



BIOSAFETY CONSIDERATIONS FOR PLANTS DEVELOPED BY GENOME EDITING AND OTHER NEW GENETIC MODIFICATION TECHNIQUES (nGMS)

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An EU Perspective on Biosafety Considerations for Plants Developed by Genome Editing and Other New Genetic Modification Techniques (nGMs)

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Plants Developed by New Genetic Modification Techniques—Comparison of Existing Regulatory Frameworks in the EU and Non-EU Countries

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QUESTIONS CONCERNING nGMs / nGM-plants



QUESTIONS CONCERNING nGMs / nGM-plants

- Scope of Techniques and Terminology
- Biosafety issues
 - Intended / unintended effects on health & environment
- Regulatory issues
 - Coverage by existing regulatory frameworks for GMOs (Regulatory trigger)
 - Future regulatory development (amendments existing regulations / new regulations)
- Enforcement issues
 - Detection and identification supporting traceability & labeling
- Sustainability issues
 - Socioeconomic considerations
 - Agroecological considerations and policies (Innovations for a sustainable agriculture)

QUESTIONS CONCERNING nGMs / nGM-plants addressed in a study commissioned by BfN

Biosafety Considerations for nGM Plants – a perspective based on an European (EU) background

Comparison of existing regulatory
frameworks for nGM plants
(EU and non-EU countries)



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- Survey of scientific literature
 - Which nGMs?
(Techniques, Objectives)
 - Plant applications?
(Crops, traits, use in agricult.)
- Risk assessment considerations
 - nGM characteristics relevant for RA
- Considerations for a case-specific framing of the RA
 - Molecular characterisation



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- Comparison of existing regulatory frameworks
 - Similarities & differences
- Pros & Cons of respective regulatory triggers
 - Product- or process-oriented trigger definitions
- (Possible) regulatory approaches
 - Options for regulation of nGM products

nGMs: GM-TECHNOLOGY & BEYOND ...

1. **Genome Editing (GEd)** applications directed to introduce genomic modifications in a targeted manner, e.g. by means of site directed nucleases (SDNs) or ODM
 - SDN-1 / SDN-2 / SDN-3 / ODM / base editing
2. **Cisgenesis or Intragensis** applications, where only genetic material derived from the parental or sexually compatible species is used for genetic modification
3. **GM-modifications** present only **transiently** or in particular plant parts
 - e.g. agroinfiltration, transgrafting (GM rootstocks)
4. **Applications** where the **GM-modification(s)** are **only present in intermediate breeding steps** and supposed to be absent from the final product
 - e.g. reverse breeding, haploid induction, accelerated breeding/early flowering, etc.
5. **Applications** directed to modify the **epigenetic regulation** in plants and their offspring rather than the DNA sequence of their genomes
 - e.g. RNA-directed DNA Methylation (RdDM), SD-epigenetic effectors

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| Applications | nGMs | Genome editing | | | | | RdDM | CG | IG | TG* | nGMs to support breeding | |
|--|------------|----------------|----------|----------|----------|----------|----------|----------|-----------|----------|--------------------------|--------------------|
| | | CRISPR* | TALEN | ZFN | MN | ODM | | | | | AI | HI |
| JAN. 2011-DEC. 2015 | | | | | | | | | | | | |
| Total number | n.a. | 10 | 17 | 5 | 1 | 6 | 7 | 4 | n.a. | 14 | 9 | Total: (73) |
| JAN. 2016-JUNE 2017* | | | | | | | | | | | | |
| Total number (172) | 114 | 8 | 7 | 1 | 1 | 1 | 2 | 4 | 23 | 4 | 7 | 172 |
| SDN-1 | 99 | 5 | 4 | — | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. |
| SDN-2 | 5 | — | — | — | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. |
| SDN-3 | 4 | 3 | 3 | 1 | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. |
| Base editing | 4 | — | — | — | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. |
| Other types of genome editing | 2 | — | — | — | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. | n.a. |
| OBJECTIVE OF APPLICATIONS (JAN. 2016-JUNE 2017) | | | | | | | | | | | | |
| Method development | 72 | 1 | 2 | 1 | — | — | 1 | 1 | 6 | — | 3 | 88 |
| Basic research | 22 | 1 | 2 | — | — | — | — | — | 7 | 4 | 1 | 37 |
| Applied development | 20 | 6 | 3 | — | 1 | 1 | 1 | 3 | 10 | — | 2 | 47 |

SDN, site-directed nuclease; CRISPR, CRISPR (Clustered regularly interspaced short palindromic repeat)-directed nuclease; TALEN, Transcription activator-like effector nuclease; ZFN, Zinc-Finger-directed nuclease; MN, Meganucleases; ODM, Oligonucleotide-directed mutagenesis; RdDM, RNA dependent DNA methylation; CG, Cisgenesis; IG, Intragensis; TG, Transgrafting; AI, Agro-infiltration; HI, Haplid induction; Other types of genome editing: different variants of CRISPR-based genome editing, including use of nickases; n.a.: not applicable.

*For the use of CRISPR-based systems for genome editing and transgrafting literature was only screened for the time period Jan. 2016-June 2017.

Bold values indicate total numbers of publications for individual nGMs for the indicated time periods.

RESULTS OF LITERATURE SURVEY /1

- Continuous interest in all nGMs (2011-2017: 321 publications, 245 + 76/CRISPR Hilscher et al. (2017) Biotechnol. J. 12, 600173)
 - Clear focus on **GEd**(75% of total publications)
 - Wide range of plant species:
model species, important crop species (grain and oilseed crops, vegetables and spices, perennial plants (fruit and forest trees) and mosses
- Focus of recent work (Jan 2016 - June 2017, 172 publications)
 - Strong focus on **GEd by SDNs** (75 % of total publications)
 - Most genome editing of **SDN-1** type (83 % of GEd publications)
Knock-out of endogenous genes (basic research, applied development)
- Strong recent focus on CRISPR-applications (88 % of GEd publications)
 - CRISPR-**technology development** (>60 % of CRISPR publications)
- Objective for use (Jan 2016 - June 2017)
 - Method development (51 %, CRISPR, haploid induction),
 - Basic research (22 %, CRISPR, agroinfiltration),
 - Applied development (27 %, TALEN, ODM, cis/intra, transgrafting)

RESULTS OF LITERATURE SURVEY /2

- Method development aims (General)
 - Increased efficacy and speed of methods
 - Increased range of plant species to be modified
 - Products without integrated transgenes
- Method development aims (Genome editing, CRISPR)
 - Enhanced specificity and targeting
 - Other CRISPR-nucleases than Cas9 (e.g. Cpf1)
 - deadCas9-fusion enzymes for nicking, base editing or transcriptional/epigenetic regulation
 - Multiplexed applications (multiple guide RNAs) – e.g. for metabolic engineering
 - Genome editing with preassembled nucleases (e.g. functional PNP-complexes, no transgenes)
 - Tool for development of gene drives

RESULTS OF LITERATURE SURVEY /3

- Basic research aims

- Screening approach for novel traits
- Functional characterisation of genetic elements or combinations of alleles
- Functional characterisation of homologous modifications in other plant species
(model species - crops, wild relatives – crop species, related crop species)
- New types of applications (Gene drives, development of epialleles, complex metabolic engineering)

- Applied development aims

- Direct modification of elite lines of plants, e.g. vegetatively propagated plant species (GEd, cis/intra)
- Faster development of traits in perennials with long generation times, e.g. fruit-trees
(GEd, cis/int, accelerated breeding)
- Specific transfer of traits from related plant species, e.g. wildforms (GEd, cis/intra)
- Improvement of non-domesticated plant species (GEd, cis/intra, haploid induction)
- Targeted, multiple modification (multiplexed GEd, molecular stacking by SDN-3)
- Plant products without integrated transgenes (GEd, transgrafting, reverse breeding, RdDM)

RISK ASSESSMENT CONSIDERATIONS (SAM 2017)

- Effects due to **intended changes** present in the modified plant
 - Trait related effects:
Herbicide resistance, disease resistance (viral, bacterial, fungal), compositional changes, enhanced fitness against environmental stressors, alteration of morphological or reproductive plant characteristics
- Effects due to **unintended changes** present in the modified plant
 - Method related effects:
e.g. due to transformation (GM tools), nGM mechanism (off-target effects), other biotechnological methods (in vitro cultivation, regeneration)
- Effects due to **characteristics of the modified plant species** and its **interaction with the receiving environment**
 - (Major) crop species, other agricultural and ornamental plants, (fruit) trees
- Effects due to the **intended use of the modified plant**

INTENDED EFFECTS – TRAIT-RELATED CONSIDERATIONS

- Herbicide resistance (HR) against broadband herbicides
 - ALS-Inhibitors (OSR, potato, rice, maize, soy, tobacco), glyphosate (strawberries, flax, cassava, cotton), glufosinate, bialaphos, 2,4-D (maize, tobacco)
- Disease resistance against plant pathogens
 - Bacterial and fungal pathogens (grapefruit, wheat, tomato, grapevine, apple, and rice)
 - Viral pathogens (cucumber)
- Compositional changes
 - sugar and starch content (potato and rice), lipid composition (*Camelina* and soybean), lignin (sugarcane), fragrance (rice)
- Enhanced fitness (environmental stressors), morphological or reproductive characteristics
 - Abiotic stress response (cold, drought, salinity)
 - Increased seed shatter resistance (oilseed rape), early maturation and facultative parthenocarpy (tomato), early flowering, larger fruit and more flower buds (tomato), *de novo* domestication (tomato)

| Trait | Mechanisms | nGMs | Comp. dev. |
|--|--|------------------------------|-----------------------------|
| Herbicide resistance (HR) (broadband herbicides) | Modification of target genes | GEd (SDN-1, SDN-2, ODM) | Class. mut., nat. selection |
| | Introduction of resistant alleles | GEd (SDN-3), cis/intra | GM |
| | Molecular stacking of multiple HR genes | GEd (SDN-3) | GM |
| Disease resistance (viral, bacterial, fungal pathogens) | Knockout of susceptibility genes (bact. and fungal path.) | GEd (SDN-1) | GM (RNAi) |
| | Knockout of viral host factors | GEd (SDN-1) | GM (RNAi) |
| | Expression of heterologous resistance genes and antimicrobials | Transgrafting, cis/intra | GM |
| Compositional changes | Knockout of biosynthetic enzymes | GEd (SDN-1) | GM (RNAi) |
| | Expression of biosynthetic genes | Cis/intra | GM |
| Altered env. fitness, morphology / reproduction | Knockout of endogenous genes | GEd (SDN-1) (multiplexed) | |
| | Expression of abiotic stress response genes | Transgrafting | GM |

TRAIT-RELATED CONSIDERATIONS - ISSUES

- Limited knowledge and familiarity (no history of safe use)
 - Novel crops / agricultural plants (new species, wildforms)
 - Novel traits (phenotypes)
 - Changed agricultural management
- Unintended effects associated with intended changes
 - Pleiotropic effects
 - Unintended effects in non-transgenic plant parts (transgrafting)
 - Complex physiological effects of multiple changes (multiplexed GEd)
 - Complex regulatory effects on morphology, development and reproduction

| Trait | Potential adverse effects | Comp. issues |
|--|---|--------------|
| Herbicide resistance (HR) (broadband herbicides) | Impacts on biodiversity due to herbicide use | GM |
| | Development of HR-weeds (selection, gene flow) | GM |
| | HR-volunteer plants in subsequent crops | GM |
| | Herbicide cocktail effects (residues, metabolites) | GM (stacks) |
| | Pleiotropic effects of overexpressed HR-genes | |
| Disease resistance (viral, bacterial, fungal pathogens) | Pleiotropic effects on plant development (e.g. multiple mlo-knockouts) | GM (RNAi) |
| | Evolution of pathogens (selection of resistant pathogens, secondary pathogens) | GM (IR) |
| | Effects on (soil) non-target organisms (antimicrobials) | GM |
| Compositional changes | Animal and human health effects (nutritional effects, toxicity, allergenicity) | GM |
| | Environmental effects due to changed composition (herbivore attractivity, NTOs, decomposition) | GM |
| | Environmental effects of morphological changes (stability) | GM |
| Altered env. fitness, morphology / reproduction | Increased invasiveness of modified plant | GM |
| | Negative effects on protected relatives (gene flow) | GM |
| | Increased fitness of weedy relatives (gene flow) | GM |
| | Unintended effects of <i>de novo</i> domesticated plants (nutritional) | |

CASE-SPECIFIC FRAMING OF RISK ASSESSMENT

Different categories of nGM applications

- nGM plants with traits and usage known from conventional approaches
 - Familiarity concerning effects upon use should be considered during assessment
- nGM plants with traits similar to existing GM plants and associated with comparable risk issues
 - e.g. herbicide resistance or disease resistance, compositional changes
 - previous experience with the risk assessment of comparable GMOs should be taken into account
- nGM plants with traits which have not yet been established and thus are novel
 - Similar approaches for risk assessment as implemented for GMOs should be applied

METHOD-RELATED CONSIDERATIONS

- Holistic assessment of unintended changes is required
 - Typically a combination of different methods is used (nGM(s), GM-methods, other breeding methods)
 - Unintended changes due to transformation procedures (GM methods, introduction of method-related components)
 - Unintended changes due to integration of unwanted genetic material (GM methods, transient introduction of genetic constructs)
 - Off-target effects genome editing – unintended as well as “intended” off-target effects (SDNs, ODM)
 - Unintended changes due to other required biotechnological methods (*in vitro* cultivation, protoplast technology, regeneration)
- Unintended changes at genomic locations other than the genomic target site(s)
 - Modifications usually not genetically linked to the desired trait(s)
- Unintended molecular changes in the vicinity of the intended site of modification
 - Different from the intended modifications, but tightly linked to the desired trait(s)

nGM CHARACTERISTICS RELEVANT FOR RA

- Combination of biotechnological and conventional methods
 - Different nGMs
 - nGMs, GM technology & other biotechnological methods
- Precision (specificity of GEd)
 - Potential to introduce off-target changes
 - Predictability of off-target changes
- Depth of Intervention
 - Single vs. multiple changes (multiplexed, serial changes)
 - Physiological effects of modified targets (specific vs. pleiotropic effects)
- Impact on time of development (observation)
 - Direct modification of elite lines, plants that are propagated vegetatively
 - Modification of plants with long generation cycles (trees)

CASE-SPECIFIC APPROACH TO RISK ASSESSMENT

- Case-specific risk assessment requirements taking into account
 - the nature of the developed trait,
 - unintended consequences of the modification introduced,
 - the available experience with comparable products, and
 - relevant protection goals specified by the respective countries.
- **Appropriate** molecular characterization to assess among other things
 - the unintentional presence of any transgenic inserts in the final product, and
 - the presence of off-target modifications and other unintended genetic changes, which might result in adverse phenotypic effects.
- Phenotypic characterization to specifically test parameters related to plausible risk issues associated with a particular nGM plant

CHARACTERISATION OF UNINTENDED EFFECTS

- Consider the specific characteristics of the nGM approach, and existing knowledge on potential for unintended changes/off-target activity
- Assess whether unlinked unintended modifications will be removed by crossbreeding steps
- Use robust bioinformatics tools to predict off-target changes and check predicted off-target activity against *in vitro* test data
- Use targeted sequencing to assess off-target changes linked to the desired modification(s), and whole genome sequencing in case of significant potential for unlinked off-target changes
- Assess whether any unintended changes might be functional relevant and significant in terms of biological effects
- Use targeted or untargeted phenotyping to assess the possible adverse effects resulting from unintended modifications/off-target

CHALLENGES FOR RISK ASSESSMENT

- Variety of methods and traits need to be considered
- No safety by default
 - The issue that certain changes could (hypothetically) be developed with conventional methods (or spontaneous mutation) is not indicative of product-safety
 - Small size genetic changes are not indicative of (environmental) safety
 - High precision of modification is not indicative of the safety of trait(s)
- Limited knowledge for assessment available
 - Novel traits and complex traits (Non-trivial physiological / phenotypical effects)
 - Limited predictability of (unintended) changes and effects
- Increased speed of development
 - Impacts observation and elimination of unintended changes

LIMPING ALONG AND LAGGING BEHIND: REGULATION

- Risks not correlated with specific types of techniques (e.g. SDN-1, SDN-2, ODM, SDN-3)
 - Rather with traits and characteristics of approach (complex, deep, fast, dirty)
 - Challenges for devising an appropriate regulatory approach (2-sets of criteria)
- Existing regulatory frameworks are not consistently addressing nGM-applications
 - Particularly they fail to consistently address the level of risk associated with different nGM-applications
 - Neither are proposed/implemented amendments increasing consistency
- Broad flexible framework probably best to address biosafety issues
 - Exclusion from biosafety regulation is not a good option – other applicable regulation is not well suited to address biosafety issues
 - General principles of GMO regulation frameworks are suitable
 - Case-specific „outcome-based“ assessment strategies need to be developed

THANK YOU FOR YOUR ATTENTION!

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