

**Working Group on Biochemical and Molecular Techniques
and DNA-Profiling in Particular****BMT/16/20****Sixteenth Session
La Rochelle, France, November 7 to 10, 2017****Original:** English
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SDN-ASSISTED PLANT BREEDING AND POTENTIAL IMPACT ON DUS TESTING*Document prepared by an expert from the European Union**Disclaimer: this document does not represent UPOV policies or guidance*

The Annex to this document contains a copy of a presentation on “SDN-assisted plant breeding and potential impact on DUS testing”, prepared by an expert from the European Union, to be made at the sixteenth session of the Working Group on Biochemical and Molecular Techniques and DNA-Profiling in Particular (BMT).

[Annex follows]

SDN-ASSISTED PLANT BREEDING AND POTENTIAL IMPACT ON DUS TESTING

Presentation prepared by an expert from the European Union

UPOV UPOV BMT meeting La Rochelle (France), Nov 6-10, 2017



CPVO · OCVV
Community Plant Variety Office
Office Communautaire des Variétés Végétales

**SDN-assisted plant breeding
and potential impact on DUS testing**

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The EC New techniques WG

The 8 NBT proposed by EC (Dec. 2011) :

1. Oligonucleotide-Directed Mutagenesis (ODM)
2. Cisgenesis and intragenesis
3. Grafting
4. Agro-infiltration
5. RNA dependent DNA methylation
6. Reverse breeding
7. Synthetic biology
8. Site-directed nucleases

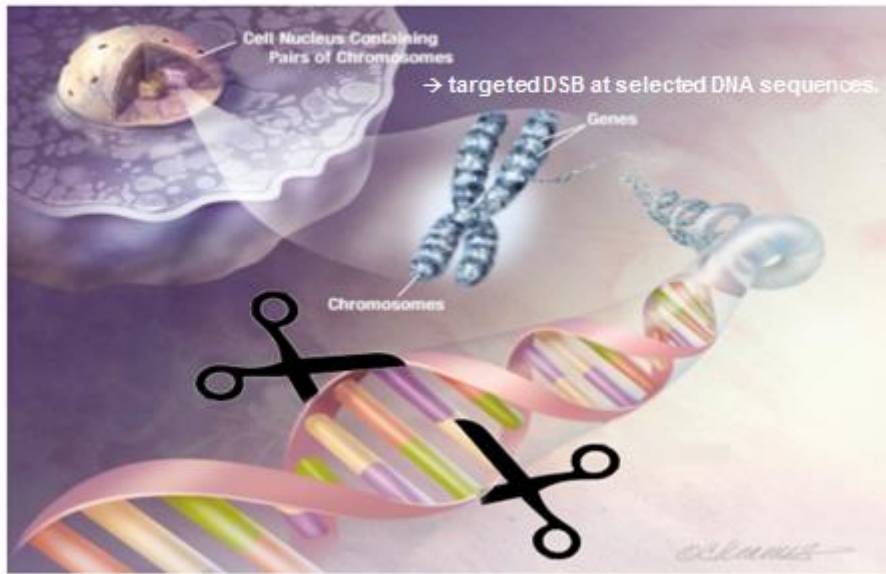
The views expressed in this report are those of an expert working group and do not necessarily represent those of the European Commission or the Competent Authorities. Only the European Court of Justice can give a binding opinion on EU law.

New Techniques Working Group

FINAL REPORT

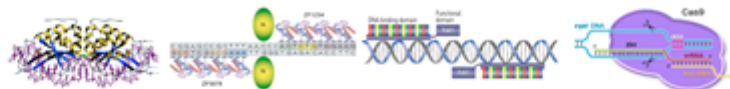
1.0 Introduction

8 – Site Directed Nucleases



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Site-Directed Nucleases



	Meganuclease	ZFN	TALEN	CRISPR/Cas
Nb of proteins required	1	2	2	1 + gRNA
Off-target	Very low (target = 18-24 bp)	Medium high (target = 2 x 12-18 bp)	Low (target = 2 x 10-30 bp)	Low (target = 19-23 bp)
Diversity of target sequences	One cutting site every 250 bp	One cutting site every 300 bp	One cutting site every 35 bp	One cutting site every 8 pb
Difficulty of production	Heavy (modification of the peptid chain and selection)	Uneasy (interaction effects on specificity)	Relatively easy (modular assembly)	Very easy (synthesis of one oligonucleotide)
Approximate price	50 000 €	5000 €	1000 €	100 €

+ Hyper-specific MegaTALE (Boissel et al., 2013)

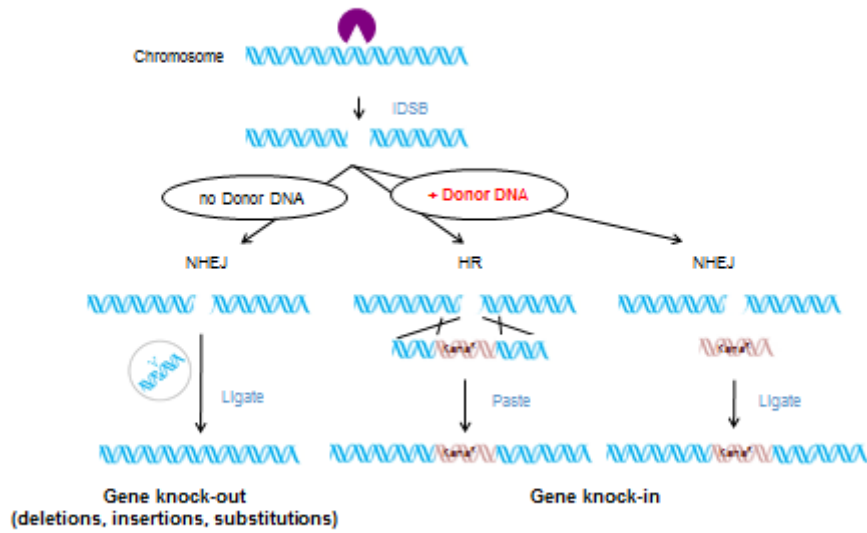


+ Hybrid nucleases (one subunit of ZFN + one subunit of TALEN) (Ibn et al., 2013)



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SDN-induced DSB

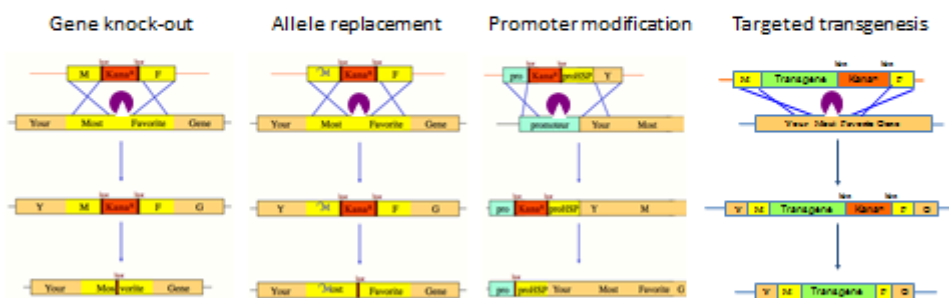


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Applications of SDNs-induced Gene Targeting

Precise modifications of the genome :

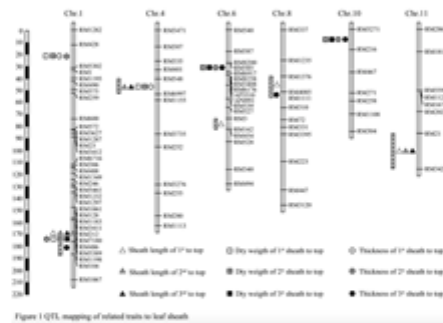
- Functional analysis of genes
- Biotechnological improvement of species



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Potential applications of SDNs for Plant Breeding

1) Validation of candidate genes by SDN-induced gene knock-out



2) Knock-out (loss of function) or knock-in (allele replacement) of the validated genes.

➤ Potentially all characters for which the genes involved are known can be modified by using SDNs.

Potential applications of SDNs for Plant Breeding

- Fast assembling of alleles and genes (simplification of QTL pyramiding, ...) + interest for perennials, species propagated vegetatively, polyploid species...



Fruit trees

- Specific applications : elimination of unfavorable alleles, selection of recessive alleles, breaking of linkage drags
- Transfer of genes of interest from a wide range of species (exploitation of genetic resources)
- Possible insertion of alleles of interest in minor or orphan crops



Genetic resources



Sorghum



Cow pea



Pigeon pea



Cassava

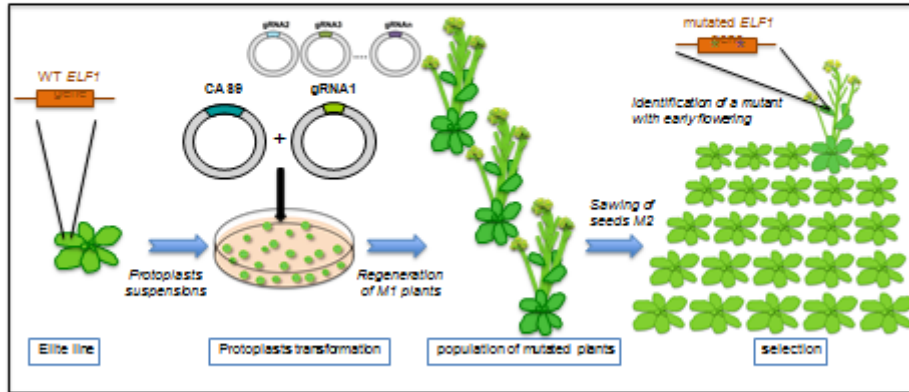


Yam

- Design of traits adapted to very specific environments
- Opportunities to increase genetic diversity
 - ➔ Induction of targeted genetic variability (TIGV)
 - ➔ cis regulatory alleles
 - ➔ « rewilding » concept

Targeted induced genetic variation (TIGV)

➤ Inducing targeted mutations in genes of interest in order to create and select new phenotypes.



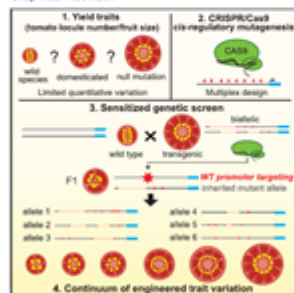
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CRISPR gene editing to advance traits discovery : creation of a new variability

CRISPR/Cas9 mutagenesis of promoters to generate **novel cis-regulatory alleles** to achieve a range of variation for quantitative traits

Engineering Quantitative Trait Variation for Crop Improvement by Genome Editing

Graphical Abstract

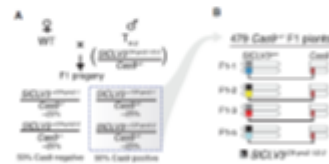


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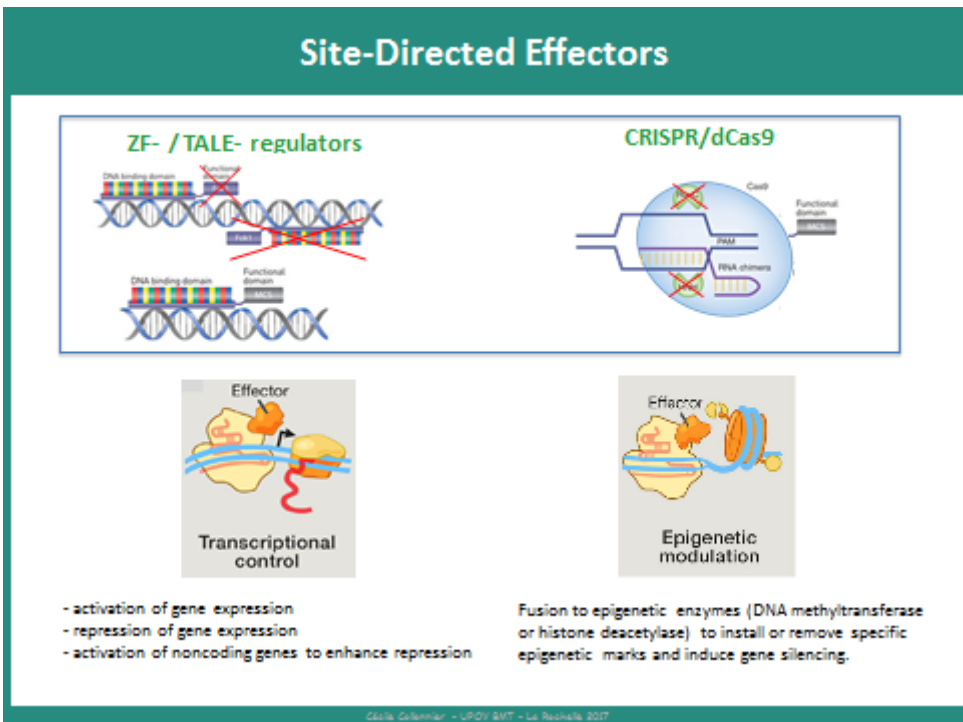
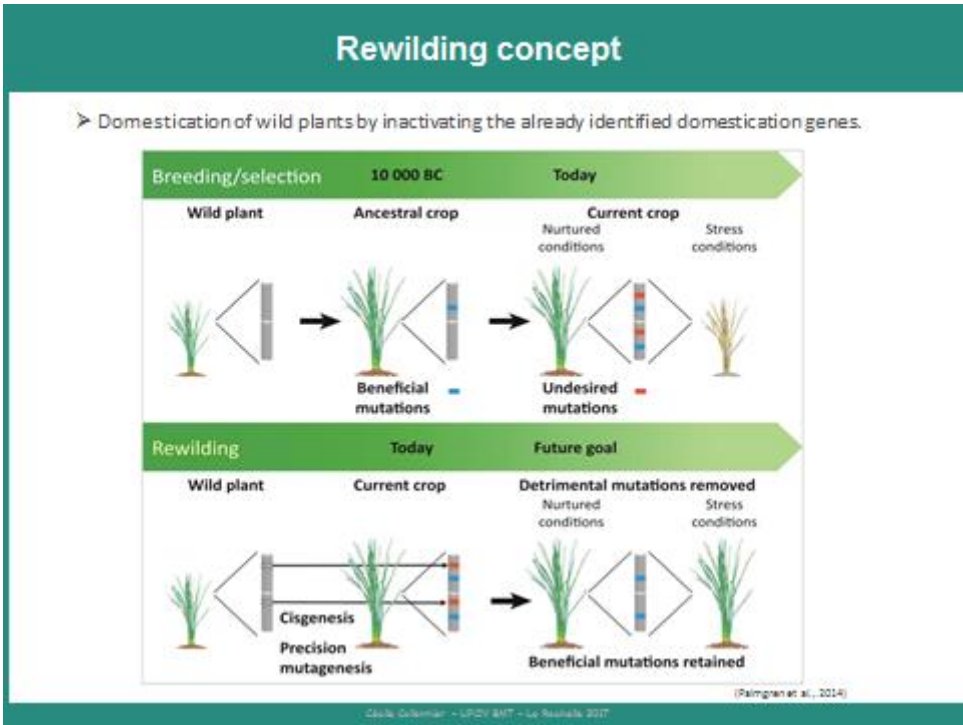
In Brief
In this article, we discuss how to use the CRISPR/Cas9 genome editing approach to dissect the biology of quantitative trait loci.

Cell



a simple genetic scheme which exploits trans-generational heritability of Cas9 activity

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Potential applications of SDNs for Plant Breeding

A great diversity of potential traits :

- **Disease resistance** (eg. target: translation initiation factors)
- **Herbicide tolerance** (eg. target: acetolactate synthase gene)
- **Drought tolerance** (eg. Target : promoters of genes activated by water stress)
- **Low anti-nutritional compounds** (eg. erucic acid in Brassicas, target: fatty acid elongases)
and allergens (eg. target: conglutin genes in peanut, gluten in wheat)
- **Improved nutritional value** (eg. via elevated carotenoids, target: zeaxanthin epoxidase)
- **Modified starches and fats for food and non-food uses**
(eg. target: starch synthases, branching enzymes and fatty acid desaturases)
- **Longer shelf life/reduced wastage** (eg. targets: aminocyclo-propane (ACC) oxidase and polygalacturonase)
- **Reduced enzymatic** (eg. target: polyphenol oxidases)
and nonenzymatic browning (eg. target: invertase genes for high quality and low acrylamide potato)
- **Improved yield via modified RuBisCO genes** (eg. increasing catalytic activity, decreasing oxygenation activity)
- **Improved biomass conversion for biofuels** (eg. lower lignin)
- **Control of meiosis** : Increase crossing overs, diplogametes, ...
- —

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Potential applications of SDNs for Plant Breeding

Qualitative and quantitative traits can be achieved.

Easier for monogenic or oligogenic traits (quality, resistance to biotic stresses...)

But more complex traits can also be improved (yield, resistance to abiotic stresses, metabolites...)

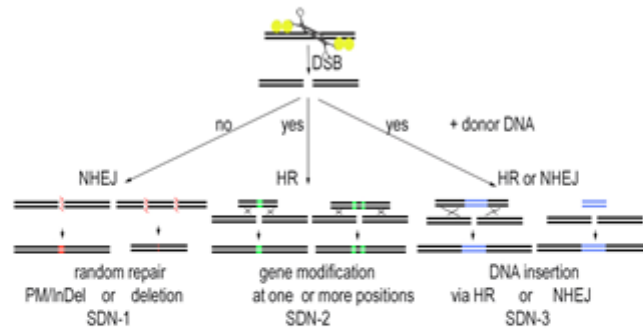
So far, easier by gene knock-out than by gene knock-in...



New products addressing from niche markets to large field crop markets

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3 types of events produced by using SDNs on plants



SDN-1 (random repair) : DSB result in site-specific random point mutations (PM) and short insertions/deletions (indel) or in excision. (no donor DNA)

SDN-2 (gene modification) : homologous donor DNA is used to induce specific nucleotide sequence changes by HR (= allele replacement)

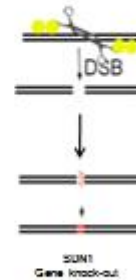
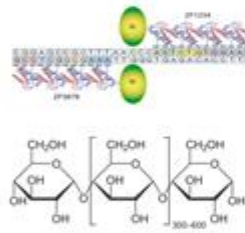
SDN-3 (DNA insertion) : DNA is integrated at a specific site of the plant genome (landing pads) using either NHEJ (cassette without homology) or HR (cassette with homology).

SDN1 / ZFNs

Potato ($2n = 4x$)

Knock out the starch branching enzyme II (SBEII) gene to **increase amylose content**.

@WUR



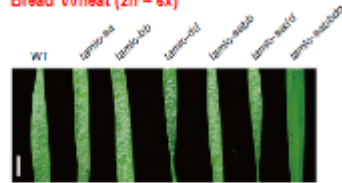
EXZACT™ Precision Technology (Dow AgroSciences)

<http://www.exzactprecisiontechnology.com/index.htm>

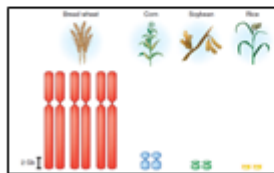
SDN1 / TALEN



Bread V/wheat (2n = 6x)



→ knocking out all six alleles encoding the MILDEW-RESISTANCE LOCUS (MLO) protein
→ mutant line with strong **resistance to powdery mildew**.



Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew **in situ** biotechnology (2014)

Yanyang Wang^{1,2}, Xi Cheng^{1,2}, Qiong Shen¹, Yi Zhang¹, Jinxing Liu¹, Gailin Guo¹ & Jin-Long Qiu¹



SDN1 / TALEN

calyxt

+ High fiber wheat
→ **still at an early stage.**

Removal of the components of gluten responsible for the immune reaction
→ **still at an early stage.**



high oleic acid and low linoleic acid
= ~20% decrease in saturated fatty acids compared to standard soybean oil

→ **30 tons produced in Argentina in 2016.**

inactivated enzyme responsible for the degradation of sugars in tubers
→ reduction of sweetening of cold-stored potatoes and of creation of acrylamide during frying.

→ **2016 = 2nd year of field trials.**

3.5% saturated fat (instead of 7%)
by deactivating one enzyme responsible for the synthesis of saturated fatty acids

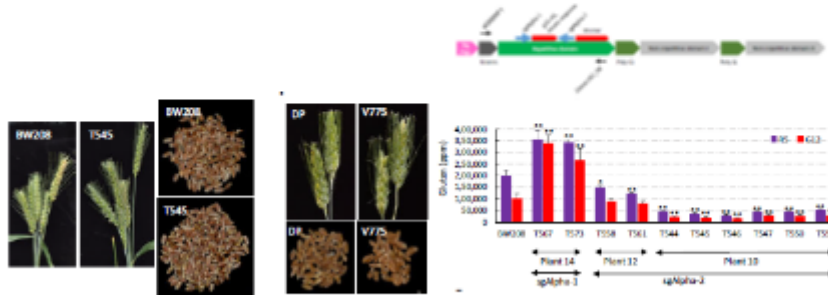
→ **On going.**

SDN1 / CRISPR-Cas

Low-gluten, non-transgenic wheat engineered with CRISPR/Cas9

Susana Sánchez-León^{1, 4}, Javier Gil-Humanes^{2, 4}, Carmen V. Ozuna¹, María J. Giménez¹, Caroline Sousa³, Daniel F. Voytas², Francisco Barro^{1,*}

two sgRNAs targeting a conserved region in the 45 gliadin genes of the WT
21 mutant lines, all showing strong reduction in gliadins.
Up to 35 different genes mutated → immunoreactivity reduced by 85%.

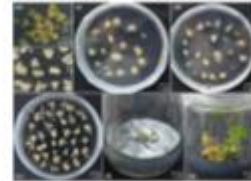


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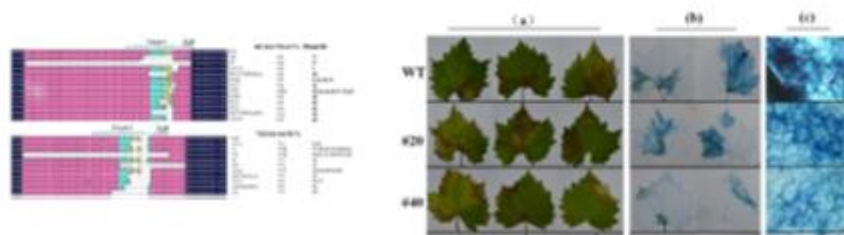
SDN1 / CRISPR-Cas

CRISPR/Cas9-mediated efficient targeted mutagenesis in grape in the first generation

Xianhong Wang^{1,2†}, Mingxiang Tu^{1,2†}, Dejun Wang^{1,2}, Aarwen Liu^{1,2},
Yipun Li^{1,2}, Zhi Li^{1,2}, Yeyun Wang^{1,2}, Xipeng Wang^{1,2*}

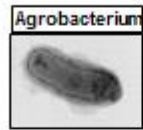


knock out of transcription factor *VvWRKY52* in grape increased the resistance to *Botrytis cinerea*.



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SDN1 / CRISPR-Cas



Tomato



Mutations in 3 regions of the RIN gene (transcription factor regulating fruit ripening)

→ **incomplete-ripening** fruits in homozygous mutants
(longer shelf-life, easier processing).

CRISPR/Cas9-mediated mutagenesis of the RIN locus that regulates tomato fruit ripening (2015)

Yoshino K^{1,2}, Aoki Nobuyasu¹, Masaki Endo¹, Masahito Mikami^{1,2}, Senichi Tada^{1,2,3}

Biochemical and Biophysical Research Communications

CRISPR/Cas9-mediated mutagenesis of the RIN locus that regulates tomato fruit ripening (2015)

SDN1 / CRISPR-Cas



Dr Yinong YANG

CRISPR/Cas9-edited white button mushroom (*Agaricus bisporus*)

Transient transformation of protoplasts (no transgene)
Small deletions (1-14 bp) in the polyphenol oxydase gene
→ anti-browning phenotype

USDA considers it as non regulated (April 13, 2016).

CRISPR/Cas9-mediated mutagenesis of the RIN locus that regulates tomato fruit ripening (2015)

SDN1 / CRISPR-Cas



(KO of 1 gene (*wx*) to block the production of amylose)



100% amylopectin corn
→ Feed, industry.

(conventional waxy cvs =
3,5 % less yield)

waxy corn hybrids

USDA considers it as non regulated (April 18, 2016).

SDN2 / CRISPR-Cas

Accepted Date : 15-Jul-2016

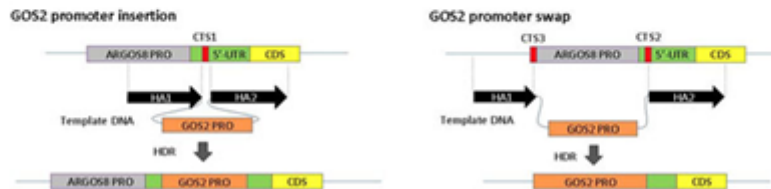
Article type : Research Article

Plant Biotechnology Journal
Open Access

ARGO88 variants generated by CRISPR-Cas9 improve maize grain yield under field drought stress conditions

Jinrui Shi*, Huirong Gao, Hongyu Wang, H. Renee Lafitte, Rayeann L. Archibald, Melzhu

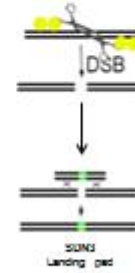
Yang, Salim M. Hakim, Hua Mo, and Jeffrey E. Habben



SDN3 / Meganuclease



- gene **stacking** using *I-Cre1*
- precise insertion of two herbicide tolerance genes (*hppd*, *epsps*) next to pre-existing Bt and bar loci in 2% of the embryogenic callus lines
- all trait genes were inherited as a single genetic unit



Plant Biotechnology Journal (2013) 11, pp. 933–941

doi: 10.1111/1365-3113.12085

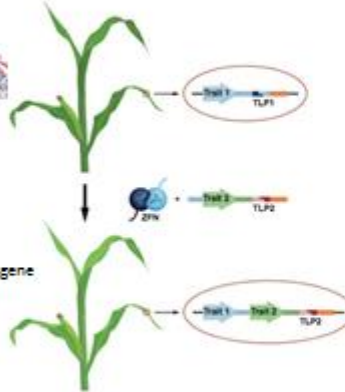
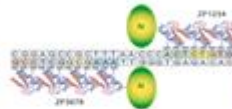
Targeted molecular trait stacking in cotton through targeted double-strand break induction

Kathleen O'Halloran¹*, Chantal Vanderstraeten¹, Jolien Van Hulle², Joanna Rosolowska¹, Ise Van Den Brande¹, Anouk Pennewaert¹, Kristel O'Hara¹, Martine Bossut¹, Derek Jantz², Rene Ruter¹ and Jean Broadbent¹

¹Syngenta CropScience N.V., Gent, Belgium
²Meridian Biotechnologies, Durham, NC, USA

© 2013 John Wiley & Sons, Ltd. *Journal of Biotechnology* 2013, 11, 933–941

SDN3 / ZFN



- **stacking** : 5% of transgenic events integrated the transgene precisely at the landing pad.

Trait stacking via targeted genome editing

William M. Ashley^{1,2}*, Lakshmi Sathya-Deni^{1,2}, Mary E. Veiter¹, Michael G. Murley¹, Bryan Zetter¹, Rainier Amorá¹, David R. Corbin¹, Rebecca R. Miles¹, Nicole L. Arnold¹, Tonya L. Strange¹, Matthew A. Simpson¹, Zehui Cao¹, Carley Carroll¹, Katherine S. Pawelczak¹, Ryan Blue¹, Kim Wiest¹, Lynn M. Rowland¹, Douglas Perkins¹, Ron Samuel¹, Cristie M. Dewen¹, Liu Shen¹, Sheedharan Sriram¹, Steven L. Evans¹, Edward J. Rebar¹, Lei Zhang¹, Philip D. Gregory¹, Proctor D. Umov¹, Steven R. Webb¹ and Joseph F. Petráš^{1,2}*

¹Syngenta CropScience LLC, Johnston, RI, USA
²Meridian Biotechnologies, Inc., Richmond, CA, USA

Plant Biotechnology Journal (2013) 11, pp. 1126–1138

© 2013 John Wiley & Sons, Ltd. *Journal of Biotechnology* 2013, 11, 1126–1138

SDN-mediated varieties and DUS

Description of SDN-mediated candidate varieties

For each PVP application CPVO Technical Questionnaire gives :

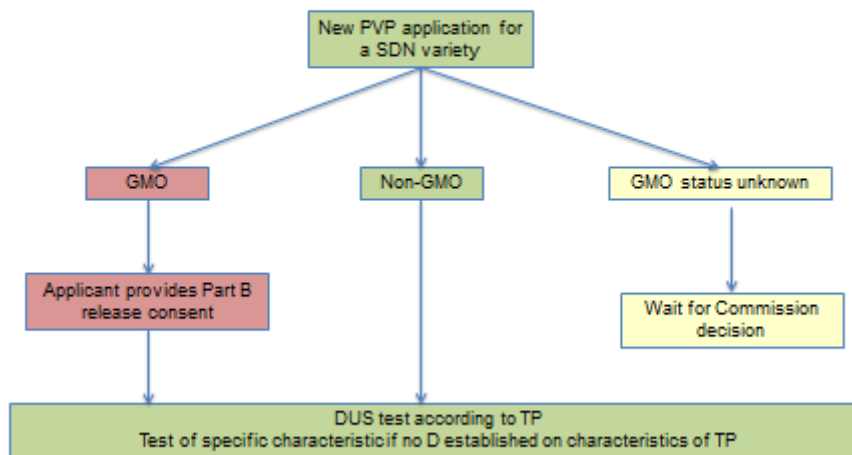
- Information on **breeding scheme and multiplication**
- Description of **specific characteristics**
- Declaration of **GMO status** according to Directive EC/2001/18

→ **Necessary loyalty**

since no detection possible without declaration for SDN1 and SDN2
(impossible to distinguish between targeted and natural mutations)

SDN-mediated varieties and DUS

DUS Procedure for SDN-mediated candidate varieties



SDN-mediated varieties and DUS

- SDNs are breeding tools to introduce traits into varieties:
 - Either these traits contribute to characteristics evaluated in the TP,
 - Or they are specific characteristics that need to be treated as additional characteristics (fulfilling UPOV requirements).
 - Distinctness is established using the same minimum distances as usually.



A priori, the use of SDN for plant breeding should not change fundamentally the process of DUS testing, but could increase the diversity of traits to evaluate.

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Thank you !



[End of Annex and of document]