagenesis efficiencies (34.0–85.2%) in the protoplast-regenerated calli and plants with the heritable mutants recovered in the next generation. This RNP delivery approach was further extended to pennycress (*Thlaspi arvense*), soybean (*Glycine max*) and *Setaria viridis* with up to 70.2% mutagenesis frequency. Together, this study sheds light on the choice of RNP reagents to achieve efficient transgene-free genome editing in plants.

<https://www.frontiersin.org/articles/10.3389/fgeed.2021.760820/full>

Thakur T, Sinha K., Kaur T., Kapoor R. et al. (2022): **Efficient Genetic Transformation of Rice for CRISPR/Cas9 Mediated Genome-Editing and Stable Overexpression Studies: A Case Study on Rice Lipase 1 and Galactinol Synthase Encoding Genes.** Agronomy 12(1), 179; |

<https://doi.org/10.3390/agronomy12010179>

Rice is a staple food crop for almost half of the world's population, especially in the developing countries of Asia and Africa. It is widely grown in different climatic conditions, depending on the quality of the water, soil, and genetic makeup of the rice cultivar. Many (a)biotic stresses severely curtail rice growth and development, with an eventual reduction in crop yield. However, for molecular functional analysis, the availability of an efficient genetic transformation protocol is essential. To ensure food security and safety for the continuously increasing global population, the development of climate-resilient crops is crucial. Here, in this study, the rice transformation protocol has been effectively optimized for the efficient and rapid generation of rice transgenic plants. We also highlighted the critical steps and precautionary measures to be taken while performing the rice transformation. We further assess the efficacy of this protocol by transforming rice with two different transformation constructs for generating galactinol synthase (Gols) overexpression lines and CRISPR/Cas9-mediated edited lines of lipase (Lip) encoding the OsLip1 gene. The putative transformants were subjected to molecular analysis to confirm gene integration/editing, respectively. Collectively, the easy, efficient, and rapid rice transformation protocol used in this present study can be applied as a potential tool for gene(s) function studies in rice and eventually to the rice crop improvement

<https://www.mdpi.com/2073-4395/12/1/179>

Lloyd, K.G., Tahon, G.(2022): **Science depends on nomenclature, but nomenclature is not science.** Nat Rev Microbiol | <https://doi.org/10.1038/s41579-022-00684-2>

The International Committee on Systematics of Prokaryotes (ICSP) has recently altered long-standing phylum names and given no guidance for taxonomy of uncultured or imperfectly cultured archaea and bacteria, disrupting progress towards a universal system of microbial taxonomy. Inclusion of new members into ICSP may help it to keep up to date.

<https://www.nature.com/articles/s41579-022-00684-2>

Lin, J., Zhang, W., Zhang, X. et al. (2022): **Signatures of selection in recently domesticated macadamia.** Nat Commun 13, 242 (2022). <https://doi.org/10.1038/s41467-021-27937-7>

Macadamia is a high value nut crop that is recently domesticated, ideal for testing the effect of artificial selection. Here, we sequence the genome of Hawaiian cultivar 'Kau' and assemble into 794 Mb in 14 pseudo-chromosomes with 37,728 genes. Genome analysis reveals a whole-genome duplication event, occurred 46.8 million years ago. Gene expansions occurred in gene families involved in fatty acid biosynthesis. Gene duplication of MADS-Box transcription factors in proanthocyanidin biosynthesis are relevant for seed coat development. Genome re-sequencing of 112 accessions reveals the origin of Hawaiian cultivars from Mount Bauple in southeast Queensland in Australia. Selective sweeps are detected in macadamia cultivars, including genes involved in fatty acid biosynthesis, seed coat development, and heat stress response. Such strong effects

of artificial selection in few generations reveals the genomic basis for 'one-step operation' for clonal crop domestication. The knowledge gained could accelerate domestication of new crops from wild species.
<https://www.nature.com/articles/s41467-021-27937-7.pdf>

Gao M. et al. (2021): "**High-Performance Deep Learning Toolbox for Genome-Scale Prediction of Protein Structure and Function,**" *2021 IEEE/ACM Workshop on Machine Learning in High Performance Computing Environments (MLHPC)*, 46-57 | DOI: [10.1109/MLHPC54614.2021.00010](https://doi.org/10.1109/MLHPC54614.2021.00010)

Computational biology is one of many scientific disciplines ripe for innovation and acceleration with the advent of high-performance computing (HPC). In recent years, the field of machine learning has also seen significant benefits from adopting HPC practices. In this work, we present a novel HPC pipeline that incorporates various machine-learning approaches for structure-based functional annotation of proteins on the scale of whole genomes. Our pipeline makes extensive use of deep learning and provides computational insights into best practices for training advanced deep-learning models for high-throughput data such as proteomics data. We showcase methodologies our pipeline currently supports and detail future tasks for our pipeline to envelop, including large-scale sequence comparison using SAdLSA and prediction of protein tertiary structures using AlphaFold2.

<https://ieeexplore.ieee.org/document/9652872>

Ringeling, F.R., Chakraborty, S., Vissers, C. et al. (2022): **Partitioning RNAs by length improves transcriptome reconstruction from short-read RNA-seq data.** *Nat Biotechnol* | <https://doi.org/10.1038/s41587-021-01136-7>

The accuracy of methods for assembling transcripts from short-read RNA sequencing data is limited by the lack of long-range information. Here we introduce Ladder-seq, an approach that separates transcripts according to their lengths before sequencing and uses the additional information to improve the quantification and assembly of transcripts. Using simulated data, we show that a kallisto algorithm extended to process Ladder-seq data quantifies transcripts of complex genes with substantially higher accuracy than conventional kallisto. For reference-based assembly, a tailored scheme based on the StringTie2 algorithm reconstructs a single transcript with 30.8% higher precision than its conventional counterpart and is more than 30% more sensitive for complex genes. For de novo assembly, a similar scheme based on the Trinity algorithm correctly assembles 78% more transcripts than conventional Trinity while improving precision by 78%. In experimental data, Ladder-seq reveals 40% more genes harboring isoform switches compared to conventional RNA sequencing and unveils widespread changes in isoform usage upon m⁶A depletion by *Mett14* knockout.

<https://www.nature.com/articles/s41587-021-01136-7>

Liu J.-B., Li Z.-F., Lu L., Wang Z.-Y., Wang L. (2022) **Glyphosate damages blood-testis barrier via NOX1-triggered oxidative stress in rats: Long-term exposure as a potential risk for male reproductive health.** *Environment International* 159, 107038 | <https://doi.org/10.1016/j.envint.2021.107038>

Blood-testis barrier (BTB) creates a privileged niche indispensable for spermatogenesis. Glyphosate (GLY), the most commonly used herbicide worldwide, has been reported to decrease sperm quality. However, whether and how GLY destroys the BTB to affect sperm quality remains to be elucidated. Herein, this study was designed to investigate the influence of GLY on the BTB *in vivo* and *in vitro* experiments. The results showed that male rats exposed to GLY for 4 months exhibited a decrease in sperm quality and quantity, accompanied by BTB integrity disruption and testicular oxidative stress. Additionally, GLY-induced reactive oxygen species (ROS) contributed to the downregulation of BTB-related proteins in primary Sertoli cells (SCs). Intriguingly, we identified a marked upregulation of oxidative stress-related gene *NOX1* in GLY-exposed *testis* based on transcriptome analysis. *NOX1* knockdown blocked the GLY-induced oxidative stress, as well as prevented BTB-related protein decrease in SCs. Furthermore, the estrogen receptor (ER)- α was significantly upregulated *in vivo* and *in vitro* models. An ER- α inhibitor decreased the expression levels of both ER- α and *NOX1*. Mechanistically, GLY directly interacted with ER- α at the site of Pro39 and Lys401 to promote ER- α activation, which boosted *NOX1* expression to trigger ROS accumulation. Collectively, these results demonstrate that long-term GLY exposure adversely affects BTB integrity, which disrupts spermatogenesis via activation of ER- α /*NOX1* axis. This study presents a better understanding of the risk of long-term GLY exposure to male fertility.

<https://www.sciencedirect.com/science/article/pii/S0160412021006632>

Chang, D., Wang, C., Ul Islam, Z. et al. (2022): **Omics analysis coupled with gene editing revealed potential transporters and regulators related to levoglucosan metabolism efficiency of the engineered *Escherichia coli*.** *Biotechnol Biofuels* 15, 2 | <https://doi.org/10.1186/s13068-022-02102-4>

Bioconversion of levoglucosan, a promising sugar derived from the pyrolysis of lignocellulose, into biofuels and chemicals can reduce our dependence on fossil-based raw materials. However, this bioconversion process in microbial strains is challenging due to the lack of catalytic enzyme relevant to levoglucosan metabolism, narrow production ranges of the native strains, poor cellular transport rate of levoglucosan, and inhibition of levoglucosan metabolism by other sugars co-existing in the lignocellulose pyrolysate. The heterologous expression of eukaryotic levoglucosan kinase gene in suitable microbial hosts like *Escherichia coli* could

overcome the first two challenges to some extent; however, no research has been dedicated to resolving the last two issues till now.

<https://biotechnologyforbiofuels.biomedcentral.com/track/pdf/10.1186/s13068-022-02102-4.pdf>

Wong-Bajracharya J. et al. (2022): **The ectomycorrhizal fungus *Pisolithus microcarpus* encodes a microRNA involved in cross-kingdom gene silencing during symbiosis**, PNAS 119 (3) e2103527119; <https://doi.org/10.1073/pnas.2103527119>

Small RNAs (sRNAs) are known to regulate pathogenic plant–microbe interactions. Emerging evidence from the study of these model systems suggests that microRNAs (miRNAs) can be translocated between microbes and plants to facilitate symbiosis. The roles of sRNAs in mutualistic mycorrhizal fungal interactions, however, are largely unknown. In this study, we characterized miRNAs encoded by the ectomycorrhizal fungus *Pisolithus microcarpus* and investigated their expression during mutualistic interaction with *Eucalyptus grandis*. Using sRNA sequencing data and in situ miRNA detection, a novel fungal miRNA, *Pmic_miR-8*, was found to be transported into *E. grandis* roots after interaction with *P. microcarpus*. Further characterization experiments demonstrate that inhibition of *Pmic_miR-8* negatively impacts the maintenance of mycorrhizal roots in *E. grandis*, while supplementation of *Pmic_miR-8* led to deeper integration of the fungus into plant tissues. Target prediction and experimental testing suggest that *Pmic_miR-8* may target the host NB-ARC domain containing transcripts, suggesting a potential role for this miRNA in subverting host signaling to stabilize the symbiotic interaction. Altogether, we provide evidence of previously undescribed cross-kingdom sRNA transfer from ectomycorrhizal fungi to plant roots, shedding light onto t

<https://www.pnas.org/content/119/3/e2103527119>

John E, Jacques S, Phan HTT, Liu L, Pereira D, Croll D, et al. (2022): **Variability in an effector gene promoter of a necrotrophic fungal pathogen dictates epistasis and effector-triggered susceptibility in wheat**. PLoS Pathog 18(1): e1010149. |

<https://doi.org/10.1371/journal.ppat.1010149>

The fungus *Parastagonospora nodorum* uses proteinaceous necrotrophic effectors (NEs) to induce tissue necrosis on wheat leaves during infection, leading to the symptoms of septoria nodorum blotch (SNB). The NEs Tox1 and Tox3 induce necrosis on wheat possessing the dominant susceptibility genes *Snn1* and *Snn3B1/Snn3D1*, respectively. We previously observed that *Tox1* is epistatic to the expression of *Tox3* and a quantitative trait locus (QTL) on chromosome 2A that contributes to SNB resistance/susceptibility. The expression of *Tox1* is significantly higher in the Australian strain SN15 compared to the American strain SN4. Inspection of the *Tox1* promoter region revealed a 401 bp promoter genetic element in SN4 positioned 267 bp upstream of the start codon that is absent in SN15, called PE401. Analysis of the world-wide *P. nodorum* population revealed that a high proportion of Northern Hemisphere isolates possess PE401 whereas the opposite was observed in representative *P. nodorum* isolates from Australia and South Africa. The presence of PE401 removed the epistatic effect of *Tox1* on the contribution of the SNB 2A QTL but not *Tox3*. PE401 was introduced into the *Tox1* promoter regulatory region in SN15 to test for direct regulatory roles. *Tox1* expression was markedly reduced in the presence of PE401. This suggests a repressor molecule(s) binds PE401 and inhibits *Tox1* transcription. Infection assays also demonstrated that *P. nodorum* which lacks PE401 is more pathogenic on *Snn1* wheat varieties than *P. nodorum* carrying PE401. An infection competition assay between *P. nodorum* isogenic strains with and without PE401 indicated that the higher *Tox1*-expressing strain rescued the reduced virulence of the lower *Tox1*-expressing strain on *Snn1* wheat. Our study demonstrated that *Tox1* exhibits both ‘selfish’ and ‘altruistic’ characteristics. This offers an insight into a complex NE-NE interaction that is occurring within the *P. nodorum* p

<https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1010149>

Andergassen D., Smith Z.D., Kretzmer H., Rinn J.L., Meissner A. (2021): **Diverse epigenetic mechanisms maintain parental imprints within the embryonic and extraembryonic lineages**, Developmental Cell, 56, Issue 21, 2995-3005.e4, |

<https://doi.org/10.1016/j.devcel.2021.10.010>

Genomic imprinting and X chromosome inactivation (XCI) require epigenetic mechanisms to encode allele-specific expression, but how these specific tasks are accomplished at single loci or across chromosomal scales remains incompletely understood. Here, we systematically disrupt essential epigenetic pathways within polymorphic embryos in order to examine canonical and non-canonical genomic imprinting as well as XCI. We find that DNA methylation and Polycomb group repressors are indispensable for autosomal imprinting, albeit at distinct gene sets. Moreover, the extraembryonic ectoderm relies on a broader spectrum of imprinting mechanisms, including non-canonical targeting of maternal endogenous retrovirus (ERV)-driven promoters by the H3K9 methyltransferase G9a. We further identify Polycomb-dependent and -independent gene clusters on the imprinted X chromosome, which appear to reflect distinct domains of *Xist*-mediated suppression. From our data, we assemble a comprehensive inventory of the epigenetic pathways that maintain parent-specific imprinting in eutherian mammals, including an expanded view of the placental lineage.

[https://www.cell.com/developmental-cell/fulltext/S1534-5807\(21\)00811-](https://www.cell.com/developmental-cell/fulltext/S1534-5807(21)00811-X?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS153458072100811X%3Fshowa)

[X?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS153458072100811X%3Fshowa](https://www.cell.com/developmental-cell/fulltext/S1534-5807(21)00811-X?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS153458072100811X%3Fshowa)

[ll%3Dtrue](https://www.cell.com/developmental-cell/fulltext/S1534-5807(21)00811-X?returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS153458072100811X%3Fshowa)

Willow J., Taning C.N.T., Cook S.M., Sulg S., Silva A.I., Smaghe G., Veromann E. (2021): **RNAi Targets in Agricultural Pest Insects: Advancements, Knowledge Gaps, and IPM**. Front. Agron 3:794312 | <https://doi.org/10.3389/fagro.2021.794312>

The unprecedented target-specificity of double-stranded RNA (dsRNA), due to its sequence-specific mode of action, puts dsRNA at the forefront of biosafe insecticide technology. Since 2007, sensitive target genes have been identified in numerous crop pest insects, with an end goal of applying RNA interference (RNAi) in pest management. Key RNAi targets identified include genes involved in (1) feeding and digestion, (2) production of dsRNases, (3) resistance to insecticides and plant allelochemicals, (4) reproductive fitness, and (5) transmission of plant viruses. Despite the advances, there remain critical knowledge gaps in each of these areas. Particular emphasis must be placed on ensuring RNAi's compatibility with integrated pest management (IPM), via further identification of molecular targets that reduce crop damage while sustaining pest (host) populations for highly specialized biocontrol agents, the latter representing a core pillar of IPM. <https://www.frontiersin.org/articles/10.3389/fagro.2021.794312/full>

Kang S., Sun D. Qin J., Guo L. et al. (2022): **Fused: a promising molecular target for an RNAi-based strategy to manage Bt resistance in *Plutella xylostella* (L.)**. Journal of Pest Science (2022) 95:101–114 | <https://doi.org/10.1007/s10340-021-01374-3>

Bacillus thuringiensis (Bt), a naturally occurring entomopathogenic soil bacterium, has been the active ingredient of sprayable Bt biopesticides for over a century. Insecticidal Bt Cry proteins are particularly well suited for use as plant-incorporated protectants in transgenic crops (Bt crops) due to their specificity against insect pests and safety for non-target organisms. The sustainability of these Bt products, however, has been challenged by the development of resistance in the field. RNA interference (RNAi), a species-specific control alternative that has been deregulated and commercialized in the USA and Canada, provides a new mode of action to complement the existing Bt products. Based on our preliminary research, we hypothesized that pyramiding/integrating Bt with RNAi can address/manage resistance issues related to Bt traits. To examine this overarching hypothesis, we (1) cloned and characterized a serine/threonine kinase gene (*fused*) of the Hedgehog (Hh) signaling pathway in the diamondback moth, *Plutella xylostella* (L.), a global superpest; (2) profiled *Pxfused* expression in Bt-resistant *P. xylostella* strains; and (3) investigated the involvement of *Pxfused* in Bt Cry1Ac resistance in *P. xylostella*. *Pxfused* expression was elevated ubiquitously in all Bt-resistant strains, and silencing of *Pxfused* led to larval and pupal mortality in both Cry1Ac-susceptible and -resistant strains, suggesting that *Pxfused* is a potential target for RNAi-based resistance management. Taken together, our results not only identify a molecular target to control a devastating lepidopteran pest, but also shed light on a novel resistance management strategy through the integration of two biotechnological techniques with distinct modes of action.

<https://link.springer.com/article/10.1007%2Fs10340-021-01374-3>

EFSA:

Food Enzymes

CEP Panel (2022): Scientific Opinion on the safety evaluation of the food enzyme cyclomaltodextrin glucanotransferase from *Anoxybacillus caldiproteolyticus* strain St-88.

EFSA Journal 2022;20(1):7004, 10 pp. <https://doi.org/10.2903/j.efsa.2022.7004>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2022.7004>

Scientific Opinion on the safety evaluation of a food enzyme containing chymosin, pepsin and gastricsin from the abomasum of suckling goats. EFSA Journal 2022;20(1):7005, 11 pp.

<https://doi.org/10.2903/j.efsa.2022.7005>

<https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2022.7005>

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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.

As always, I thank you all for hints and for publications. Most of the pdf files can be downloaded directly from the links.

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