EEA-RESEARCH-64

EDIT GRASS 4FOOD

Legislative proposal for plants produced by NGTs: implications for abiotic stress tolerance breeding

LAMMC, 27 October 2023

“EditGrass4Food”, ID No EEA-RESEARCH-64, Contract No EEZ/BPP/VIAA/2021/4 is financially supported by European Economic Area (EEA) grants

EditGrass4Food project

- Background of the project
- Genome editing in the context of EU GMO regulation
- EC legislative proposal
- Further initiatives to support EC proposal and to facilitate legislative process

Improving adaptability and resilience of perennial ryegrass for safe and sustainable food systems through CRISPR-Cas9 technology (EditGrass4Food)

EEA-RESEARCH-64

Principal Investigator: Nils Rostoks

Promoter: University of Latvia

Partners:

- Norwegian University of Life Sciences, NMBU , Norway
- Tallinn University of Technology, TalTech, Estonia
- Lithuanian Research Centre for Agriculture and Forestry, LAMMC, Lithuania

From **01.05.2021** to **30.04.2024** (36 months)

Website: https://www.editgrass4food.lu.lv/en/

Lolium perenne

- *Lolium perenne* (perennial ryegrass)
- Native to Southern Europe, the Middle East and North Africa
- Important pasture and forage plant, extensively used in seed mixes
- High yield in fertile soil
- Lacks adaptation to climate conditions in Nordic and Baltic region, but due to the climate change this situation can change
- For cultivation in Nordic and Baltic countries perennial ryegrass needs improved freezing and drought tolearance

Lolium perenne

- *Lolium perenne* exhibits perennial growth habit
- *L. perenne* is an outcrossing, wind-pollinated species
- Selfing is largely prevented by a gametophytic, two-locus incompatibility system (*SZ*)
- Genome is heterozygous and the varieties consist of a mixture of related genotypes
- Genotypes exhibit different efficiciency of *Agrobacterium*-mediated transformation (CRISPR/Cas constructs) and variable regeneration capacity

Project goals

EEA-RESEARCH-64

Aim of the project is to utilize transcriptomics and functional genomics to increase sustainability in agriculture through improvement of perennial ryegrass with better adaptation to frost and drought for current and future climates.

1. Establish a diverse perennial ryegrass core association panel by utilization of data from ongoing projects (WP1),
2. Screen the association panel in order to detect haplotype-resolved single-nucleotide variants and structural variation in the targeted genes/alleles for freezing and drought genes (WP1),
3. Identify novel genes and characterize drought and freezing tolerance genes by comparing their expression for pathway related genes in non-edited and mutant plants (WP2),
4. Develop CRISPR-Cas9 constructs and generate CRISPR-edited perennial ryegrass mutants for freezing and mild drought tolerance (WP3),
5. Validate and characterize the role of the genes and their sequence variations in the freezing and drought mechanisms (WP4).

WPs

- WP1. Establishment and screening of perennial ryegrass association panel for freezing and drought related traits. Coordinator: NMBU; Involved partners: NMBU, LAMMC
- WP2. Transcriptome regulation of freezing and drought tolerance in perennial ryegrass. Coordinator: NMBU; Involved partners: NMBU, LAMMC
- WP3. Functional characterization of frost and drought candidate genes in perennial ryegrass by CRISPR-Cas9. Coordinator: TalTech; Involved partners: LU, NMBU
- WP4. Validation of improved freezing and water shortage tolerance. Coordinator: LAMMC; Involved partners: TalTech, NMBU, LU
- WP5. Management and coordination of research activities and dissemination of results. Coordinator: LU; Involved partners: TalTech, NMBU, LAMMC

Bottlenecks in genome editing

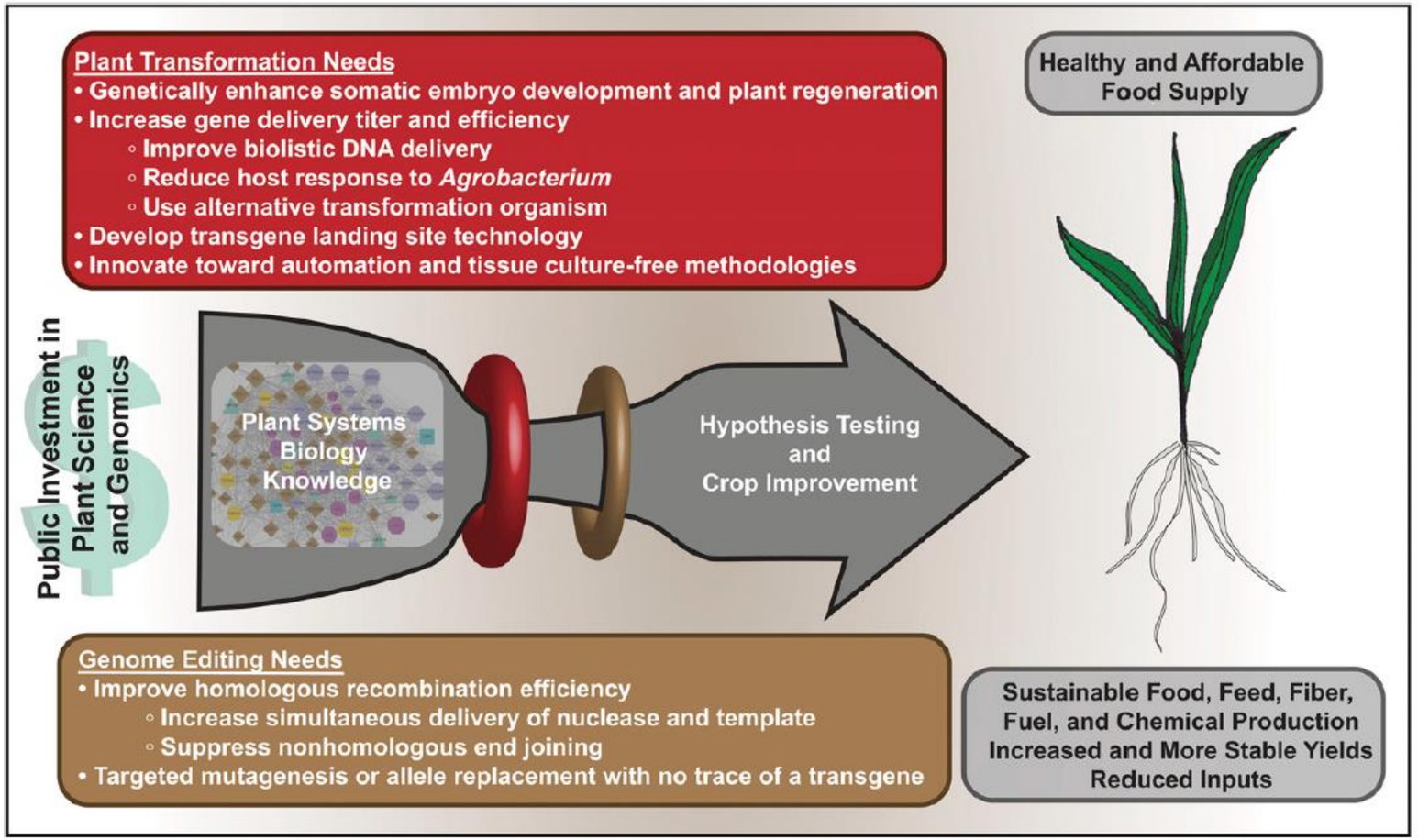

Figure 1. Current Bottlenecks in Applying Genome Editing to Crop Functional Genomics and Crop Improvement.

The main bottleneck is in plant transformation and regeneration. A secondary bottleneck is in the delivery of genome editing reagents to plant cells to produce the intended effects.

Altpeter et al. (2016) Advancing crop transformation in the era of genome editing. The Plant Cell 28:1510-1520

Exmaples of genetic engineering for abiotic stress tolerance

Journal of Experimental Botany, Vol. 70, No. 5 pp. 1669–1681, 2019
doi:10.1093/jxb/erz037 Advance Access Publication 6 February 2019
This paper is available online free of all access charges (see https://academic.oup.com/jxb/pages/openaccess for further details)

RESEARCH PAPER

Field-grown transgenic wheat expressing the sunflower gene *HaHB4* significantly outyields the wild type

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Editor: Greg Rebetzke, CSIRO Agriculture and Food, Australia

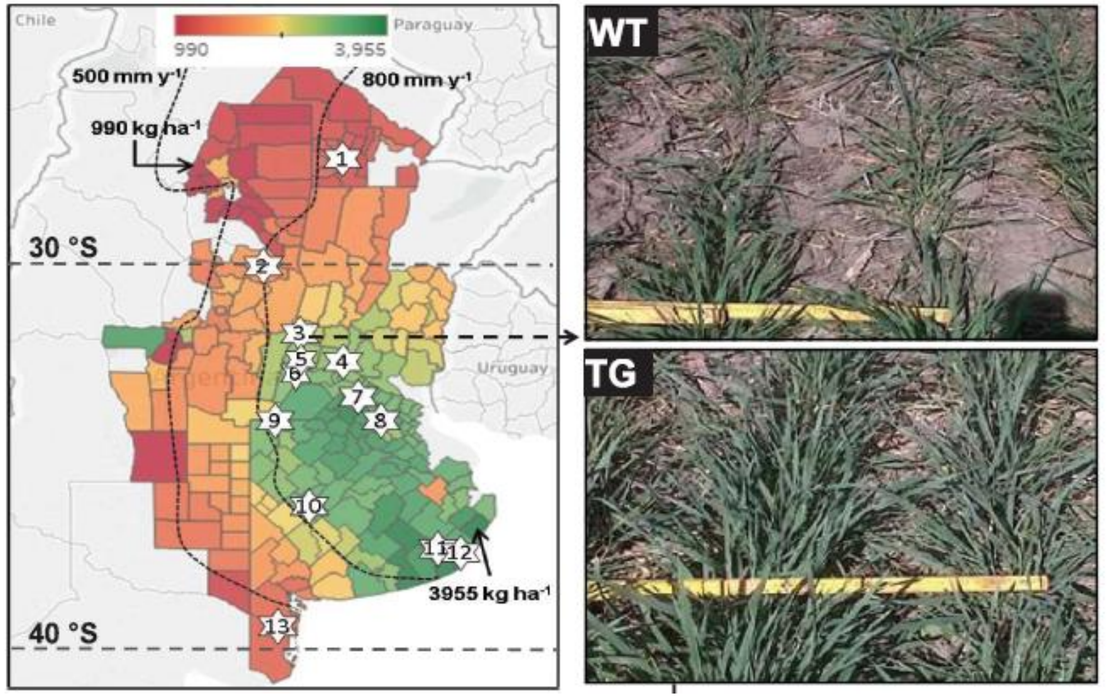
Abstract

HaHB4 is a sunflower transcription factor belonging to the homeodomain-leucine zipper I family whose ectopic expression in Arabidopsis triggers drought tolerance. The use of PCR to clone the *HaHB4* coding sequence for wheat transformation caused unprogrammed mutations producing subtle differences in its activation ability in yeast. Transgenic wheat plants carrying a mutated version of *HaHB4* were tested in 37 field experiments. A selected transgenic line yielded 6% more ($P<0.001$) and had 9.4% larger water use efficiency ($P<0.02$) than its control across the evaluated environments. Differences in grain yield between cultivars were explained by the 8% improvement in grain number per square meter ($P<0.0001$), and were more pronounced in stress (16% benefit) than in non-stress conditions (3% benefit), reaching a maximum of 97% in one of the driest environments. Increased grain number per square meter of transgenic plants was accompanied by positive trends in spikelet numbers per spike, tillers per plant, and fertile florets per plant. The gene transcripts associated with abiotic stress showed that HaHB4's action was not dependent on the response triggered either by RD19 or by DREB1a, traditional candidates related to water deficit responses. HaHB4 enabled wheat to show some of the benefits of a species highly adapted to water scarcity, especially in marginal regions characterized by frequent droughts.

Keywords: Drought tolerance, grain yield determination, HaHB4, sunflower transcription factor, transgenic wheat, water use efficiency, wheat field trials.

Introduction

Plants have evolved molecular mechanisms to deal with stress conditions, enabling their survival and reproduction. Among abiotic stress factors, drought is the major limiting constraint on agricultural productivity (Wang *et al.*, 2003). Drought tolerance has been used as a key parameter to select transgenic stress-tolerant model plants and crops (Araus and Cairns,



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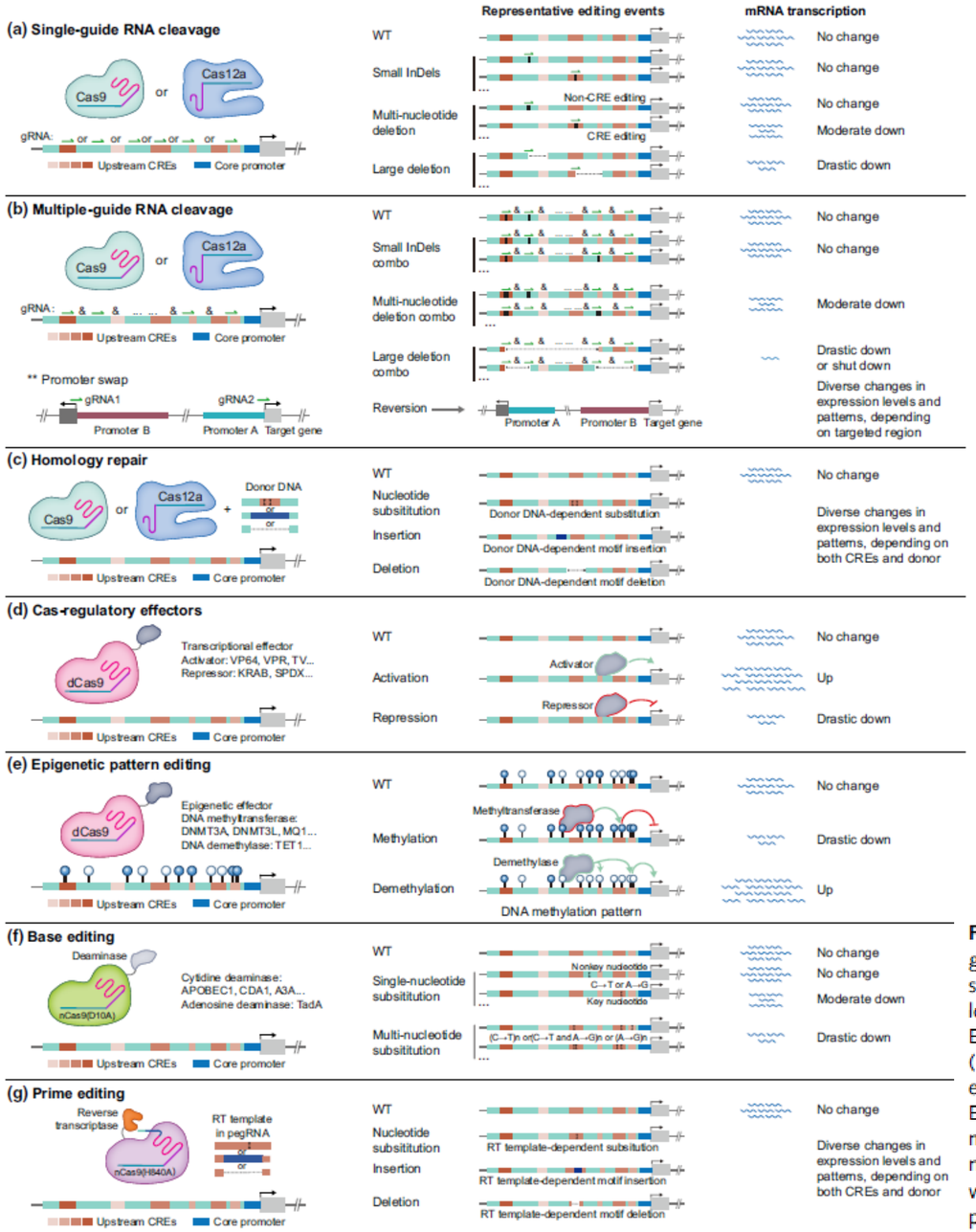
New Phytologist



Promoter editing strategies

Fig. 3 Editing plant promoters using various CRISPR-Cas tools and editing strategies. (a) Single-guide RNA cleavage mediated promoter editing. Using a single-guide RNA, the Cas nuclease can be directed to target the promoter region, inducing small InDels, multi-nucleotide deletion, or large deletion. This is the simplest approach to editing plant promoters. (b) Multiple-guide RNA cleavage mediated promoter editing. Using multiple-guide RNAs to generate multiple loci InDels, large deletions, or mixed editing events. In most cases, the genotypes of editing events are complex. (c) Homologous template-directed repair. Exogenous donor DNA can be utilized to repair DSBs at the promoter regions, enabling the introduction of specific modifications to the promoter region. (d) Cas-regulatory effectors on based gene regulation. The strategy relies on the use of catalytically inactive Cas9 proteins (dCas9) fused to transcriptional effectors, such as activators or repressors, to control gene expression by binding to specific DNA sequences in the promoter region. (e) Epigenetic editing. Epigenetic editing involves fusing the dCas9 protein with epigenetic effectors such as DNA methyltransferases or demethylases to selectively alter the DNA methylation level at the promoter regions and thereby modulate gene expression. (f) Base editing. Base editors, composed of a deaminase and a Cas9 nickase, can achieve single or multiple nucleotide substitutions in the promoter regions. (g) Prime editing. This strategy is based on the fusion of a Cas nickase with reverse transcriptase and pegRNA. By utilizing pegRNA with specific RT templates, prime editing can introduce various types of changes in the promoter regions, such as nucleotide substitutions, insertions, deletions, and combinations of these.

Plant Biotechnology Journal

Plant Biotechnology Journal (2017) **15**, pp. 207–216 doi: 10.1111/pbi.12603

ARGOS8 variants generated by CRISPR-Cas9 improve maize grain yield under field drought stress conditions

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Summary

Maize *ARGOS8* is a negative regulator of ethylene responses. A previous study has shown that transgenic plants constitutively overexpressing *ARGOS8* have reduced ethylene sensitivity and improved grain yield under drought stress conditions. To explore the targeted use of *ARGOS8* native expression variation in drought-tolerant breeding, a diverse set of over 400 maize inbreds was examined for *ARGOS8* mRNA expression, but the expression levels in all lines were less than that created in the original *ARGOS8* transgenic events. We then employed a CRISPR-Cas-enabled advanced breeding technology to generate novel variants of *ARGOS8*. The native maize GOS2 promoter, which confers a moderate level of constitutive expression, was inserted into the 5′-untranslated region of the native *ARGOS8* gene or was used to replace the native promoter of *ARGOS8*. Precise genomic DNA modification at the *ARGOS8* locus was verified by PCR and sequencing. The *ARGOS8* variants had elevated levels of *ARGOS8* transcripts relative to the native allele and these transcripts were detectable in all the tissues tested, which was the expected results using the GOS2 promoter. A field study showed that compared to the WT, the *ARGOS8* variants increased grain yield by five bushels per acre under flowering stress conditions and had no yield loss under well-watered conditions. These results demonstrate the utility of the CRISPR-Cas9 system in generating novel allelic variation for breeding drought-tolerant crops.

Keywords: maize, ARGOS, CRISPR-Cas9, genome editing, drought tolerance, grain yield.

Introduction

Developing more drought-tolerant crops in a sustainable manner is one means to meet the demand of an increasing human population that will require more food, feed and fuel. Improvement in drought tolerance of crops is ultimately measured by an increase in grain yield under water-limiting conditions. The physiological processes and metabolic networks underlying drought tolerance are complicated and often difficult to delineate. Nevertheless, the phytohormone ethylene is known to play an important role in regulating plant response to abiotic stress, including water deficits and high temperature (Hays *et al.*, 2007; Kawakami *et al.*, 2010, 2013). Field studies have shown that reducing ethylene biosynthesis by silencing *1-aminocyclopropane-1-carboxylic acid synthase6* in transgenic maize plants improves grain yield under drought stress conditions (Habben *et al.*, 2014). A higher yield also can be achieved by decreasing the sensitivity of maize to ethylene (Shi *et al.*, 2015). *ARGOS* genes are negative regulators of the ethylene response and modulate ethylene signal transduction, enhancing drought tolerance when overexpressed in transgenic maize plants (Guo *et al.*, 2014; Shi *et al.*, 2015).

In addition to a transgenic approach, natural genetic variation for traits that impact drought tolerance has also been used in maize breeding programmes to improve grain yield. By applying precision phenotyping and molecular markers as well as understanding the genetic architecture of quantitative traits, maize breeders developed hybrids (AQUAmax®) with increased grain yield under drought stress conditions (Cooper *et al.*, 2014; Gaffney *et al.*, 2015). The drought tolerance in these hybrids is governed by multiple genes which individually have small effects. Potentially, some of these key genes could be identified and altered to generate new alleles to produce a larger effect, thus enhancing the breeding process. However, until recently, generating such allelic variation with physically or chemically induced mutagenesis was a random process, which made it difficult to produce intended DNA sequence changes at a target locus. In the past few years, efficient genome editing technologies have emerged, enabling rapid and precise manipulation of DNA sequences, and setting the stage for developing drought-tolerant germplasm by editing major genes in their natural chromosomal context.

Four genome editing tools, meganucleases, zinc-finger nucleases (ZFN), transcription activator-like effector nucleases (TALEN) and the clustered regularly interspaced short palindromic repeat (CRISPR)/CRISPR-associated nuclease protein (Cas) system, have provided targeted gene modification in plants (Čermák *et al.*, 2015; Gao *et al.*, 2010; Li *et al.*, 2012, 2013; Shukla *et al.*, 2009). Among these, the CRISPR-Cas9 system is easiest to implement and is highly efficient. The system consists of a Cas9 endonuclease derived from *Streptococcus pyogenes* and a chimeric single guide RNA that directs Cas9 to a target DNA sequence in the genome. CRISPR-Cas9 genome editing is accomplished by introducing a DNA double-strand break in the target locus via Cas9, followed by DNA repair through either the endogenous imprecise nonhomologous end-joining (NHEJ) or the high-fidelity homology-directed repair (HDR) pathways. NHEJ can induce small insertions or deletions at the repair junction while HDR stimulates precise sequence alterations, including programmed sequence correction as well as DNA fragment insertion and swap, when a DNA repair template is exogenously supplied. The system has been successfully tested in staple crops, such as maize, wheat, rice and soybean (Cai *et al.*, 2015; Du *et al.*, 2016; Jacobs *et al.*, 2015; Jiang *et al.*, 2013; Li *et al.*,

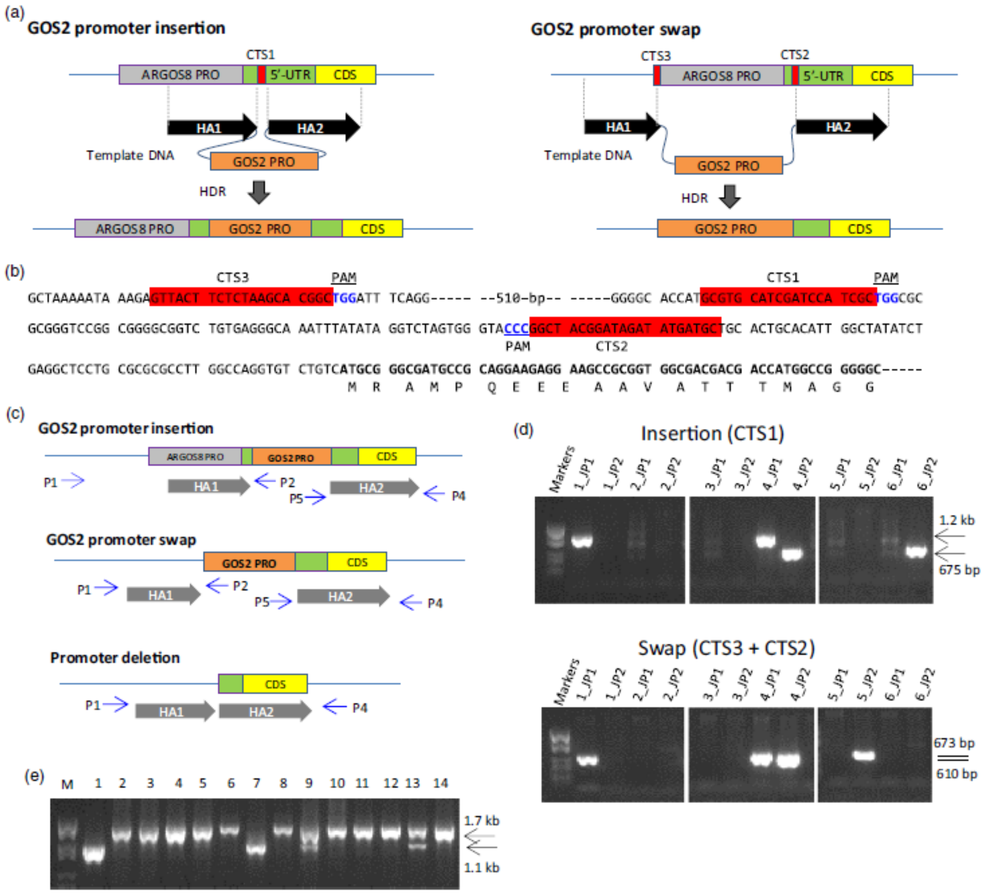

Figure 2 Editing the *ARGOS8* genomic sequence using the CRISPR/Cas9 system to generate variants with constitutive expression. (a) Schematic drawing illustrating the insertion of GOS2 PRO into the 5′-UTR of *ARGOS8* and the promoter swap. CTS, CRISPR-RNA target site; HA, homology arm; HDR, homology-directed repair; GOS2 PRO, maize GOS2 promoter and the 5′-UTR with an intron. (b) Genomic sequence of the *ARGOS8* 5′-UTR and the upstream region. The CRISPR-RNA target sites (CTS) are highlighted in red, and the protospacer adjacent motifs (PAM) are shown in blue font. The *ARGOS8* coding region is shown in bold font. (c) Diagram showing primers used in junction PCR for genotyping regenerated shoots and long PCR for amplifying and sequencing the entire modification region in homozygous plants. The relative position and direction of PCR primers (P) are indicated by arrows. P1 and P2 for the HR1 junction; P5 and P4 for the HR2 junction; P1 and P4 for the long PCR. (d) Junction PCR analysis of regenerated shoots. Agarose gel images are shown for representative regenerated shoots positive for one junction or two junctions and shoots negative in the junction PCR assay. JP1, HR1 junction PCR with the primer P1 and P2; JP2, HR2 junction PCR with P5 and P4. (e) PCR screening regenerated shoots for deletion in the *ARGOS8* locus. An agarose gel image is shown for PCR products amplified with the primer P1 and P4 in representative shoots (Lanes 1-14) generated from the *CRISPR RNA-3* and *RNA-1* transformation. M, DNA molecular weight markers.

GMO definition

Directive 2001/18/EC on the deliberate release into the environment of genetically modified organisms and repealing Council Directive 90/220/EEC, Article 2:

«genetically modified organism (GMO) means an organism, with the exception of human beings, in which the genetic material has been altered in a way that does not occur naturally by mating and/or natural recombination»

Within the terms of this definition:

(a) genetic modification occurs at least through the use of the techniques listed in Annex I A, part 1;

(b) the techniques listed in Annex I A, part 2, are not considered to result in genetic modification

Methods of genetic modification

Directive 2001/18/EC Annex IA

Techniques of genetic modification referred to in Article 2(2)(a) are inter alia:

(1) recombinant nucleic acid techniques involving the formation of new combinations of genetic material by the insertion of nucleic acid molecules produced by whatever means outside an organism, into any virus, bacterial plasmid or other vector system and their incorporation into a host organism in which they do not naturally occur but in which they are capable of continued propagation;

(2) techniques involving the direct introduction into an organism of heritable material prepared outside the organism including micro-injection, macro-injection and micro-encapsulation;

(3) cell fusion (including protoplast fusion) or hybridisation techniques where live cells with new combinations of heritable genetic material are formed through the fusion of two or more cells by means of methods that do not occur naturally

Exemptions

Directive 2001/18/EC Annex IA

Techniques/methods of genetic modification yielding organisms to be excluded from the Directive, on the condition that they do not involve the use of recombinant nucleic acid molecules or genetically modified organisms other than those produced by one or more of the techniques/methods listed below are:

(1) mutagenesis,

(2) cell fusion (including protoplast fusion) of plant cells of organisms which can exchange genetic material through traditional breeding methods.

Press and Information

Court of Justice of the European Union
PRESS RELEASE No 111/18
Luxembourg, 25 July 2018

Judgment in Case C-528/16
Confédération paysanne and Others v Premier ministre and Ministre de l'Agriculture, de l'Agroalimentaire et de la Forêt

Organisms obtained by mutagenesis are GMOs and are, in principle, subject to the obligations laid down by the GMO Directive

However, organisms obtained by mutagenesis techniques which have conventionally been used in a number of applications and have a long safety record are exempt from those obligations, on the understanding that the Member States are free to subject them, in compliance with EU law, to the obligations laid down by the directive or to other obligations

GENOME EDITED (TARGETED MUTAGENESIS) ORGANISMS ARE GMO

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EFSA and genome editing

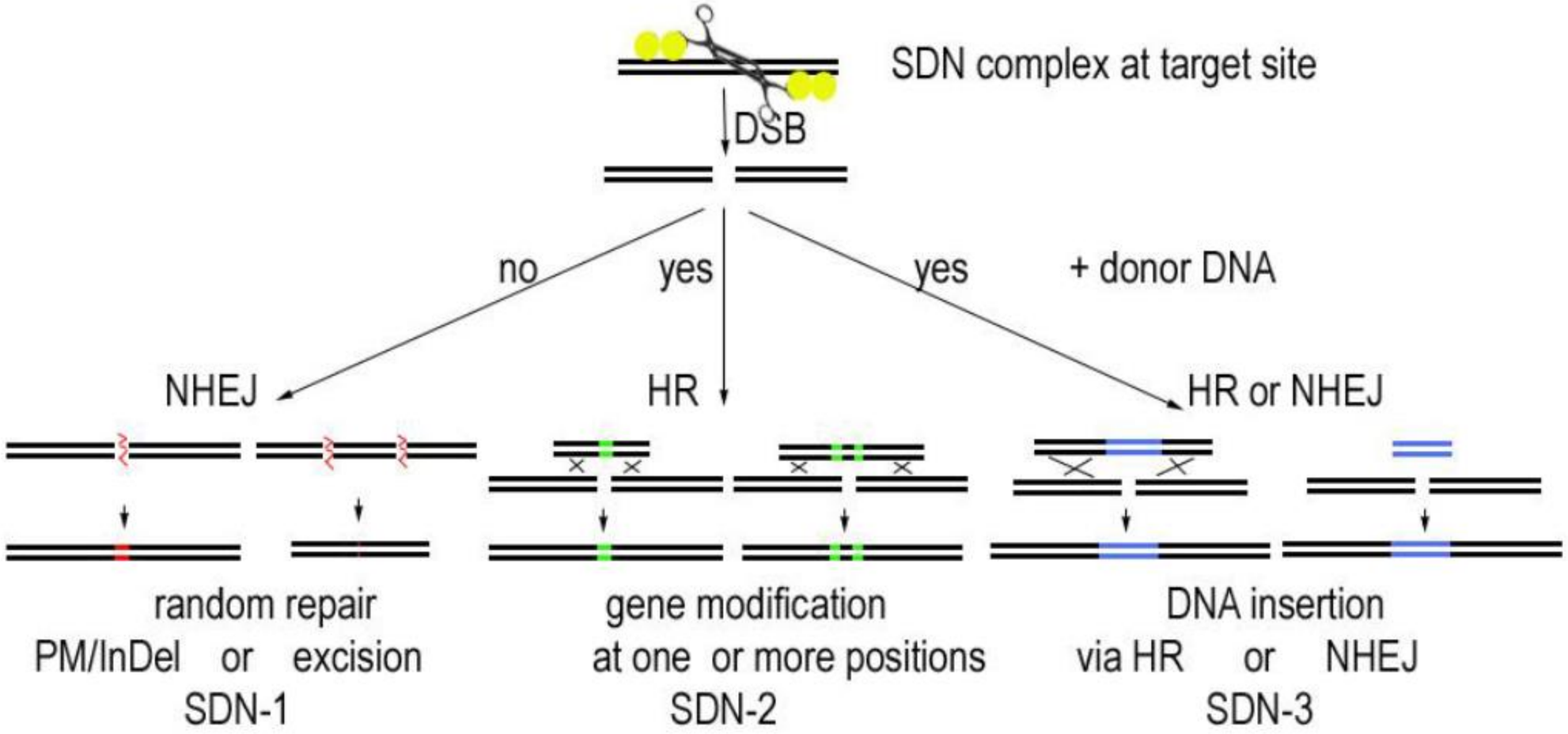
- EFSA Scientific Opinion on SDN-3 plants (transgenic) in 2012.

- EFSA GMO Panel, ….., Rostoks N (2020) Applicability of the EFSA Opinion on site-directed nucleases type 3 for the safety assessment of plants developed using site-directed nucleases type 1 and 2 and oligonucleotide-directed mutagenesis. EFSA Journal 18:e06299

SDN risk assessment

- SDN1 and SDN2 genome modifications (small insertions, deletions and nucleotide substitutions) are technically indistinguishable from natural genetic diversity in species genomes (targeted mutagenesis)
- SDN3 plants contain fragments of exogenous DNA, but unlike regular transgenic plants, the insertion of DNA is directed to a specific, precisely defined genome region which facilitates the risk assessment

SDN scenarious



EFSA conclusions on SDN-1, SDN-2 un ODM

- Conclusions:

In relation to ToR1, the GMO Panel concludes that the assessment methodology presented in section 4 of the EFSA opinion on SDN3 is partially applicable to SDN1, SDN2, and ODM. Since these approaches aim at modifying an endogenous DNA sequence, in case the final product does not contain any transgene, intragene, or cisgene, these plants will not present any of the hazards potentially associated to the inserted transgene, intragene, or cisgene found in plants obtained using the SDN-3 approach. Moreover, the GMO Panel did not identify any additional hazard associated to the use of the SDN1, SDN2 and ODM approaches as compared to both SDN3 and conventional breeding techniques which include conventional mutagenesis.

In relation to ToR2, the GMO Panel concludes that the existing Guidances for food and feed (EFSA GMO Panel, 2011) and environmental risk assessment (EFSA GMO Panel, 2010) are sufficient but are only partially applicable for the risk assessment of plants generated via SDN1, SDN2, and ODM approaches. Indeed, as SDN1, SDN2 and ODM aim at modifying endogenous DNA sequence(s) without integrating exogenous DNA, a number of requirements of the existing guidances that are linked to the presence of a transgene are not relevant for the assessment of SDN1, SDN2 and ODM plants. The amount of experimental data needed for the risk assessment will mainly depend on the modified trait introduced and, therefore, the GMO Panel considers that principle of the case-by-case approach for the risk assessment is particularly relevant for SDN1, SDN2 and ODM plants.

Criteria for risk assessment of plants produced by targeted mutagenesis, cisgenesis and intragenesis

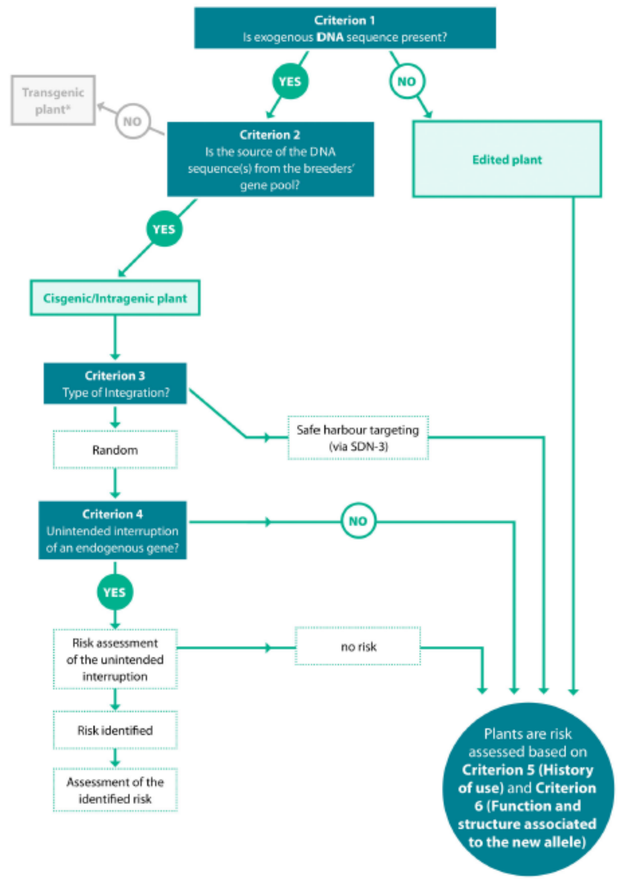
EFSA Panel on Genetically Modified Organisms (GMO),
Ewen Mullins, Jean-Louis Bresson, Tamas Dalmay, Ian Crawford Dewhurst,
Michelle M Epstein, Leslie George Firbank, Philippe Guerche, Jan Hejatko,
Francisco Javier Moreno, Hanspeter Naegeli, Fabien Nogué, Nils Rostoks,
Jose Juan Sánchez Serrano, Giovanni Savoini, Eve Veromann, Fabio Veronesi,
Antonio Fernandez, Andrea Gennaro, Nikoletta Papadopoulou, Tommaso Raffaello and
Reinhilde Schoonjans

Abstract

EFSA was asked by the european Commission to develop criteria as advice for consideration for the risk assessment of plants produced by targeted mutagenesis, cisgenesis and intragenesis. EFSA proposes in this statement six main criteria to assist the risk assessment of these plants. The first four criteria are related to the molecular characterisation of the genetic modification introduced in the recipient plant. The four criteria evaluate whether any exogenous DNA sequence(s) is/are present (Criterion 1), whether such sequence derives from the breeders' gene pool (Criterion 2), the type of integration (Criterion 3) and whether any endogenous plant gene is interrupted (Criterion 4). Depending on the evaluation of the above criteria, the product can be a genome edited plant where no exogenous DNA sequence is present, or a cisgenic or intragenic plant where the cisgenic and intragenic sequence are introduced by targeted insertion and no plant endogenous genes are interrupted. In these cases, two more criteria are assessed to evaluate the history of safe use (Criterion 5) and the structure and function of the new allele (Criterion 6). If cisgenic and intragenic sequence are introduced by random integration without interruption of an endogenous gene, or when no risk is identified when an endogenous gene is interrupted, the criteria 5 and 6 will also be assessed. Evaluating the history of safe use is an important part of the proportionate risk assessment of cisgenic, intragenic and genome-edited plants since the newly introduced allele may already be present in nature. However, when the history of safe use cannot be sufficiently demonstrated, the function and structure of the introduced allele should be carefully assessed. Recommendations are also included on the aspects that need further elaboration for full applicability of the criteria proposed herein are also included.

Keywords: cisgenesis, intragenesis, targeted mutagenesis, criteria, risk assessment, GM plant, new genomic techniques

EFSA CRITERIA FOR RISK ASSESSMENT OF NGT PLANTS



*Please note that plants obtained by transgenesis are out of the scope of the EC initiative to propose a legal framework for plants obtained by targeted mutagenesis and cisgenesis and for their food and feed products.

Figure 1: Decision tree according to proposed EFSA criteria for the risk assessment of plants developed through targeted mutagenesis, cisgenesis and intragenesis

EFSA DECISION TREE ON NGT PLANTS

Commission proposal on plants obtained by certain new genomic techniques (NGTs)

WHAT ARE NEW GENOMIC TECHNIQUES?

NGTs
are techniques
of genetic modification
that can help breed new plant
varieties faster, and with higher
precision than conventional breeding
techniques.
NGTs can produce a wide diversity
of plant products. These plants may
have only small changes that might
also occur in nature or through
conventional breeding or they
may have more complex
modifications.

Objectives of the proposal

- High level of protection of health and environment
- Developments to contribute to sustainability and climate adaptation in a wide range of plant species, especially for the agri-food system
- Opportunities for research and innovation, including for SMEs

Scope of the proposal

	of…
• **Deliberate release** into the environment for any other purpose than placing on the market (e.g. field trials)	• Plants obtained by targeted mutagenesis and cisgenesis, including intragenesis (‘**NGT plants**’)
• **Placing on the market**	• **NGT plants** • NGT **food/feed** • **Other products** containing/consisting of NGT plants

Category 1 NGT plants: Verification criteria

NGT plants that could have been obtained naturally or by conventional breeding methods

A NGT plant is considered equivalent to conventional plants when it differs from the recipient/parental plant by no more than 20 genetic modifications of the types referred to in points 1 to 5, in any DNA sequence sharing sequence similarity with the targeted site that can be predicted by bioinformatic tools.

(1) substitution or insertion of no more than 20 nucleotides;

(2) deletion of any number of nucleotides;

(3) on the condition that the genetic modification does not interrupt an endogenous gene:

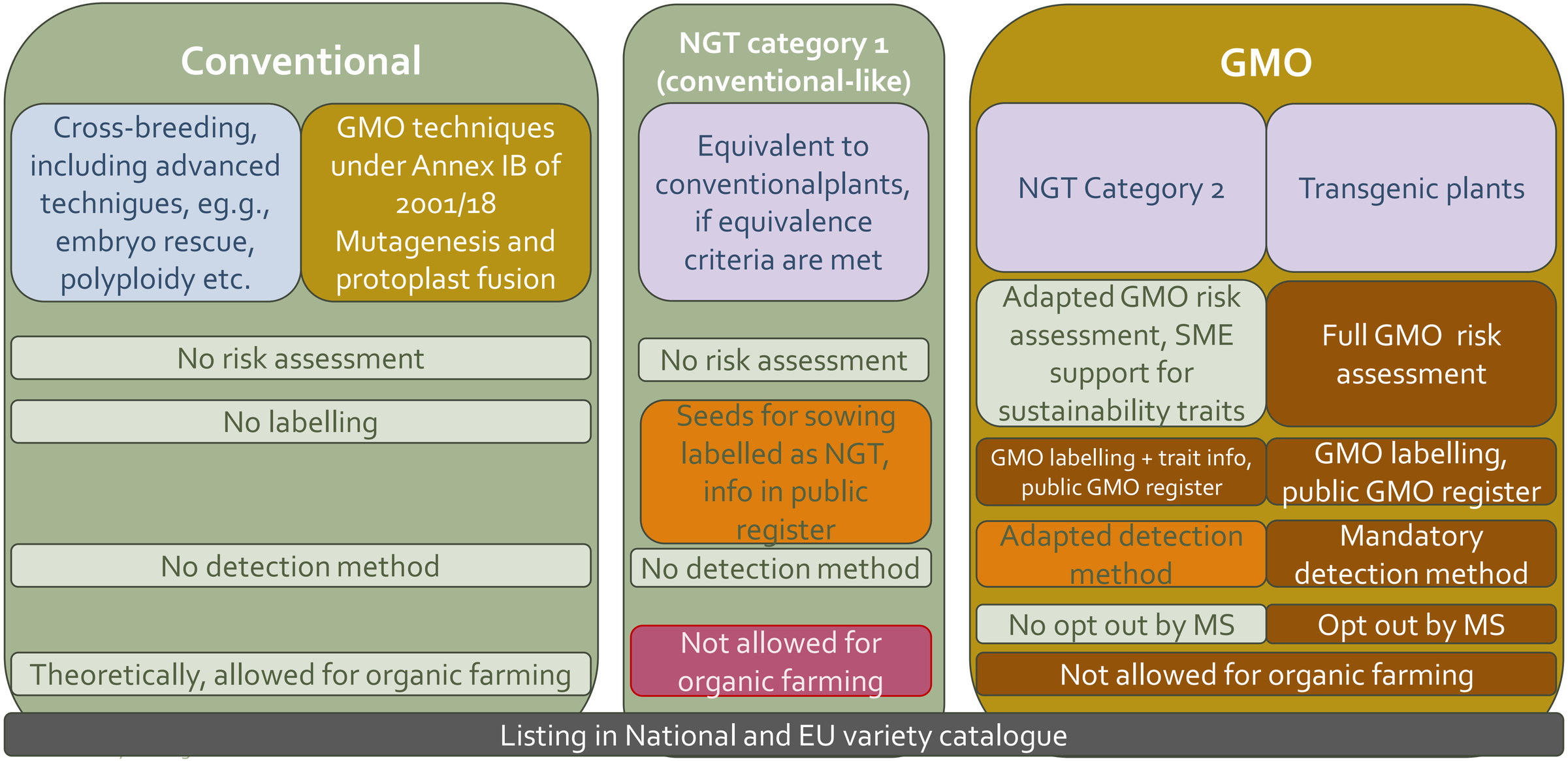
(a) targeted insertion of a contiguous DNA sequence existing in the breeder's gene pool;

(b) targeted substitution of an endogenous DNA sequence with a contiguous DNA sequence existing in the breeder's gene pool;

(4) targeted inversion of a sequence of any number of nucleotides;

(5) any other **targeted modification** of any size, on the condition that the resulting DNA sequences already occur (possibly with modifications as accepted under points (1) and/or (2)) in a species from the breeders' gene pool.

Plant product classification



Specific provision for category 2 NGT plants

- **Incentives** for traits relevant for sustainability
  - ♦ Food & feed: Fast track assessment by EFSA
  - ♦ Pre-submission advice on risk hypotheses
  - ♦ SMEs: - Extended pre-submission advice (also on studies)
    - Food & feed: no financial contribution for detection method validation
- Voluntary **labelling of traits** conveyed by the genetic modification
- **Coexistence** measures
- **No opt-out**

Traits qualifying for incentives

Traits **justifying the incentives**:

- yield, including yield stability and yield under low-input conditions;
- tolerance/resistance to biotic stresses, including plant diseases caused by nematodes, fungi, bacteria, viruses and other pests;
- tolerance/resistance to abiotic stresses, including those created or exacerbated by climate change;
- more efficient use of resources, such as water and nutrients;
- characteristics that enhance the sustainability of storage, processing and distribution;
- improved quality or nutritional characteristics;
- reduced need for external inputs, such as plant protection products and fertilisers.

Traits **excluding the application of incentives**:

- tolerance to herbicides

GeneBEcon

Funded by
the European Union

GeneBEcon – 6 regulatory options at a glance

1. Status Quo

- GMO-legislation stays intact
- No changes by future ECJ judgments

- Trans-, cisgenic and genome edited organisms = GMO
- Authorisation via comitology procedure

2. Use existing possibilities

- Use of leeways in current GMO legislation to facilitate the use of NGT
- Reduction of ERA-requirements
- Amendment of Reg. (EU) 503/2013

- Trans-, cisgenic and genome edited organisms = GMO

3. Regulatory differentiation of NGT plants according to their risk profiles

- GMO-legislation stays intact for transgenic organisms
- Regulatory relaxation for cisgenic & genome edited plants

- Simplified authorization for cis and GE plants
- Authorisation via comitology procedure

4. Product based approach

- Authorisation of organisms according to their traits and properties
- Risk assessment of all organisms

- Authorisation by EU authority
- Organisms are regulated by properties – no matter how they were produced

5. Foreign DNA approach

- Specific regulation only for organisms with foreign DNA*
- No risk assessment for other organisms

- Cisgenic and genome edited organisms:
- Official determination of lack of foreign DNA if necessary

6. REACH based approach

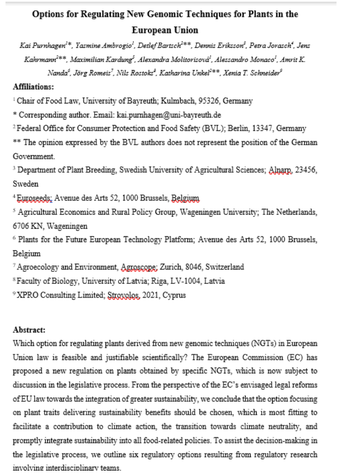
- Private sector responsibility
- Registration of GMOs

- Registered according to their classification: Cisgenic, transgenic, SDN-1, -2, -3, ..

Additional information

- Regulation of genome editing and GMOs in EU
- «Regulatory Aspects of CRISPR Edited Plants in EU», Elsevier book chapter

- Purnhagen et al. Options for Regulating New Genomic Techniques for Plants in the European Union. Nature Plants, accepted



Options for Regulating New Genomic Techniques for Plants in the European Union

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Abstract:

Which option for regulating plants derived from new genomic techniques (NGTs) in European Union law is feasible and justifiable scientifically? The European Commission (EC) has proposed a new regulation on plants obtained by specific NGTs, which is now subject to discussion in the legislative process. From the perspective of the EC's envisaged legal reforms of EU law towards the integration of greater sustainability, we conclude that the option focusing on plant traits delivering sustainability benefits should be chosen, which is most fitting to facilitate a contribution to climate action, the transition towards climate neutrality, and promptly integrate sustainability into all food-related policies. To assist the decision-making in the legislative process, we outline six regulatory options resulting from regulatory research involving interdisciplinary teams.

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