植物基因編輯技術的原理與進展

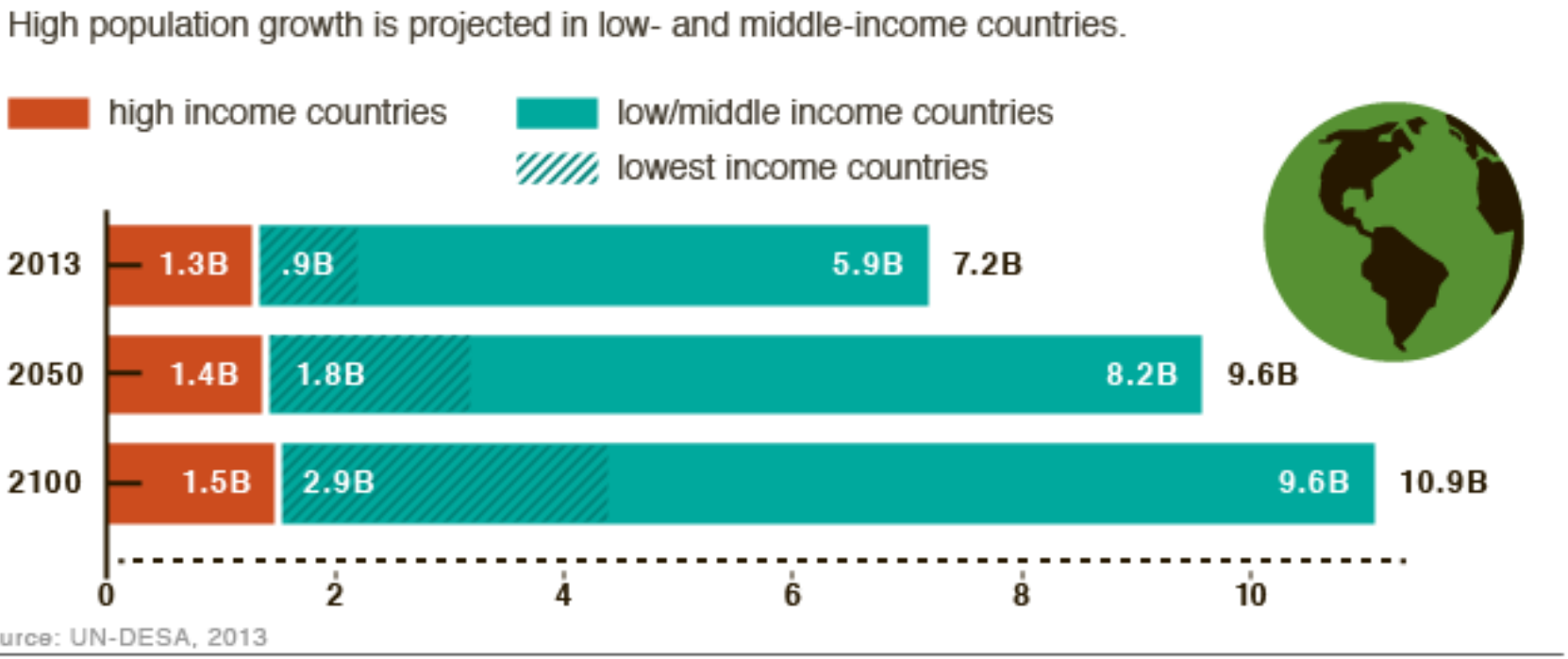
洪傳揚博士，臺灣大學農業化學系

Chwan-Yang Hong, Ph.D.

Professor, Department of Agricultural Chemistry,
National Taiwan University

2022.7.21 基因編輯產品近況與展望研討會

How do we feed 10 billion people?

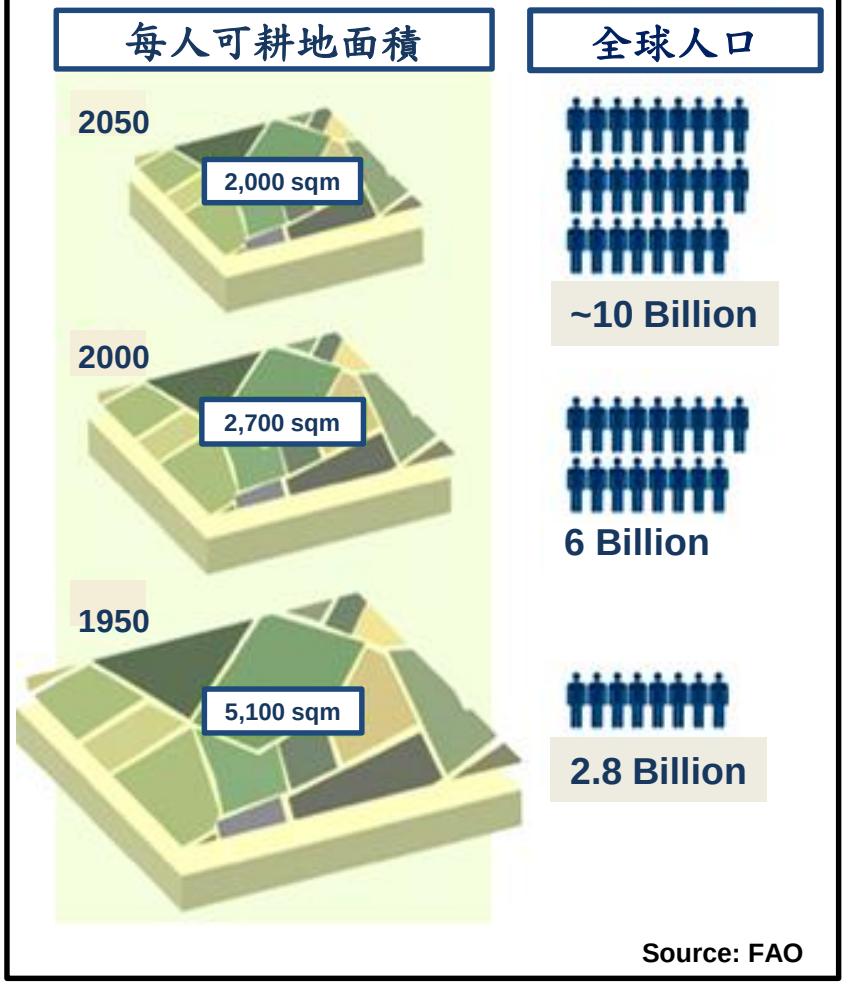


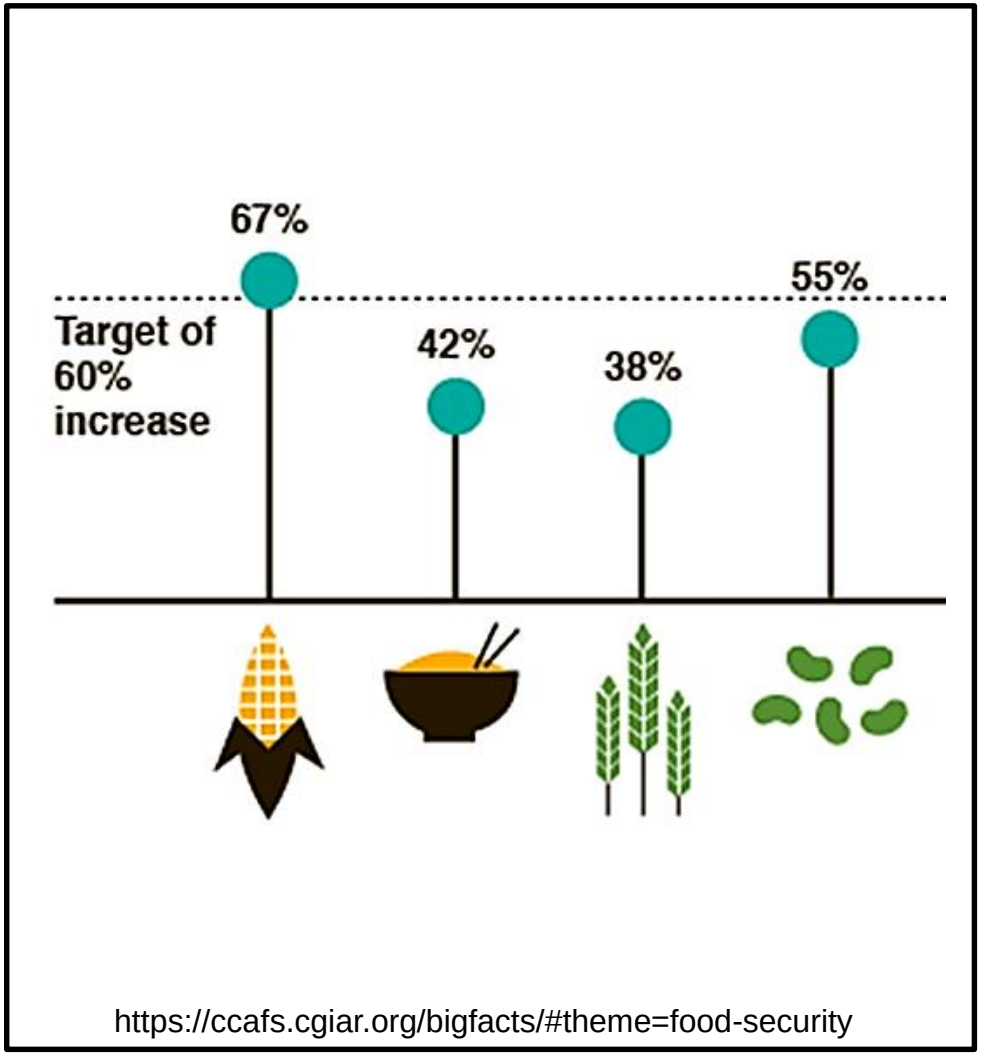
Big Facts
ccafs.cgiar.org/bigfacts

CGIAR RESEARCH PROGRAM ON Climate Change, Agriculture and Food Security — CCAFS

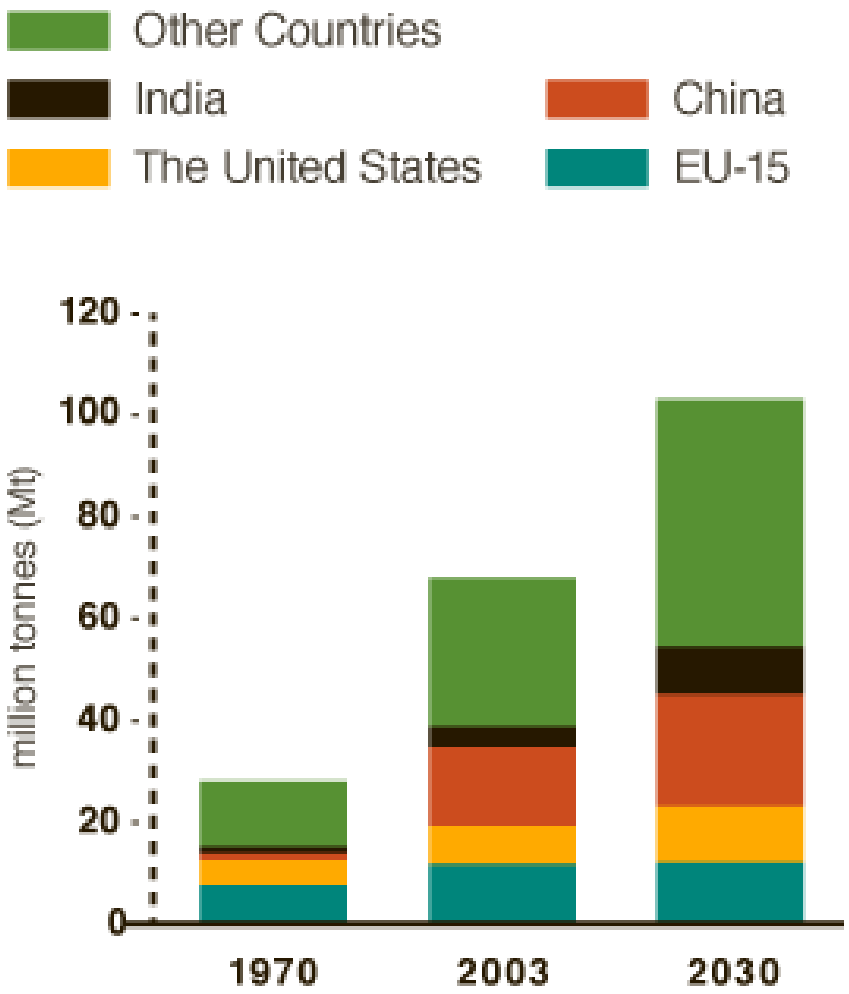
https://ccafs.cgiar.org/news/big-facts-focus-food-security

With current global trends in diets and population, 60% more food will be needed in 2050





Demand for animal protein is increasing



https://ccafs.cgiar.org/news/big-facts-focus-food-security

Source: Kastner et al. 2012

Food security 糧食確保
Food safety　糧食安全
Sustainability 農業永續

https://www.euractiv.com/section/biofuels/news/biofuels-impact-on-food-security-debate-resurfaces-amid-ukraine-war/

In Sri Lanka, Organic Farming Went Catastrophically Wrong

A nationwide experiment is abandoned after producing only misery.

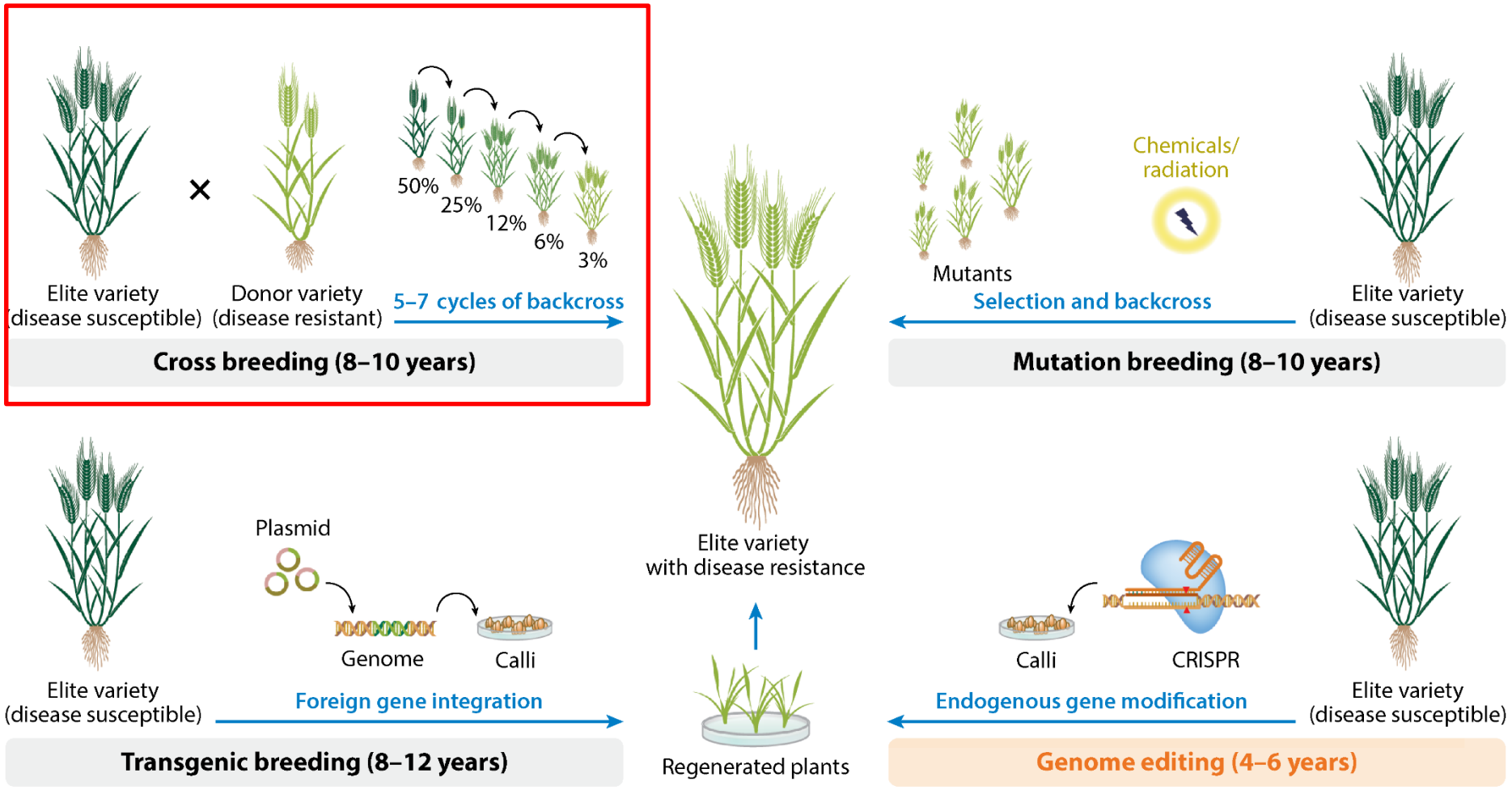
MARCH 5, 2022, 7:00 AM

https://mua.fandom.com/wiki/Hulk

https://slate.com/technology/2022/04/end-of-astronauts-excerpt-mars-robots-humans.html

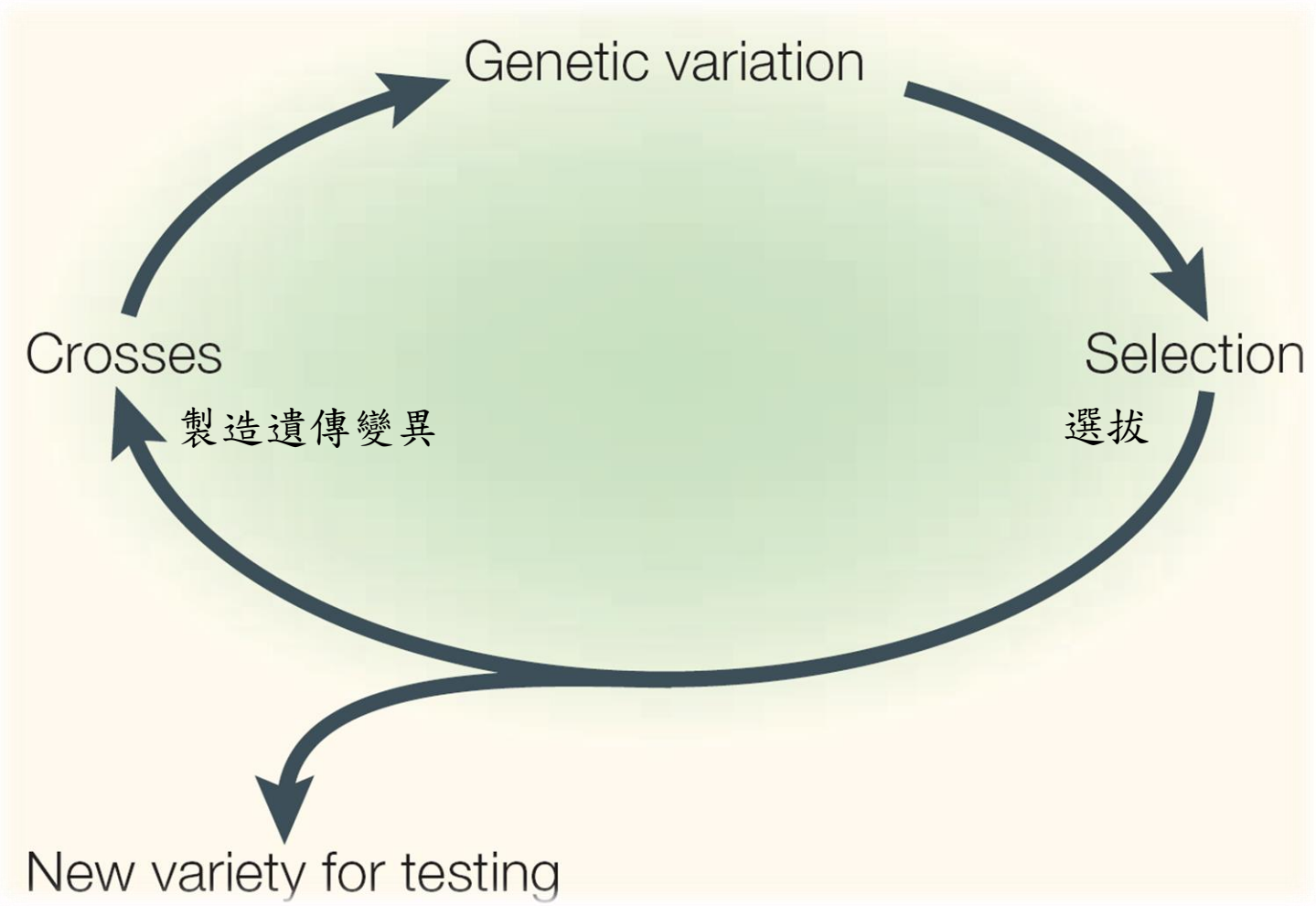
http://www.nbtplatform.org/frequently-asked-questions

Comparison of breeding methods used in modern agriculture



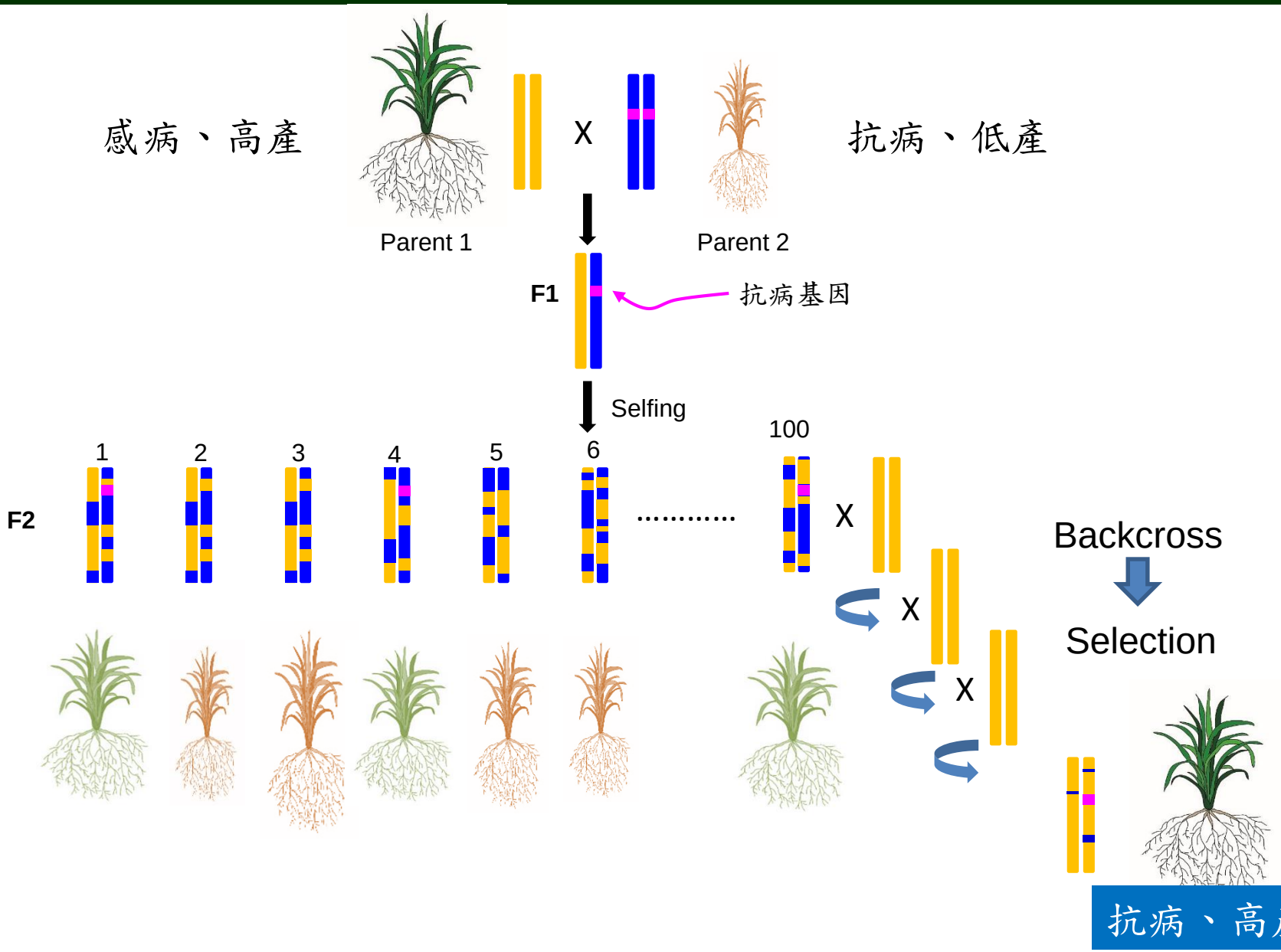
Chen K, et al. 2019.
Annu. Rev. Plant Biol. 70:667–97

The process of conventional breeding in plants



Modified from Nature Review (2001)

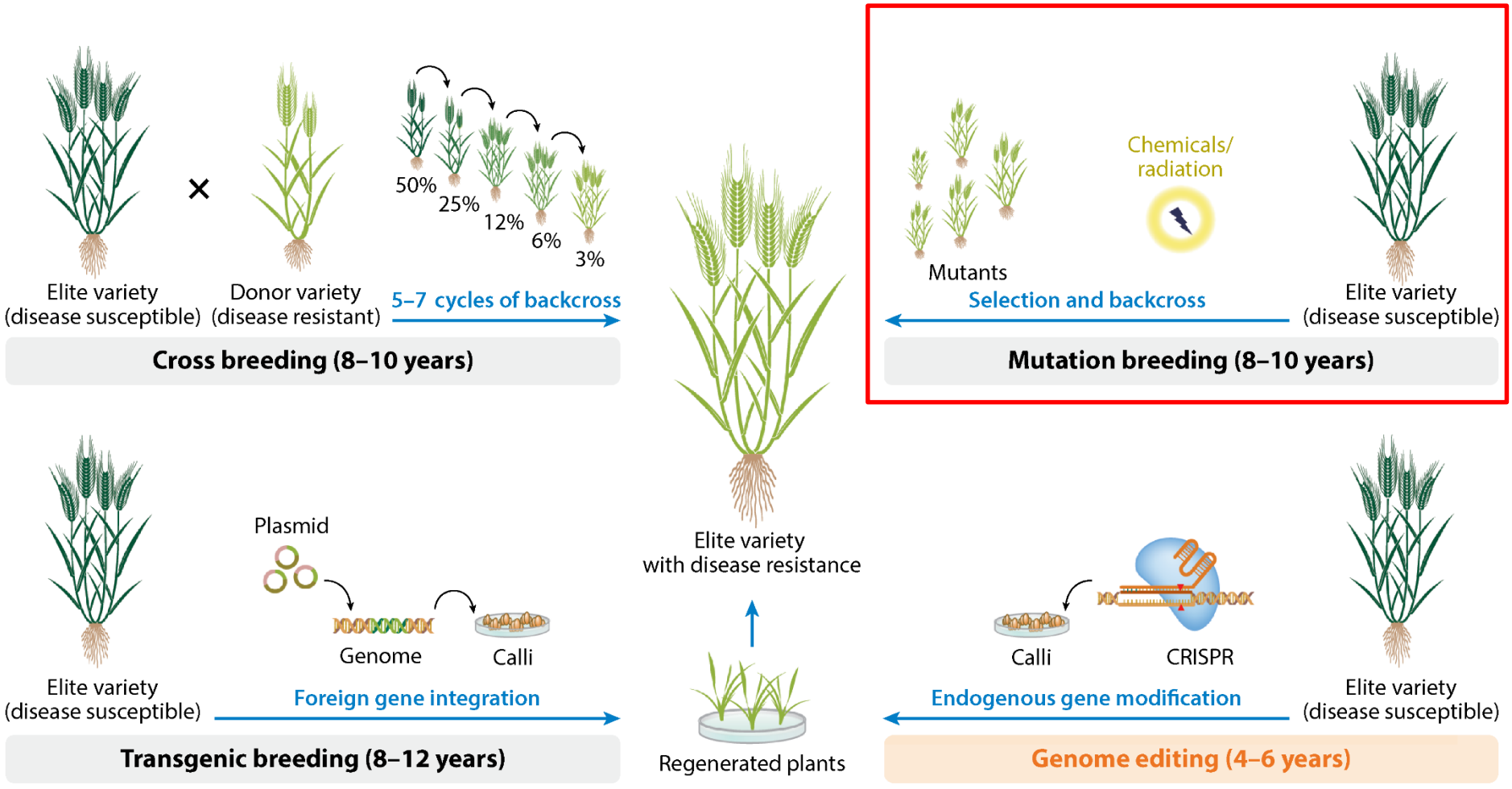
How traditional breeding works?



Bottleneck of crossing breeding

1. Linkage drag. 連鎖累贅
2. Abiotic stress tolerance is controlled by a complex pathway.
   非生物性逆境抗性路徑過於複雜不易進行
3. Cannot be applied to vegetatively propagated plants.
   無種子的植物無法進行
4. Restricted Germplasms. 種源有限
5. The breeding of many woody horticultural crops such as apple and walnut can take as many as 20–30 years to assort several favorable traits together in a single individual. 木本植物育種時間太久
6. Breeding is difficult to apply in polyploid crops. 多倍體育種難度高

Comparison of breeding methods used in modern agriculture



Chen K, et al. 2019.
Annu. Rev. Plant Biol. 70:667–97

Mutation breeding

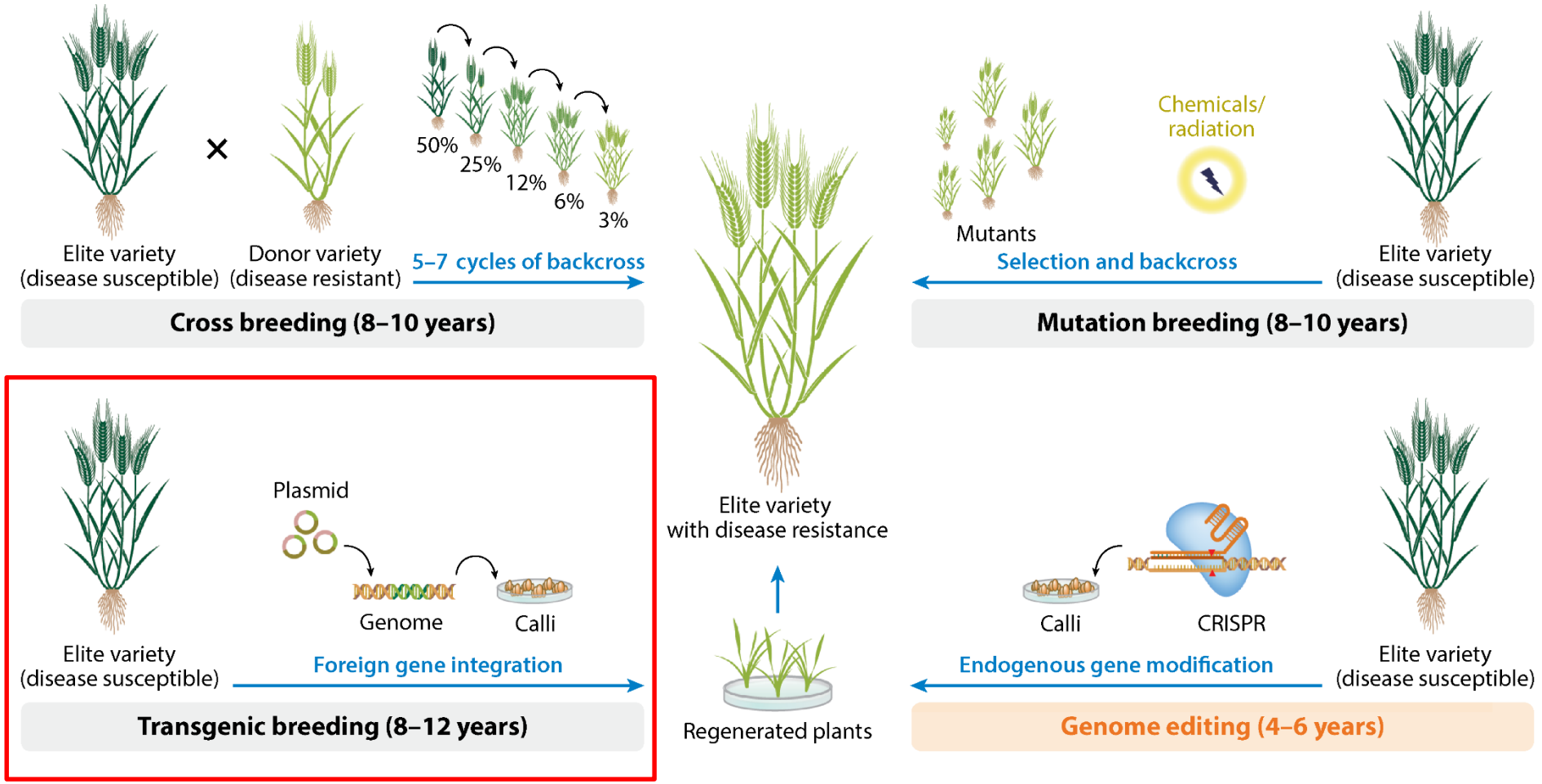
Random Mutation 逢機突變

Spontaneous mutation	Induced mutation
• Radiation	• Chemical mutation
• Transposon	• Physical mutation
• Error in DNA duplication	• Biological mutation
•••••	

- More than 3333 officially released mutant varieties from 228 different plant species in more than 73 countries throughout the world (2019 FAO/IAEA Mutant Variety Database).

Front Plant Sci (2019) https://doi.org/10.3389/fpls.2019.01326

Comparison of breeding methods used in modern agriculture



Chen K, et al. 2019.
Annu. Rev. Plant Biol. 70:667–97

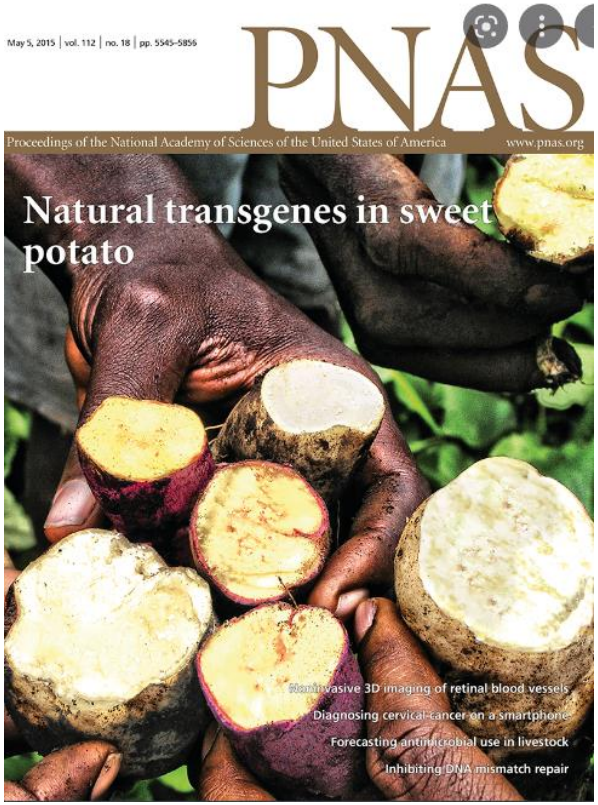
來自農桿菌的轉基因存在部分植物基因組

PNAS

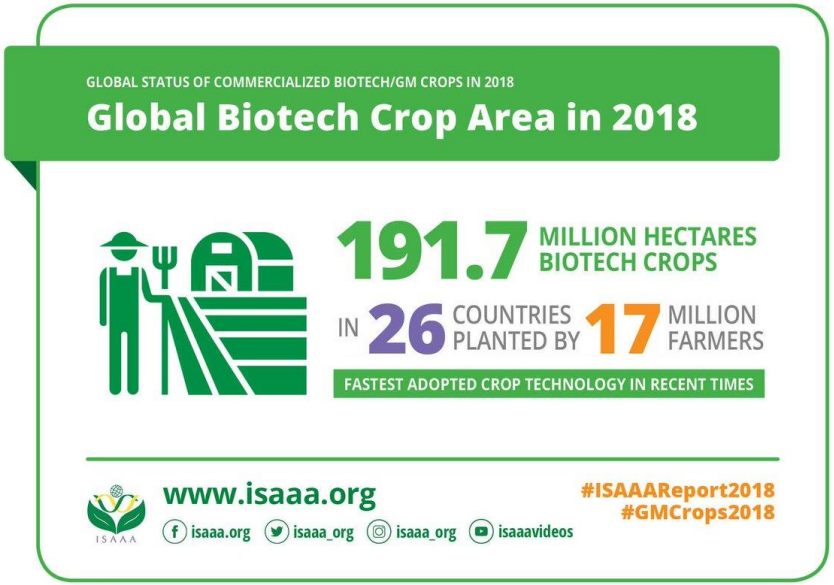
The genome of cultivated sweet potato contains *Agrobacterium* T-DNAs with expressed genes: An example of a naturally transgenic food crop

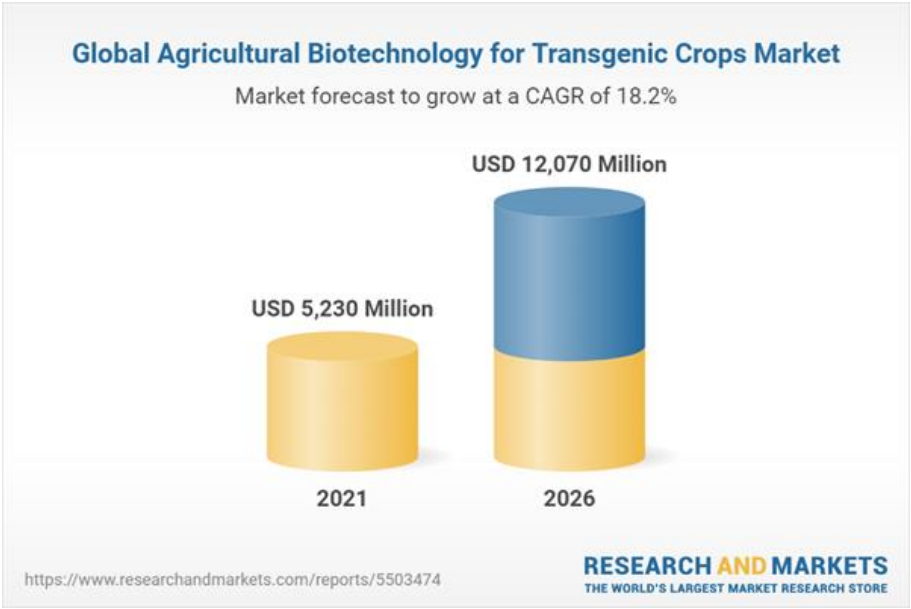
Tina Kyndt[a,1], Dora Quispe[a,b,1], Hong Zhai[c], Robert Jarret[d], Marc Ghislain[b], Qingchang Liu[c], Godelieve Gheysen[a], and Jan F. Kreuze[b,2]

[a]Department of Molecular Biotechnology, Ghent University, 9000 Ghent, Belgium; [b]International Potato Center, Lima 12, Peru; [c]Beijing Key Laboratory of Crop Genetic Improvement/Laboratory of Crop Heterosis and Utilization, Ministry of Education, China Agricultural University, Beijing, China, 100193; and [d]Plant Genetic Resources Unit, US Department of Agriculture, Agricultural Research Service, Griffin, GA 30223

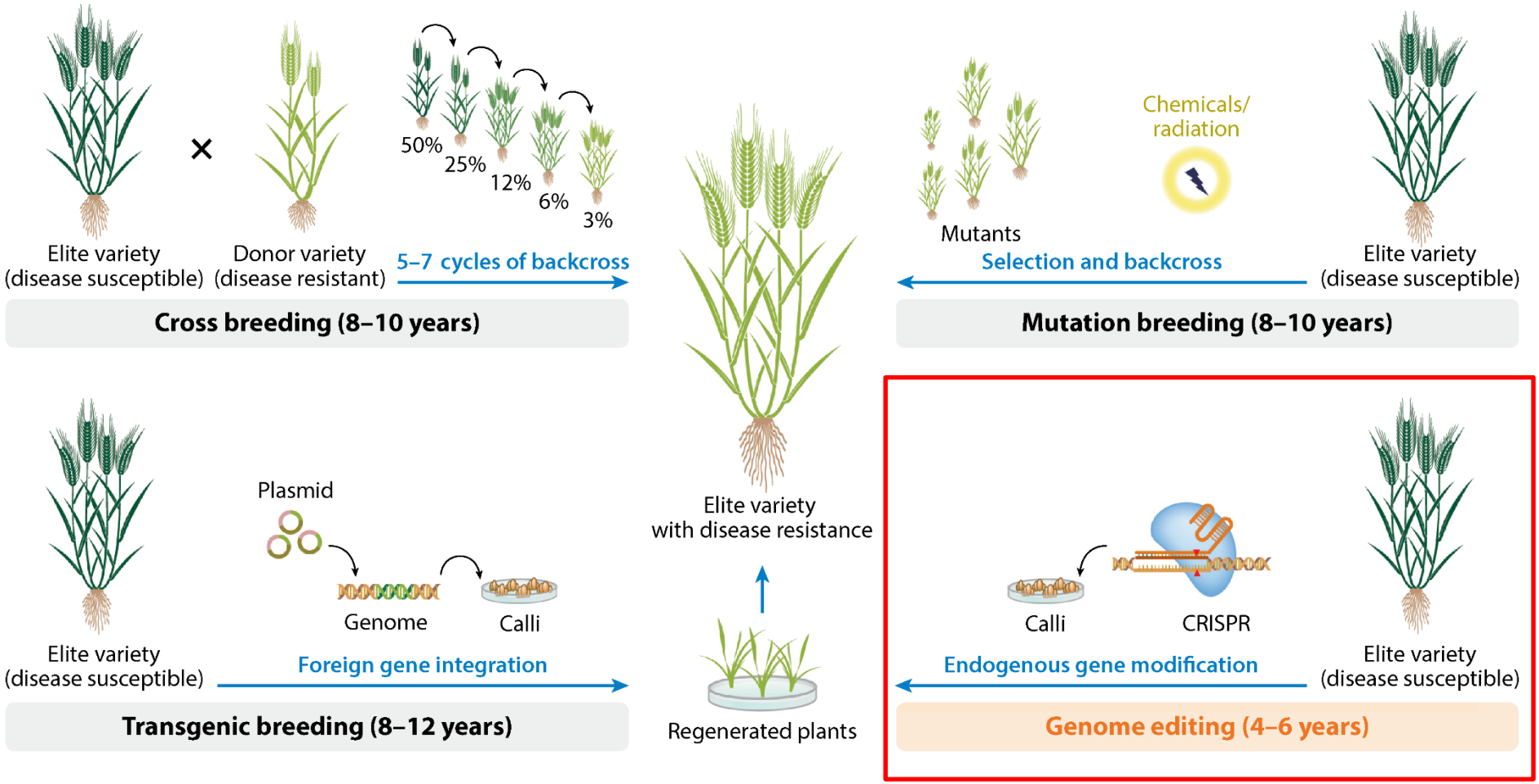


Global Agricultural Biotechnology for Transgenic Crops Market





Comparison of breeding methods used in modern agriculture



Chen K, et al. 2019.
Annu. Rev. Plant Biol. 70:667–97

What is genome editing?

- Genome editing is a method that lets scientists change the DNA of many organisms, including plants, bacteria, and animals.
- Editing DNA can lead to changes in agronomic traits, like yield, quality and disease/stress resistance.
- Scientists use different technologies to do this.

How does gene-editing work?

Break

DNA double strand breaks (DSBs)

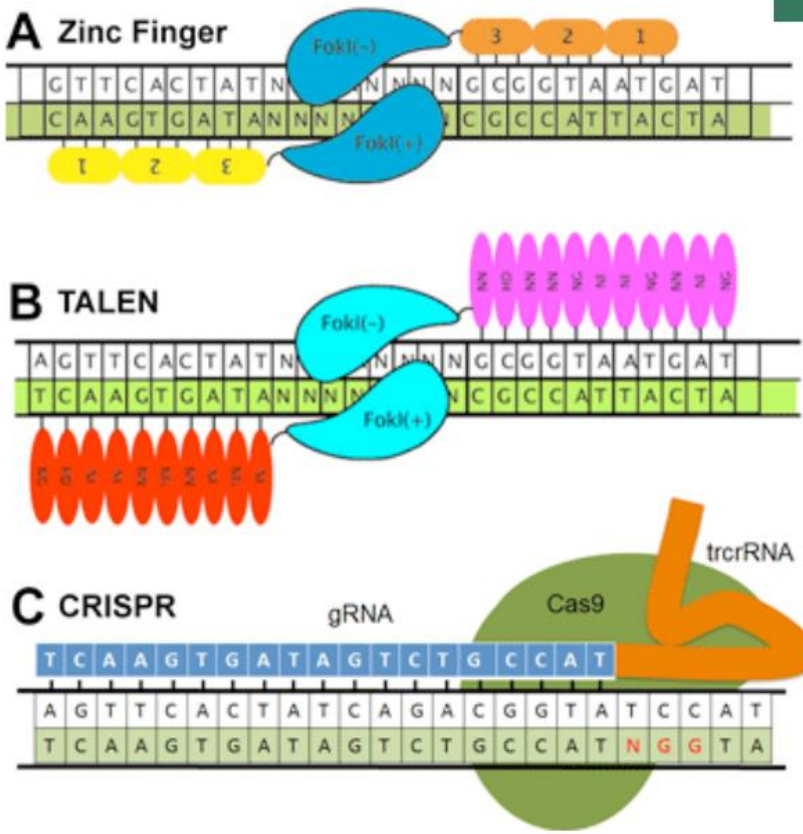
Repair

-Homology directed repair (HDR)
-Non-homologous end joining (NHEJ)

Continuous improvement of the specificity

TARGETING

CUTTING



specificity ≥ 24 bp
Protein recognition
no obvious code

Dimer nuclease

specificity ≥ 33-35 bp
Protein recognition
one-to-one rule

Dimer nuclease

specificity 19 bp
RNA recognition
one-to-one rule

Monomer nuclease
3-nt upstream
of the PAM site

DOUBLE STRAND BREAK

From: Marie-Bérengère TROADEC, 2018

There's CRISPR in Your Yogurt

We've all been eating food enhanced by the genome-editing tool for years.

By Kerry Grens | January 1, 2015

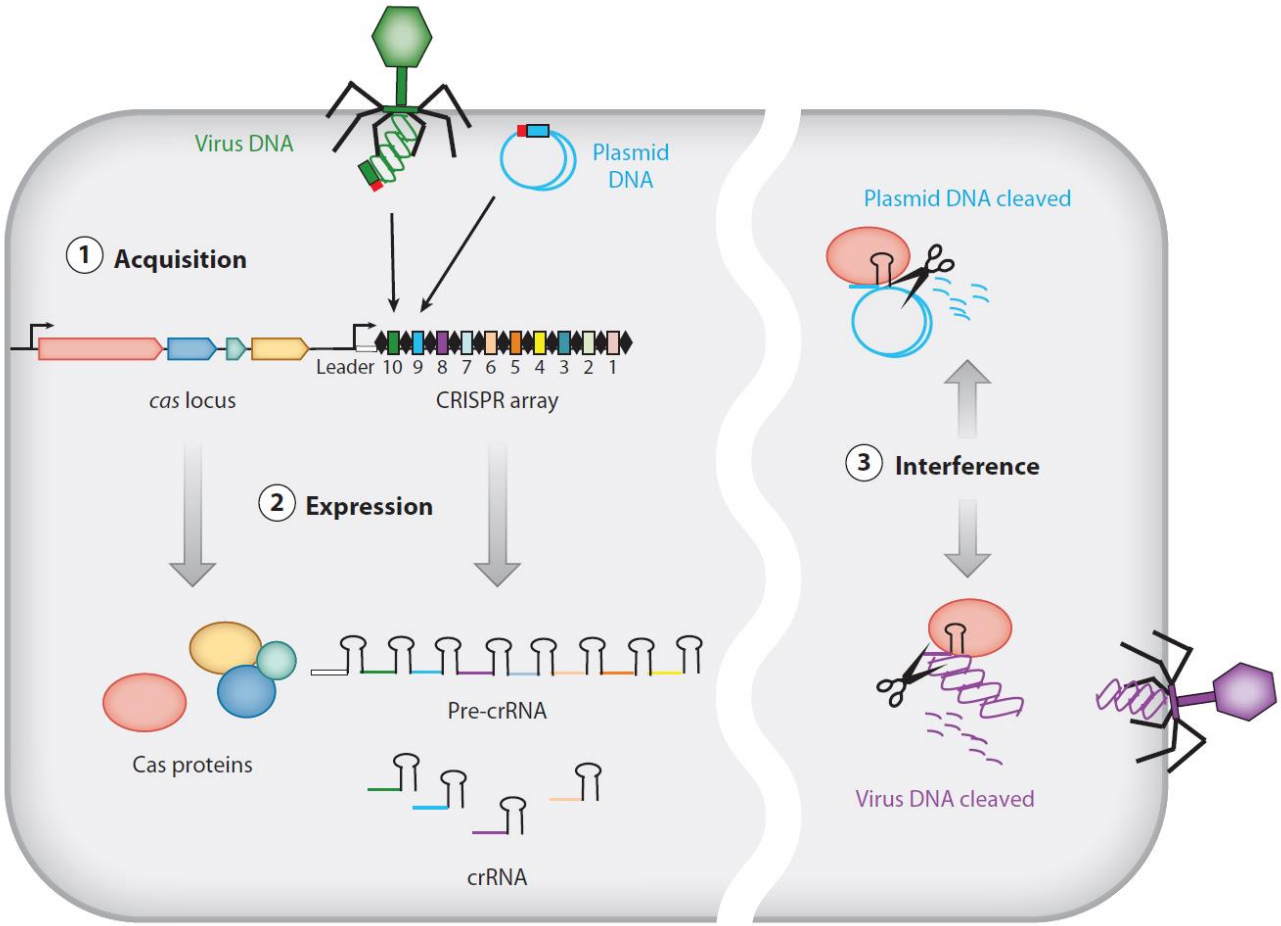
TheScientist 21
EXPLORING LIFE, INSPIRING INNOVATION

ANDRZEJ KRAUZE

Streptococcus thermophilus, a workhorse of yogurt and cheese production.

嗜熱鏈球菌

CRISPR: Bacteria Immune System



CRISPR array的protospace序列轉錄成RNA，當外源DNA再次入侵時，系統中的Cas蛋白(核酸酶)會利用這些RNA片段(crRNA)去結合並切斷入侵的相似序列，造成雙股DNA斷裂(Double-strand break)。

Annu. Rev. Genet. 2011. 45:273–97

2020 Nobel Chemistry Prize Awarded for CRISPR ‘Genetic Scissors’

NOBELPRISET I KEMI 2020
THE NOBEL PRIZE IN CHEMISTRY 2020

KUNGL. VETENSKAPS-AKADEMIEN
THE ROYAL SWEDISH ACADEMY OF SCIENCES

Emmanuelle Charpentier

Jennifer A. Doudna

Born in France, 1968

Max Planck Unit for the Science of Pathogens, Germany

Born in the USA, 1964

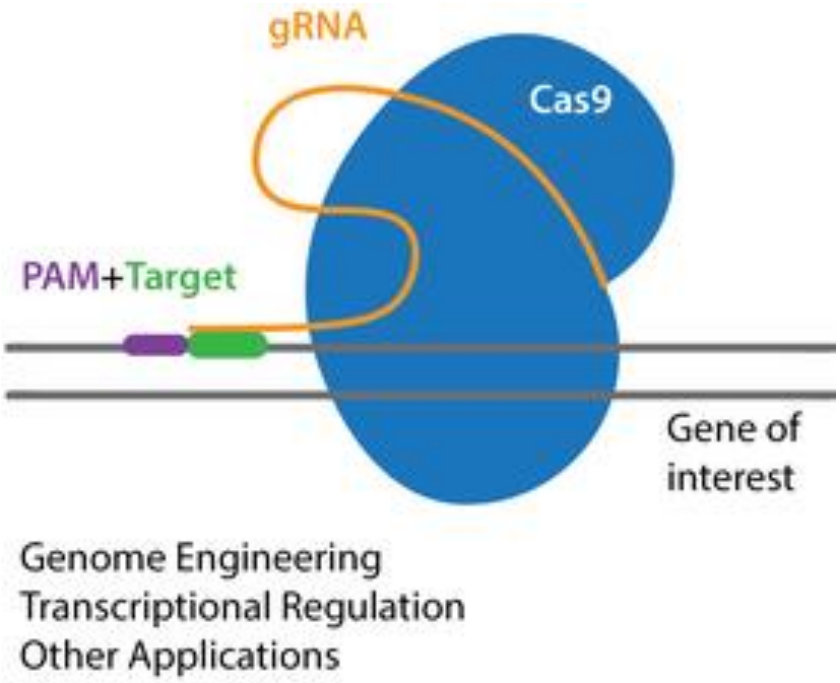
University of California, Berkeley, USA
Howard Hughes Medical Institute

https://www.nobelprize.org/prizes/chemistry/2020/press-release/

The CRISPR/Cas9 system

- CRISPR-Cas9 genome editing includes two key components: a single-guide RNA (gRNA) and a CRISPR-associated endonuclease (Cas).

- The sgRNA and Cas9 are combined into a ribonucleoprotein complex when they are used in CRISPR experiments.

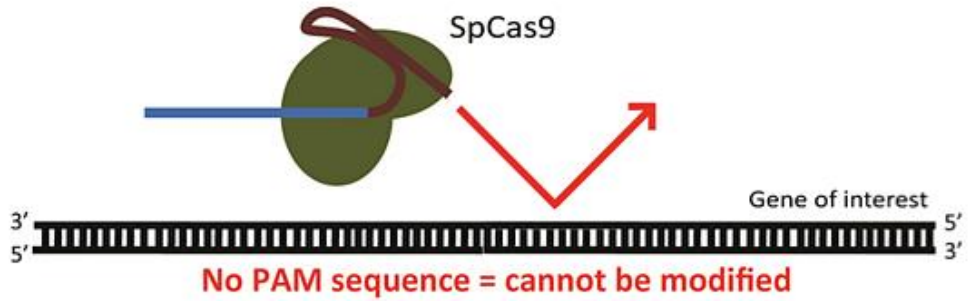


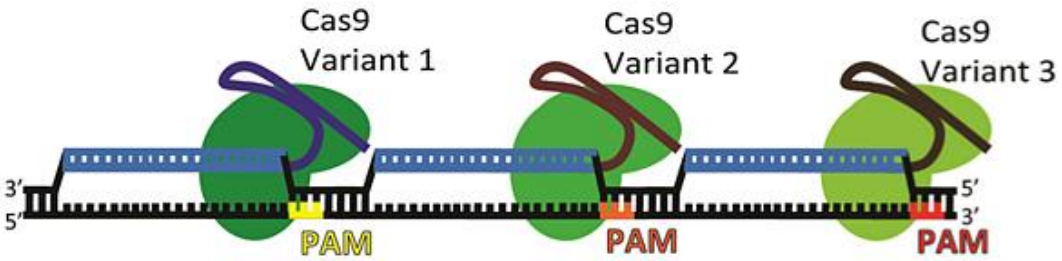
https://www.addgene.org/guides/crispr/

Protospacer Adjacent Motif (PAM sequence)

- Cas9 can be used to modify any desired genomic target provided that the sequence is located just upstream of a Protospacer Adjacent Motif (PAM sequence).

- The 3-5 nucleotide PAM sequence serves as a binding signal for Cas9 and this sequence is a strict requirement for Cas9-mediated DNA cleavage.





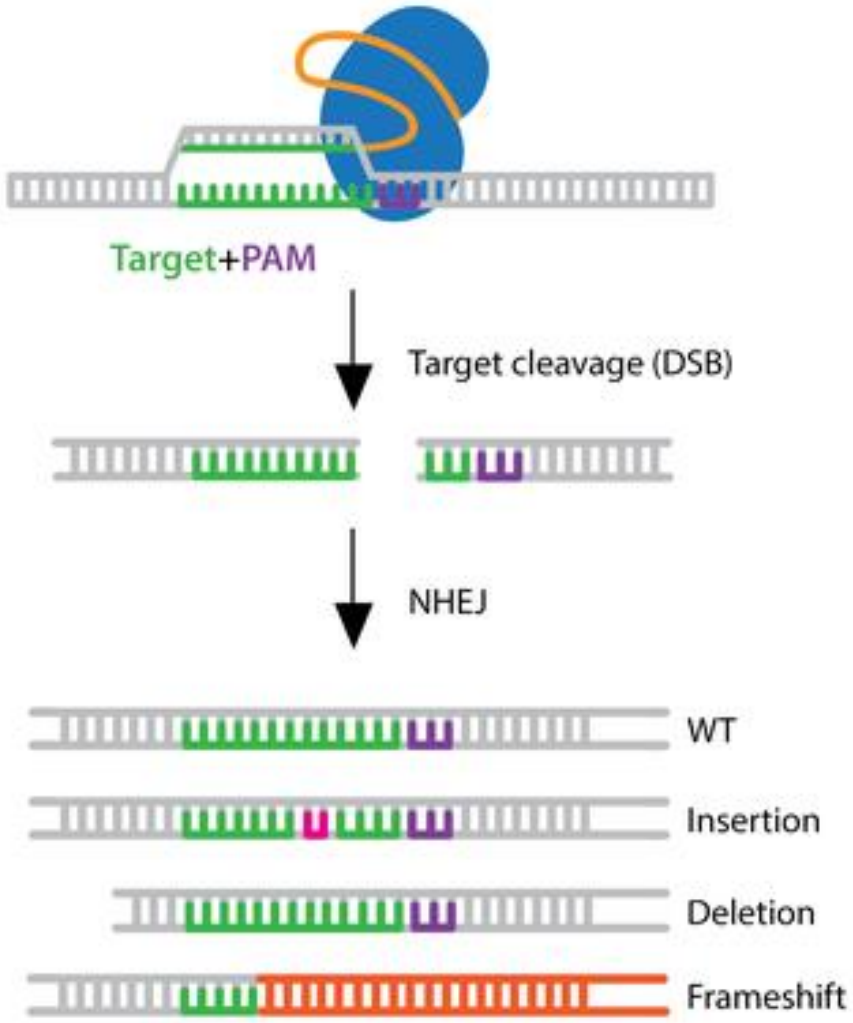
https://blog.addgene.org/the-pam-requirement-and-expanding-crispr-beyond-spcas9

The CRISPR/Cas tools

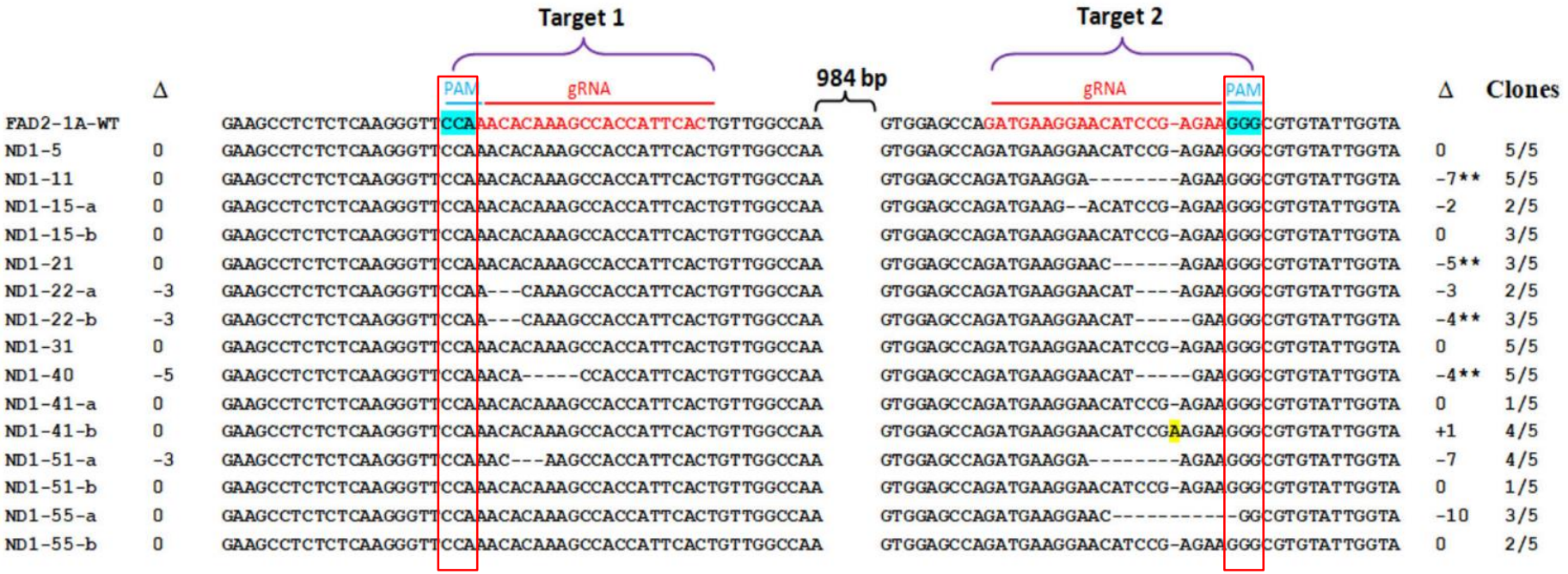
Summary of Cas and other nuclease variants used in CRISPR experiments and their PAM sequences

CRISPR Nucleases	Organism Isolated From	PAM Sequence (5’ to 3’)
SpCas9	*Streptococcus pyogenes*	3' NGG
SpCas9 D1135E variant	*Streptococcus pyogenes*	3' NGG (reduced NAG binding)
SpCas9 VRER variant	*Streptococcus pyogenes*	3' NGCG
SpCas9 EQR variant	*Streptococcus pyogenes*	3' NGAG
SpCas9 VQR variant	*Streptococcus pyogenes*	3' NGAN or NGNG
xCas9	*Streptococcus pyogenes*	3' NG, GAA, or GAT
SpCas9-NG	*Streptococcus pyogenes*	3' NG
SaCas9	*Staphylococcus aureus*	3' NNGRRT or NNGRR(N)
AsCpf1 and LbCpf1	*Acidaminococcus sp. and Lachnospiraceae bacterium*	5' TTTV
AsCpf1 RR variant	*Acidaminococcus sp.*	5' TYCV
LbCpf1 RR variant	*Lachnospiraceae bacterium*	5' TYCV
AsCpf1 RVR variant	*Acidaminococcus sp.*	5' TATV
Campylobacter jejuni (CJ)		3' NNNNRYAC
Neisseria meningitidis (NM)		3' NNNNGATT
Streptococcus thermophilus (ST)		3' NNAGAAW
Treponema denticola (TD)		3' NAAAAC
Additional Cas9s from various species		PAM sequence may not be characterized

Cutting + Repairing



CRISPR/Cas9-induced mutations in soybean



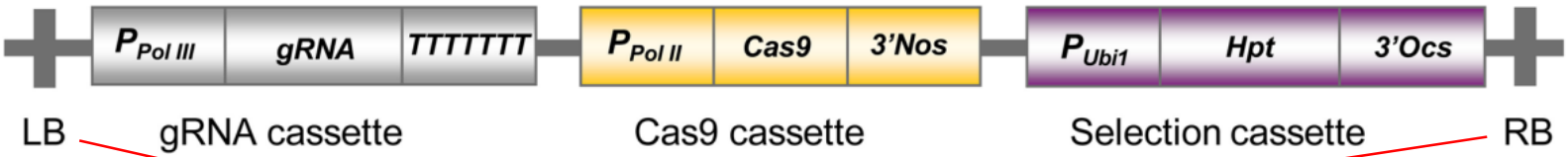
	Δ		Δ	Clones
FAD2-1A-WT		GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACATCCG-AGAAGGGCGTGTATTGGTA		
ND1-5	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACATCCG-AGAAGGGCGTGTATTGGTA	0	5/5
ND1-11	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGA--------AGAAGGGCGTGTATTGGTA	-7**	5/5
ND1-15-a	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAG--ACATCCG-AGAAGGGCGTGTATTGGTA	-2	2/5
ND1-15-b	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACATCCG-AGAAGGGCGTGTATTGGTA	0	3/5
ND1-21	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAAC------AGAAGGGCGTGTATTGGTA	-5**	3/5
ND1-22-a	-3	GAAGCCTCTCTCAAGGGTTCCAA---CAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACAT----AGAAGGGCGTGTATTGGTA	-3	2/5
ND1-22-b	-3	GAAGCCTCTCTCAAGGGTTCCAA---CAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACAT-----GAAGGGCGTGTATTGGTA	-4**	3/5
ND1-31	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACATCCG-AGAAGGGCGTGTATTGGTA	0	5/5
ND1-40	-5	GAAGCCTCTCTCAAGGGTTCCAAACA-----CCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACAT-----GAAGGGCGTGTATTGGTA	-4**	5/5
ND1-41-a	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACATCCG-AGAAGGGCGTGTATTGGTA	0	1/5
ND1-41-b	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACATCCGAAGAAGGGCGTGTATTGGTA	+1	4/5
ND1-51-a	-3	GAAGCCTCTCTCAAGGGTTCCAAAC---AAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGA--------AGAAGGGCGTGTATTGGTA	-7	4/5
ND1-51-b	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACATCCG-AGAAGGGCGTGTATTGGTA	0	1/5
ND1-55-a	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAAC----------GGCGTGTATTGGTA	-10	3/5
ND1-55-b	0	GAAGCCTCTCTCAAGGGTTCCAAACACAAAGCCACCATTCACTGTTGGCCAA	GTGGAGCCAGATGAAGGAACATCCG-AGAAGGGCGTGTATTGGTA	0	2/5

BMC Plant Biology (2019) 19:311

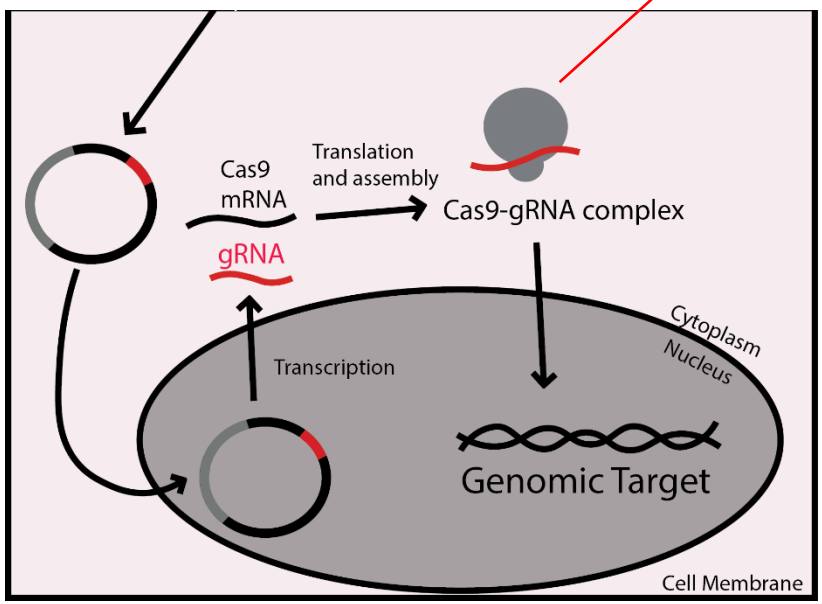
How does genome-editing work in plants?

如何將基因編輯工具送入植物基因組

1. 透過農桿菌轉殖質體DNA到植物基因組進行基因編輯



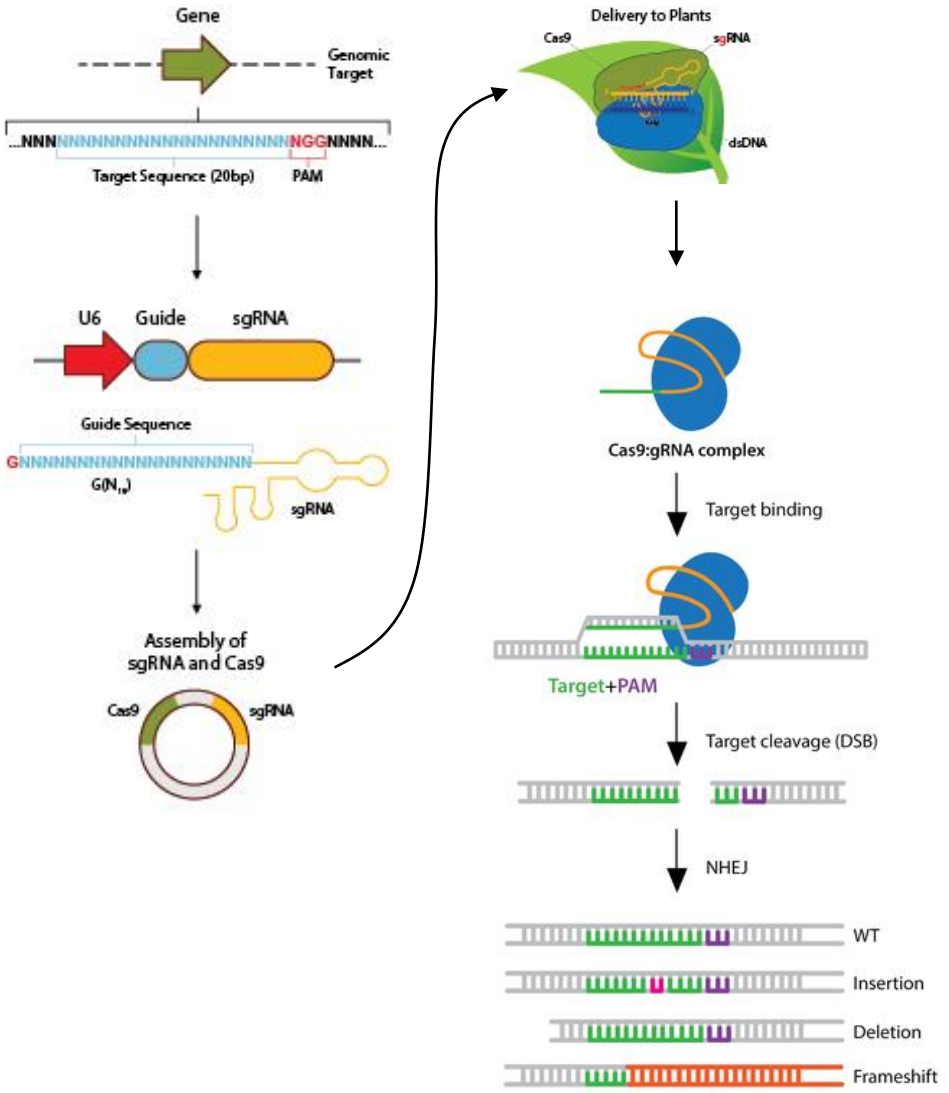
RNA-蛋白質(核酸酶)複合體



https://blog.addgene.org/genome-engineering-using-cas9/grna-ribonucleoproteins-rnps

Basic strategy for CRISPR/Cas9 editing in plants

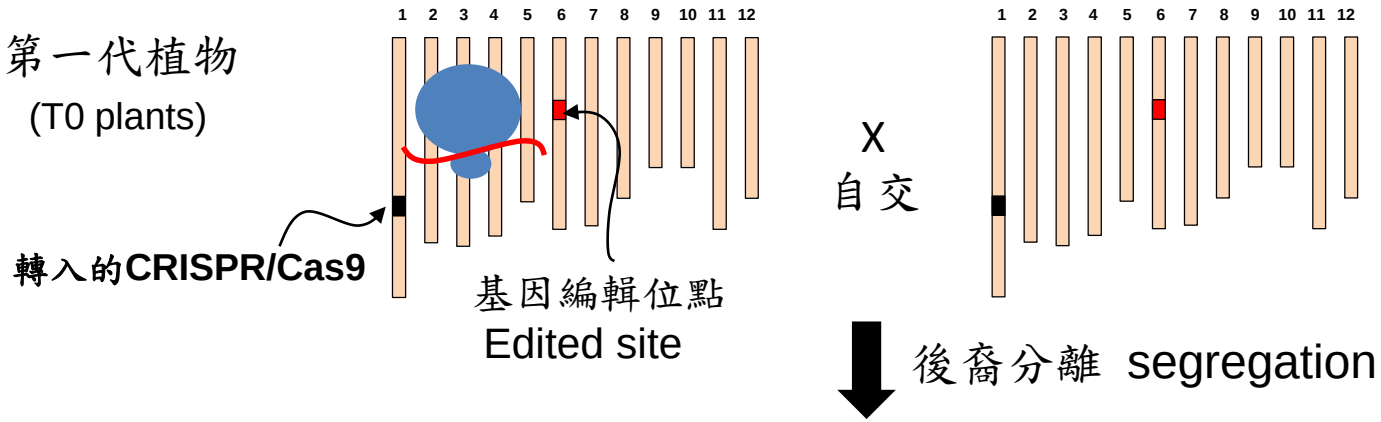
1. Design and synthesize specific and effective gRNA spacers.
2. Assemble gRNA/Cas9 construct or ribonucleotide protein complex.
3. Deliver gRNA/Cas9 construct or RNP complex into the plant cell.
4. Regenerate intact plants.
5. Genotyping and molecular characterization
6. Phenotyping, functional genomics and agronomic trait evaluation.

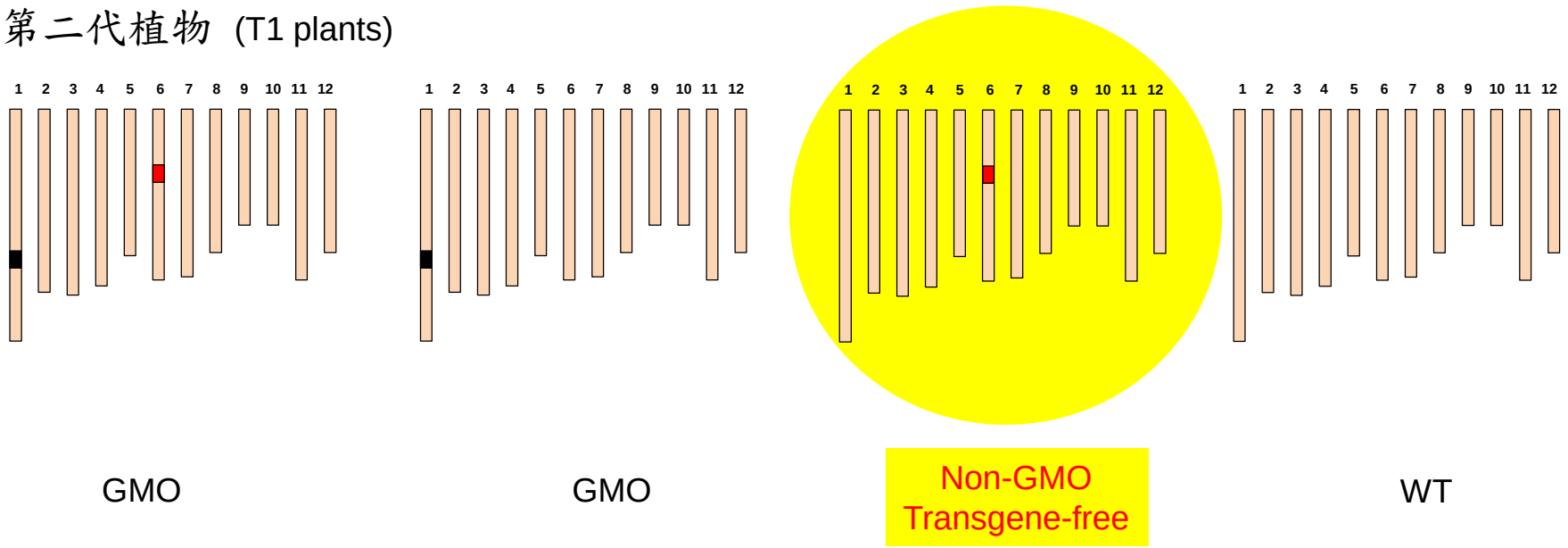


https://www.sigmaaldrich.com/technical documents/articles/biology/genome-editing-in-plants-with-crispr-cas9.html

https://www.addgene.org/guides/crispr/

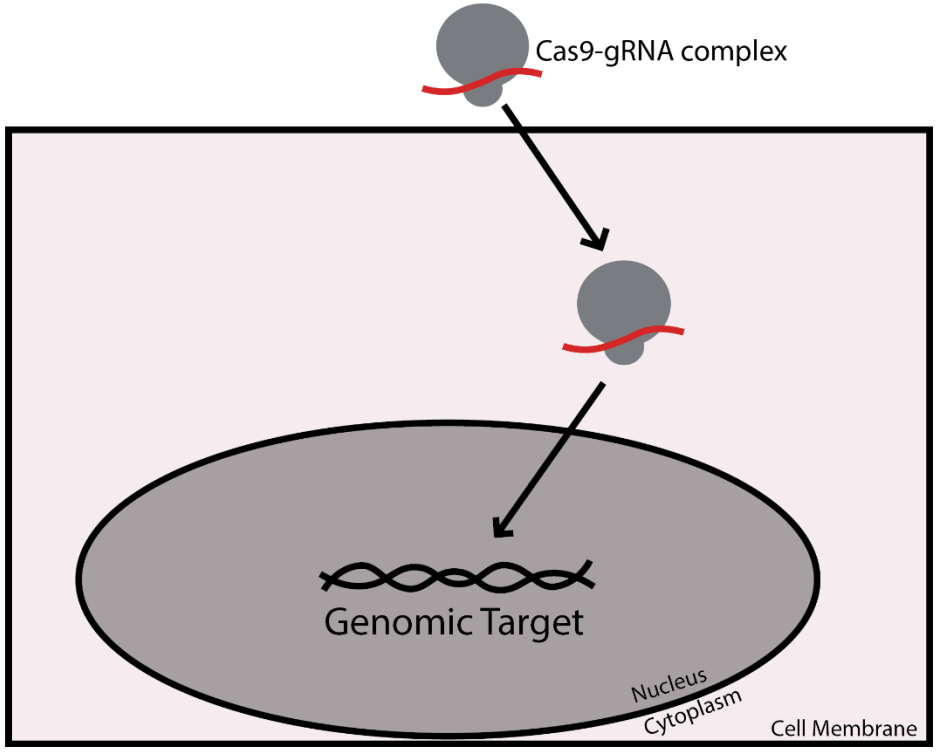
Generating transgene free GE plants by genetic segregation





Basic strategy for CRISPR/Cas9 editing in plants

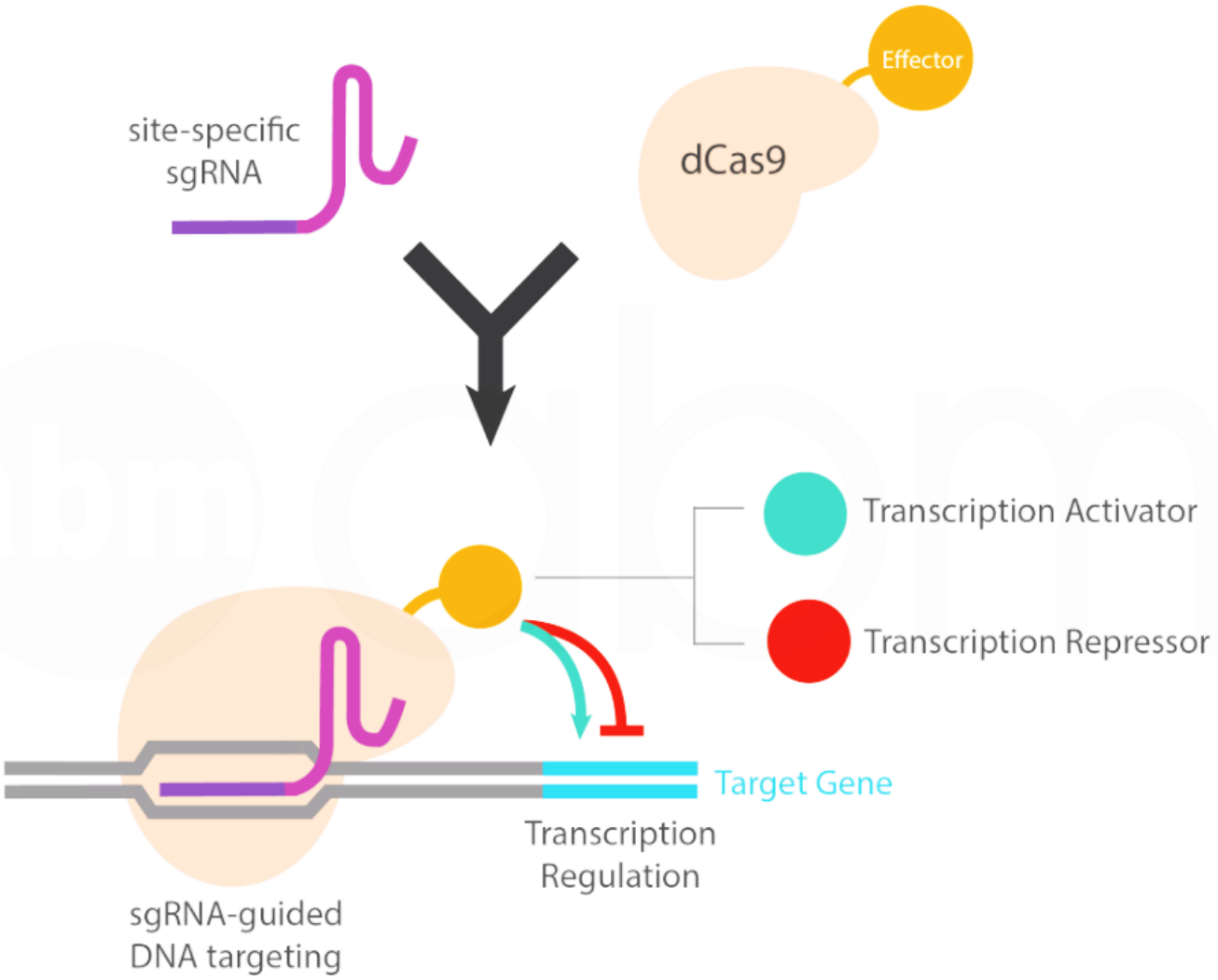
2. 直接送入RNA-蛋白質複合體RNP (ribonucleoprotein) 進行基因編輯



Without DNA integration

https://blog.addgene.org/genome-engineering-using-cas9/grna-ribonucleoproteins-rnps

dCas9 can easily be fused to effectors for targeted gene regulation



Gilbert et al. (2013)

Advantages of CRISPR/Cas9 system

- Simplicity and efficiency 簡單、高效
- Precise editing with relatively low cost 精準、低成本
- Multiplex genome editing 同時編輯多個基因
- Works well in editing polyploidy plants 多倍體育種利器
- Relieve genetic erosion 緩解遺傳質流失

  --breeding landrace to become the primary genetic background of modern varieties.
- Overcome linkage drag 克服遺傳累贅
- Transgene free 無轉基因

Off-target issue

a. Plant breeding is different from animal breeding

- Crop produces hundreds of seeds.
- Progenies with abnormal phenotypes were all discarded by selection.
- Variation is the basis of plant breeding.

b. Off target can be validated by whole genome sequencing.

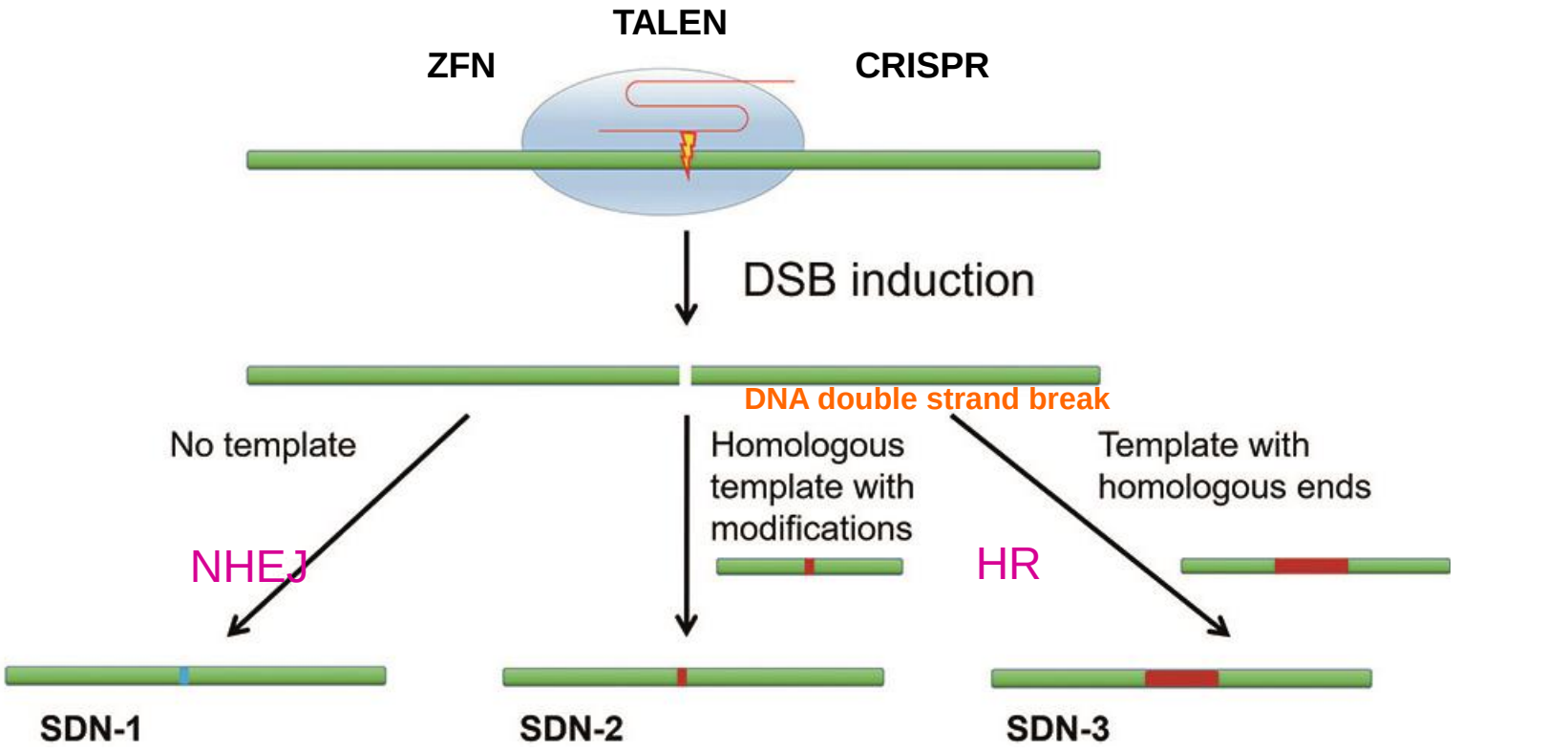
c. Crops edited by SDN1-type gene-editing is as safe as mutation breeding.

	Method	Mechanism of mutation	Mutation frequency	Estimated mutation events
Chemical mutagen	EMS	G/C to A/T transitions or G/C to C/G or G/C to T/A transversions	2-10 mutations/Mb (Till et al. 2007)	860-4300
Physical mutagen	γ-rays	Single nucleotide substitution, inversion and deletion	7.5-9.8 /Mb (Li et al., 2016)	3450-44178
Biological mutagen	Retro-Transposon	Random sequence insertion	1 insertion/100-kb (Miyao et al., 2003)	4300
Gene editing	CRISPR/Cas9	Small indels (≤10pb), often single nucleotides and deletions	85%-100% (reviewed in Zhu et al., 2017)	1 (+ when off target happens)

製造植物遺傳變異方法的優缺點

變異來源	優缺點
天然突變	機率非常低
人為誘變	效率低、隨機突變、須建立龐大族群篩選、誘變往往伴隨多種性狀變化
種原導入	種原有限、連鎖累贅、多倍體育種難度高、時間長
基因轉殖	隨機嵌入染色體、GMO issue
基因編輯	精準、簡單、快速、非轉基因

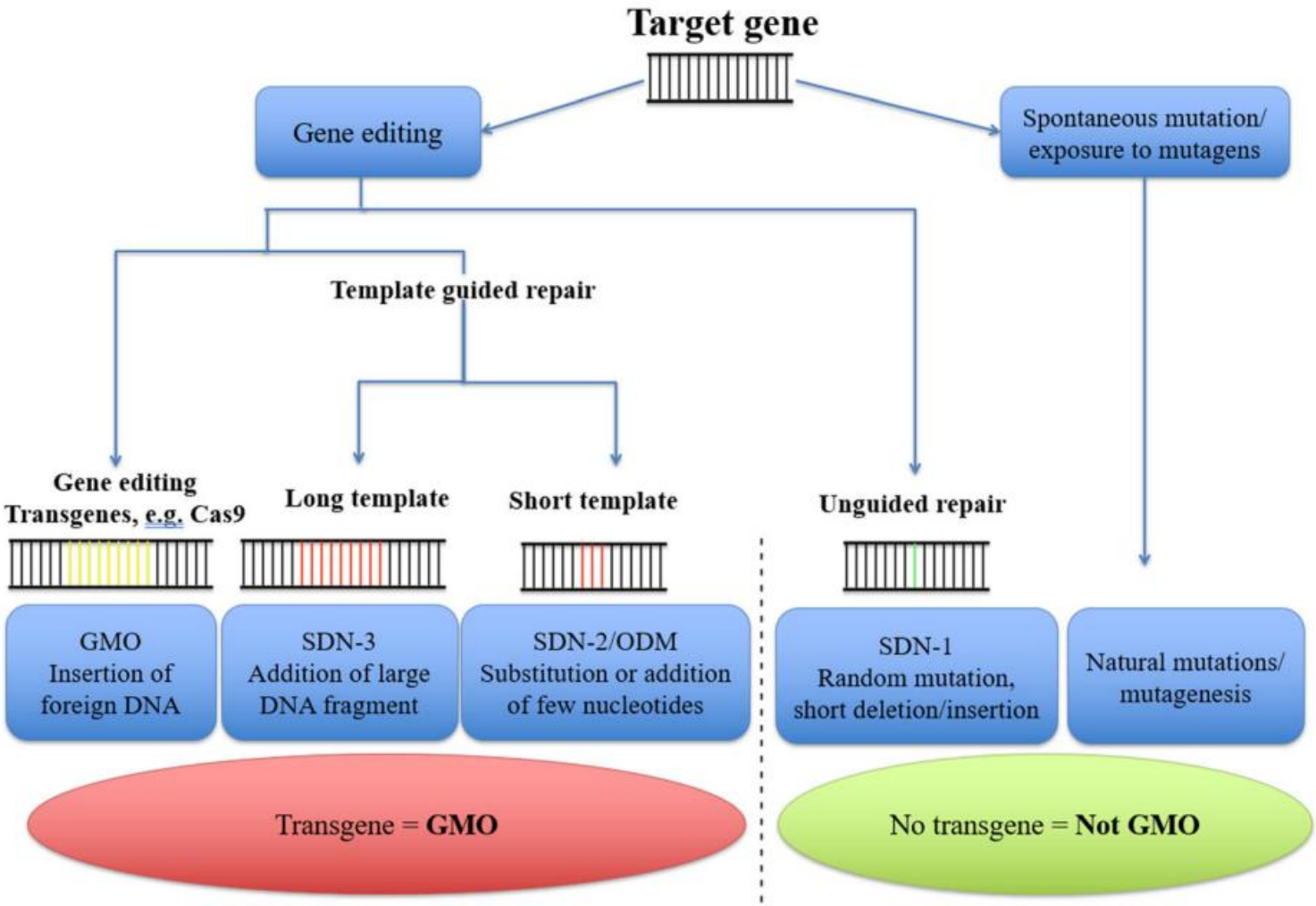
Gene-edited crops using SDNs are divided into three types



斷裂的DNA經過修補後，產生鹼基缺失、表達框架位移(SDN1)或嵌入一段相類似的DNA(SDN 2& 3)，最終造成**基因功能喪失、基因序列修復、或基因嵌入**

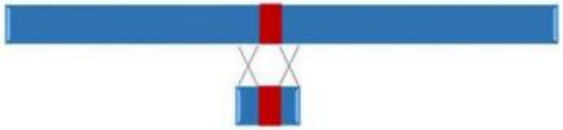
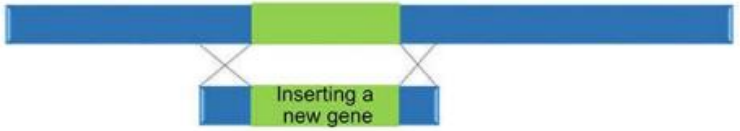
https://www.laboratory-journal.com/science/life-sciences-biotech/molecular-scissors-revolutionize-plant-breeding

Current Australian regulatory status of organisms developed via gene editing techniques, natural mutations and mutagenesis



In Vitro Cellular & Developmental Biology - Plant (2021) 57:574–583

Regulatory overview of genome-edited organisms in Japan

Division of the applications of SDNs		Definitions
SDN-1	Site-directed mutagenesis 	Non-LMOs
SDN-2	Templated editing 	LMOs
SDN-3	Site-directed insertion 	LMOs

Front. Bioeng. Biotechnol. (2019)7:387

Breaking News: India Issues Ruling Favourable to Gene Editing

By **Alex Martin** - March 31, 2022

144 0

On March 31, the Ministry of Environment, Forest and Climate Change of India revised its rules concerning the applications of gene editing in agriculture. The ruling states gene editing will be excluded from the GMO classification.

Philippines Releases Regulations for Gene-edited Plants on May 25, 2022

Republic of the Philippines
OFFICE OF THE SECRETARY
Elliptical Road, Diliman,
Quezon City 1100, Philippines

MEMORANDUM CIRCULAR
No. 08
Series of 2022

Subject: **RULES AND PROCEDURE TO EVALUATE AND DETERMINE WHEN PRODUCTS OF PLANT BREEDING INNOVATIONS (PBIs) ARE COVERED UNDER THE DOST-DA-DENR-DOH-DILG JOINT DEPARTMENT CIRCULAR NO. 1, SERIES OF 2021 (JDC1, s2021) BASED ON THE NCBP RESOLUTION NO. 1, SERIES OF 2020**

Pursuant to (a) the DOST-DA-DENR-DOH-DILG Joint Department Circular no. 1, series of 2021, ***Rules and Regulations for the Research and Development, Handling and Use, Transboundary Movement, Release into the Environment, and Management of Genetically Modified Plant and Plant Products Derived from the Use of Modern Biotechnology***, or JDC1, s2021 – which revised the previous DOST-DA-DENR-DOH-DILG Joint Department Circular no. 1, series of 2016, or JDC1, s2016 – and (b) the National Committee on Biosafety of the Philippines (NCBP) Resolution no. 001, series of 2020, ***The Regulation of Plant and Plant Products Derived from the Use of Plant Breeding Innovations (PBIs) or New Plant Breeding Techniques (NBTs),*** which tasked the Department of Agriculture to issue guidelines and take the lead in evaluating and

英國推出新法案欲放寬基因編輯限制！第一批基因編輯番茄將在2023年問世

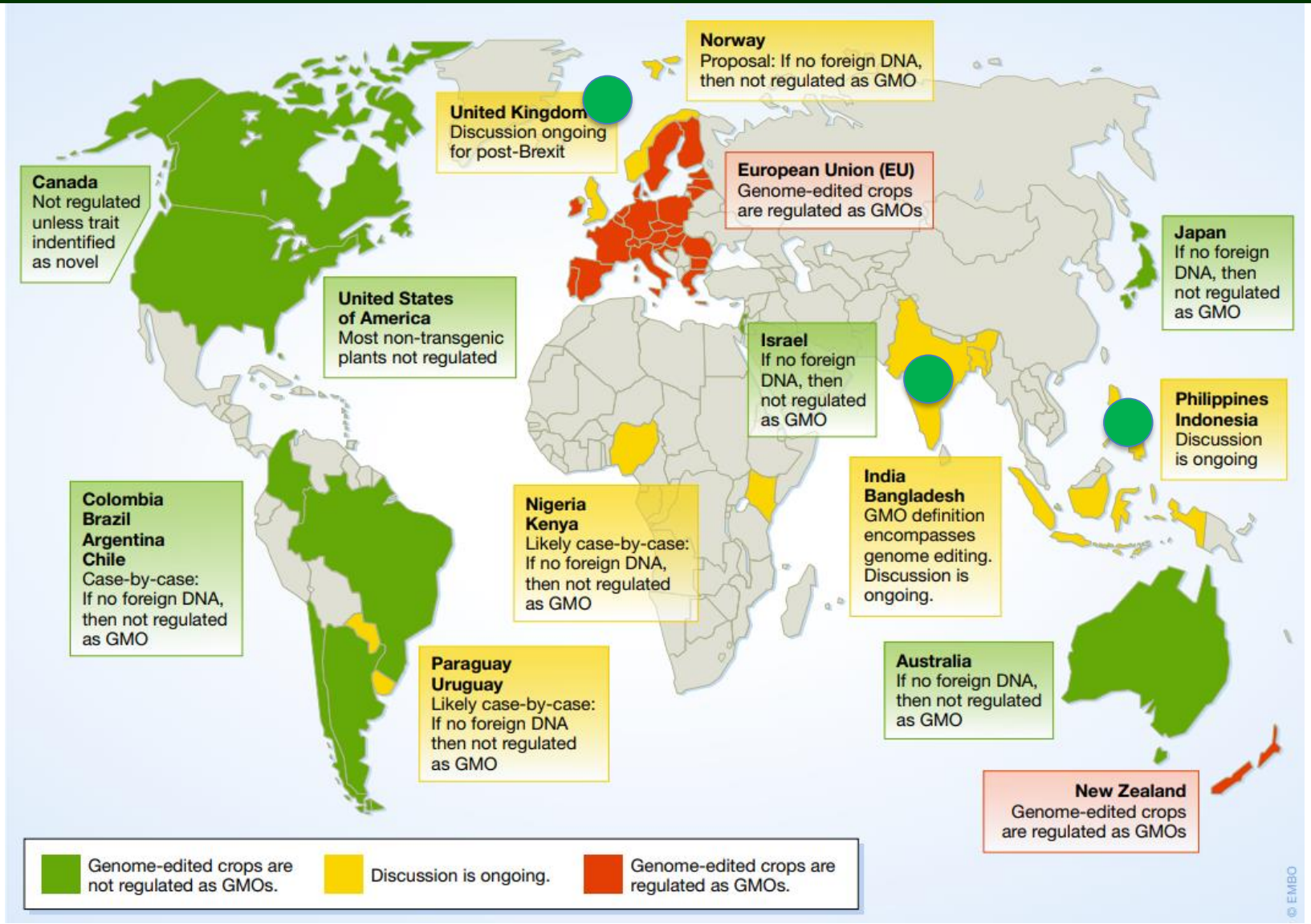
2022/06/09

撰文 = 謝承學

在2022年5月25日，英國環境、食品和農村事務部（Department of Environment, Food and Rural Affairs，DEFRA）向國會提出《基因技術法案（Genetic Technology Bill）》，又稱精確育種（Precision Breeding）法案，該法案將基因編輯的植物與基因改造作物做出區別，支持基因編輯作物技術發展。

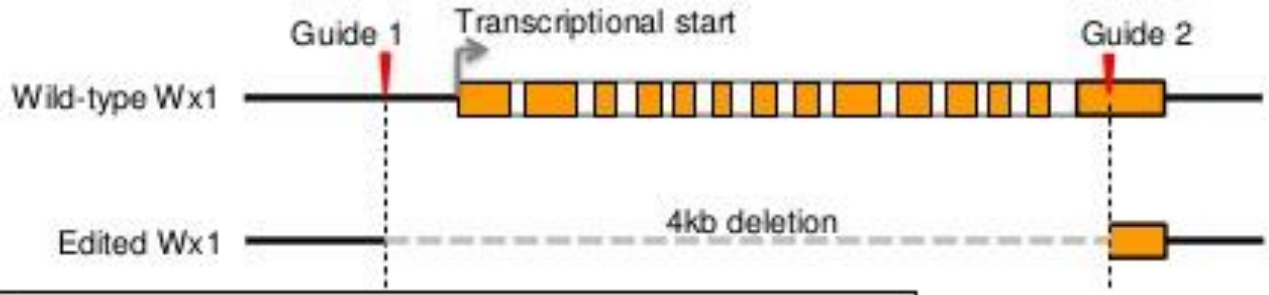
對此，DEFRA首席科學顧問Gideon Henderson以同樣在2022年5月發表在《nature plants》的基因編輯番茄研究為例表示，透過基因編輯技術可提升番茄中的維生素D含量。「這可以透過傳統育種技術達成，但速度將非常緩慢，可能需要幾十年才能駕馭。」他說道。

Current state of genome-editing legislation



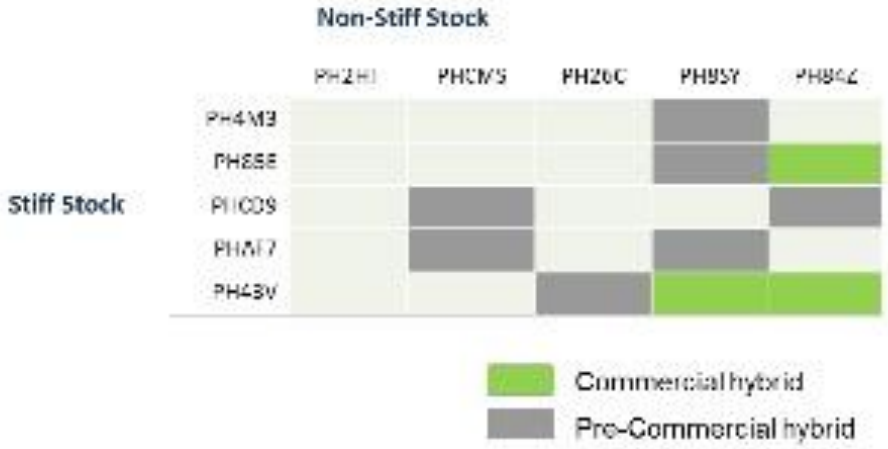
EMBO reports 21: e50680 | 2020

Waxy corn – edited allele strategy



Summary:

- Created alleles directly in multiple commercial inbreds
- Tested in greenhouse and field under standard testing strategy for late stage hybrids
- Sep 2015 initiated transformation of new elite inbreds "on demand"
- Waxy deletions recovered in all 11 inbred lines



DUPONT PIONEER.

Waxy corn generated by CRISPR/Cas9

No. 2 Yellow Dent Corn

- Translucent appearance
- Feed / ethanol / food
- Starch:

75% Amylopectin

25% Amylose

Waxy Corn

- Candlewax-like appearance
- Food / industrial
- Starch:

>97% Amylopectin

Gene-edited high oleic acid soybean oil now available in the US

- 在大豆種子和植株中，Fatty Acid Desaturase 2 (FAD2) 是控制單元不飽和脂肪生成的關鍵基因，FAD2催化油酸成為亞麻油酸，因此只要將低 FAD2 基因表達，即可提高油酸這個單元不飽和脂肪酸含量。

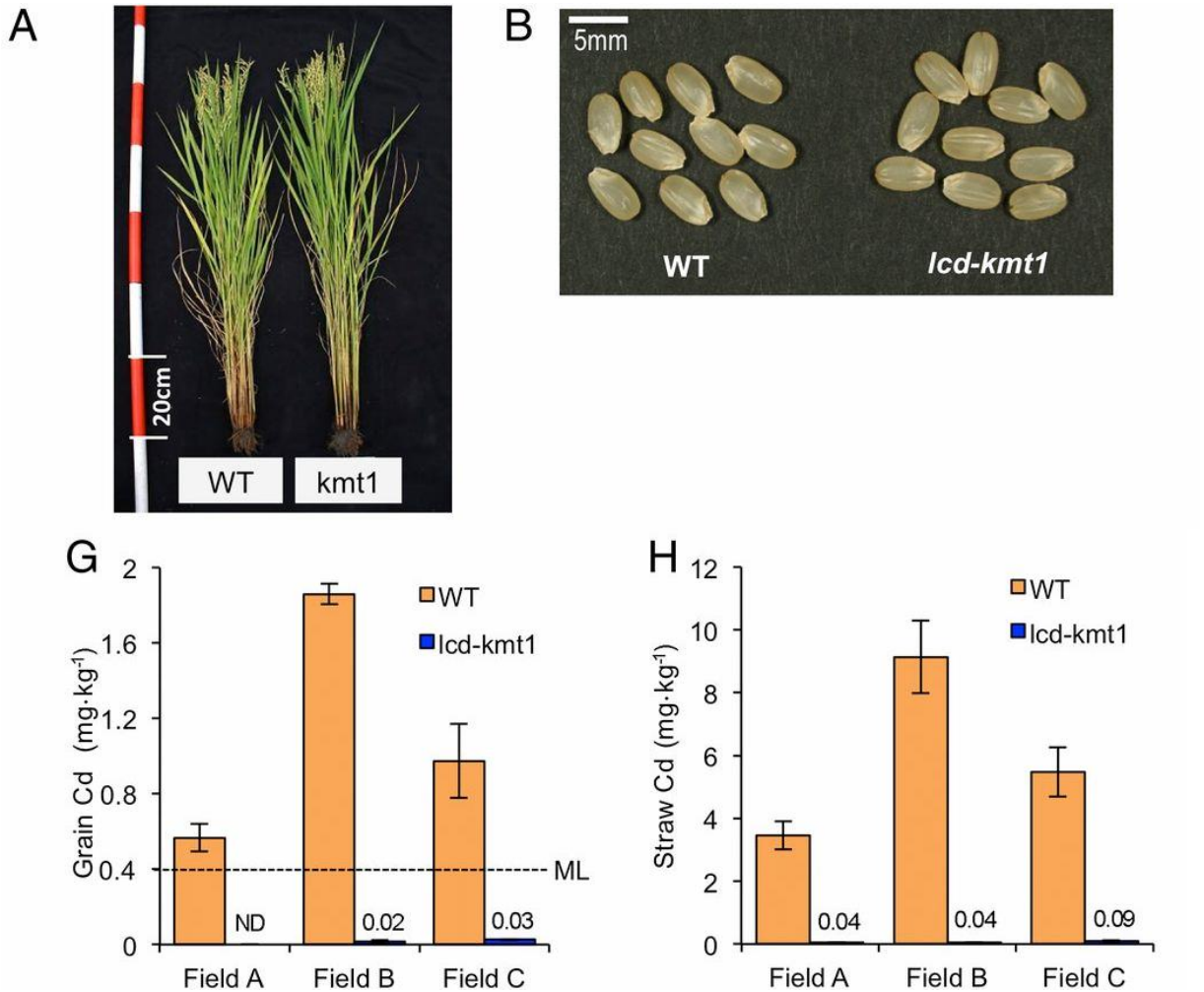
- 利用基因編輯敲除大豆FAD基因，油酸 (Oleic acid) 含量從 20% 提高到 80%，亞油酸 (linoleic acid)含量則由 50% 降至 4%，大幅改善大豆油的品質。

Calyxt/ GE

Dupont/RNAi

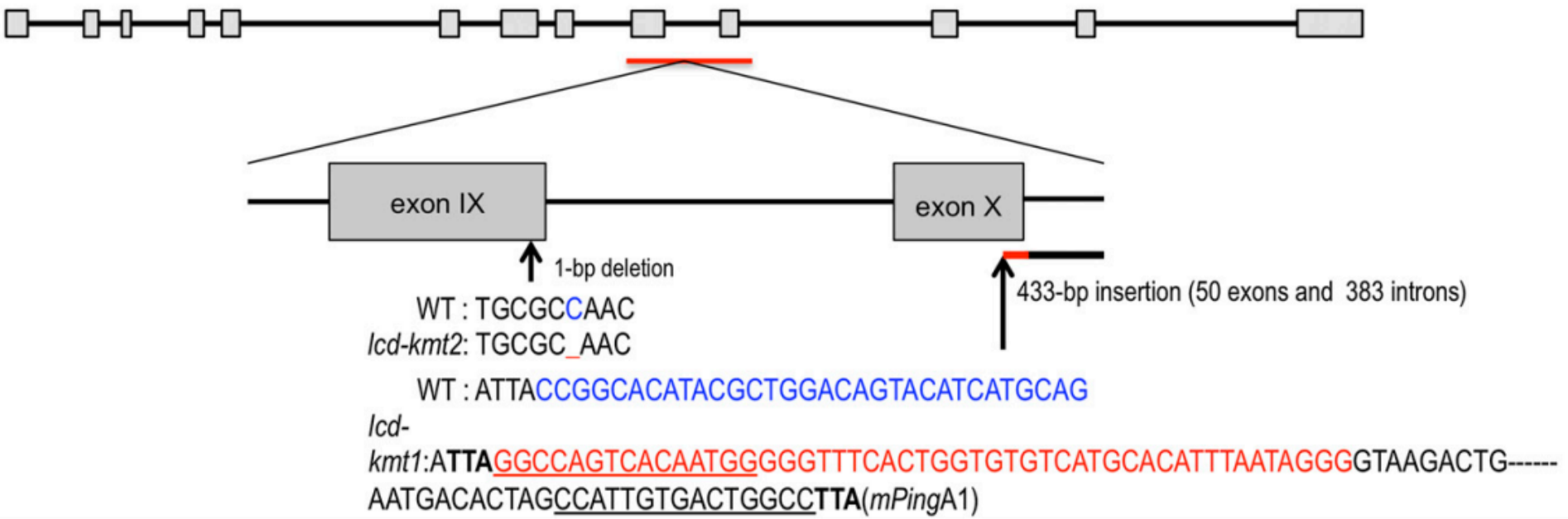
https://www.isaaa.org/kc/cropbiotechupdate/article/default.asp?ID=17345

低鎘累積越光米之育成



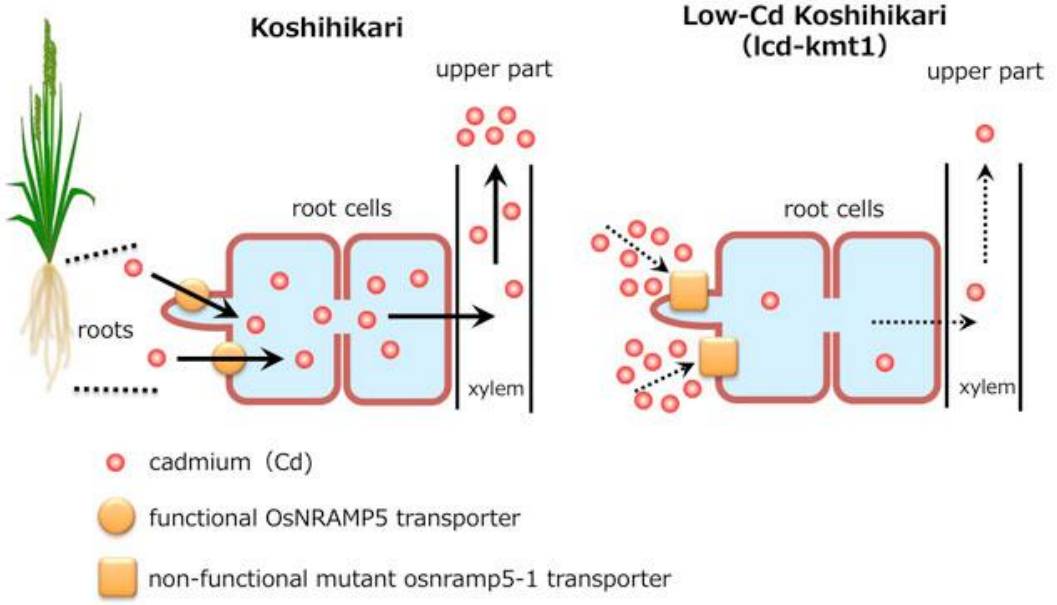
Satoru Ishikawa et al. PNAS 2012;109:19166-19171

Structure of OsNRAMP5 and the mutation sites in lcd-kmt1 and lcd-kmt2



Gene responsible for low-cadmium rice identified in Koshihikari

- Three rice mutants with grains containing less than 0.05 mg cadmium (Cd) per kilogram were identified.
- The group produced the mutants by carbon ion-beam irradiation and also identified the responsible gene for reduced Cd uptake:OsNRAMP5 gene, which encodes a Mn, Fe and Cd transporter



カドミウムを吸収しない水稲品種「コシヒカリ環1号」

土壌からのカドミウム吸収量を大幅に減らすことが可能な品種

研究開発の背景

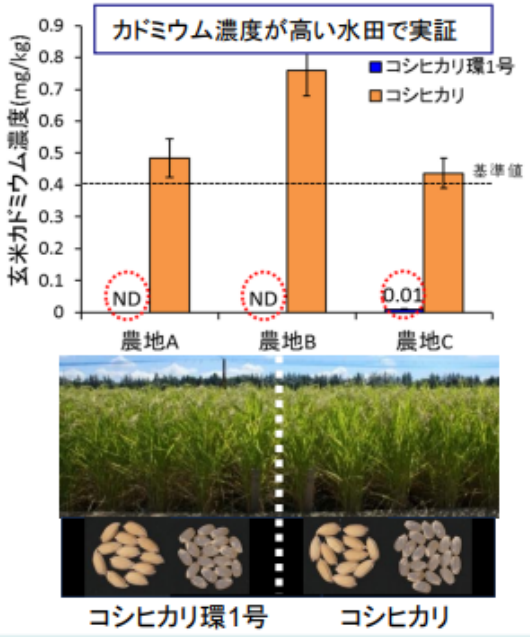
・コメ中のカドミウム濃度を低減させる従来の技術（客土や湛水管理等）は、コストや水の確保の面から適用範囲が限定される。
・従来の稲作栽培法をそのまま適用できる低カドミウム水稲品種の開発が求められている。

研究成果の内容

イオンビーム照射による突然変異処理で育成した「コシヒカリ環1号」

1. 品種特性：
　カドミウム濃度が高い水田で、低減対策をとらずに栽培しても、「コシヒカリ環1号」の玄米カドミウム濃度はほぼ検出限界（0.01mg/kg）以下になる。

2. 生育特性：
　コシヒカリ環1号の出穂期、玄米収量や稈長、穂長等の形質はコシヒカリとほぼ同等。外部機関による食味も同等の評価。



導入メリット

コメ由来のカドミウム摂取を減らすことが可能

1. コメ由来のカドミウム摂取量がほぼなくなる

・「コシヒカリ環1号」やカドミウム吸収抑制形質が導入された水稲品種が全国で栽培されることにより、農作物からのカドミウム摂取量が大きく減少する。

2. 長期の湛水管理が不要

・出穂前後の長期の湛水管理が不要になるため、夏期の大量の農業用水の確保や機械収穫時の作業性の低下を避けることが可能。

3. コメ中のヒ素低減対策にも有効

・「コシヒカリ環1号」を節水栽培することで、カドミウムとヒ素の同時低減が可能。

期待される効果

・土壌からのカドミウム吸収量の低減に寄与。
・他の品種や有望系統にもカドミウム吸収抑制形質を導入し、新たな低カドミウム品種の育成に貢献。

導入をオススメする対象
コシヒカリ栽培地域

開発機関：農研機構農業環境変動研究センター、次世代作物開発研究センター、予算区分【競争的資金】

https://www.maff.go.jp/j/kanbo/kihyo03/gityo/new_tech_cultivar/attach/pdf/2017-45.pdf

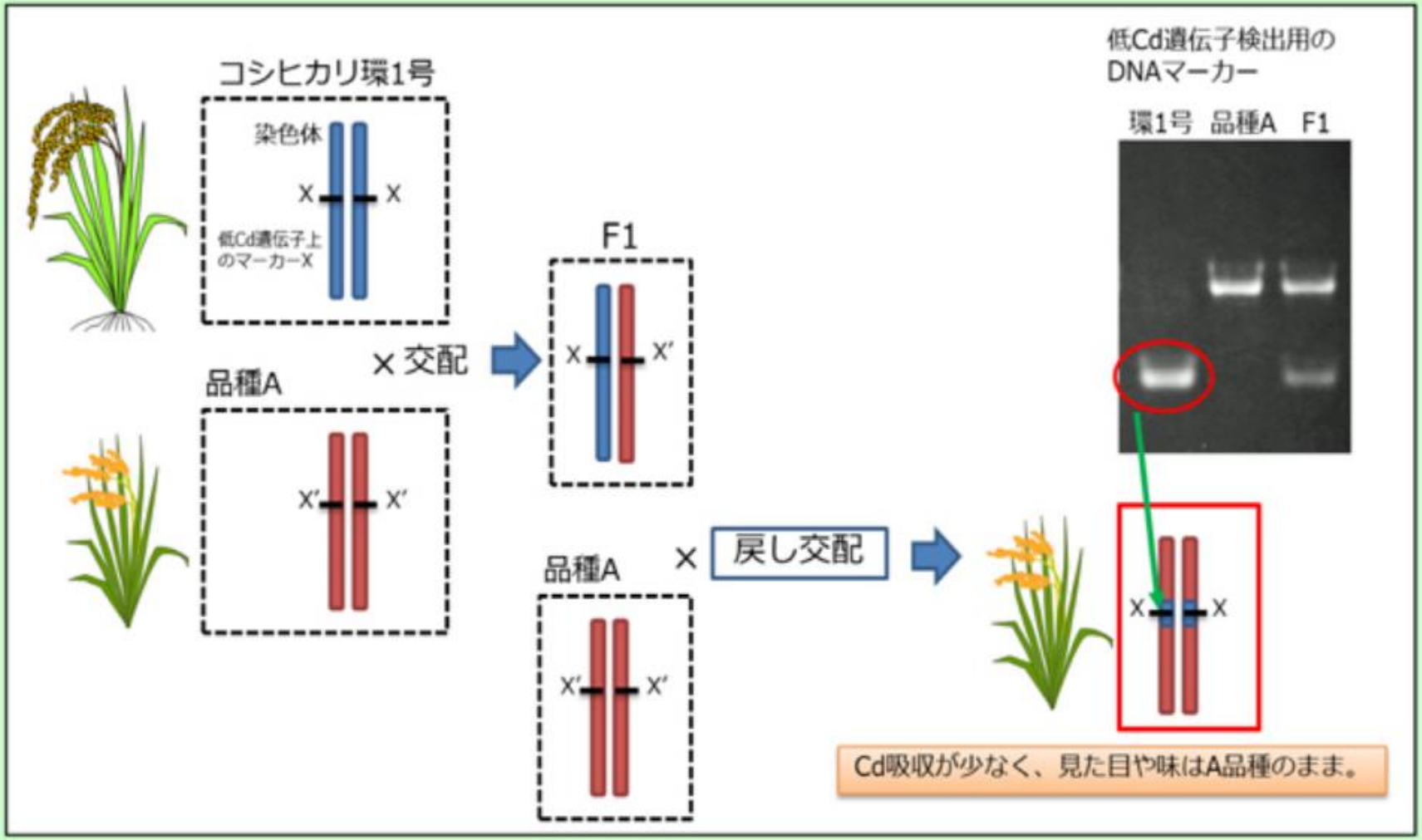
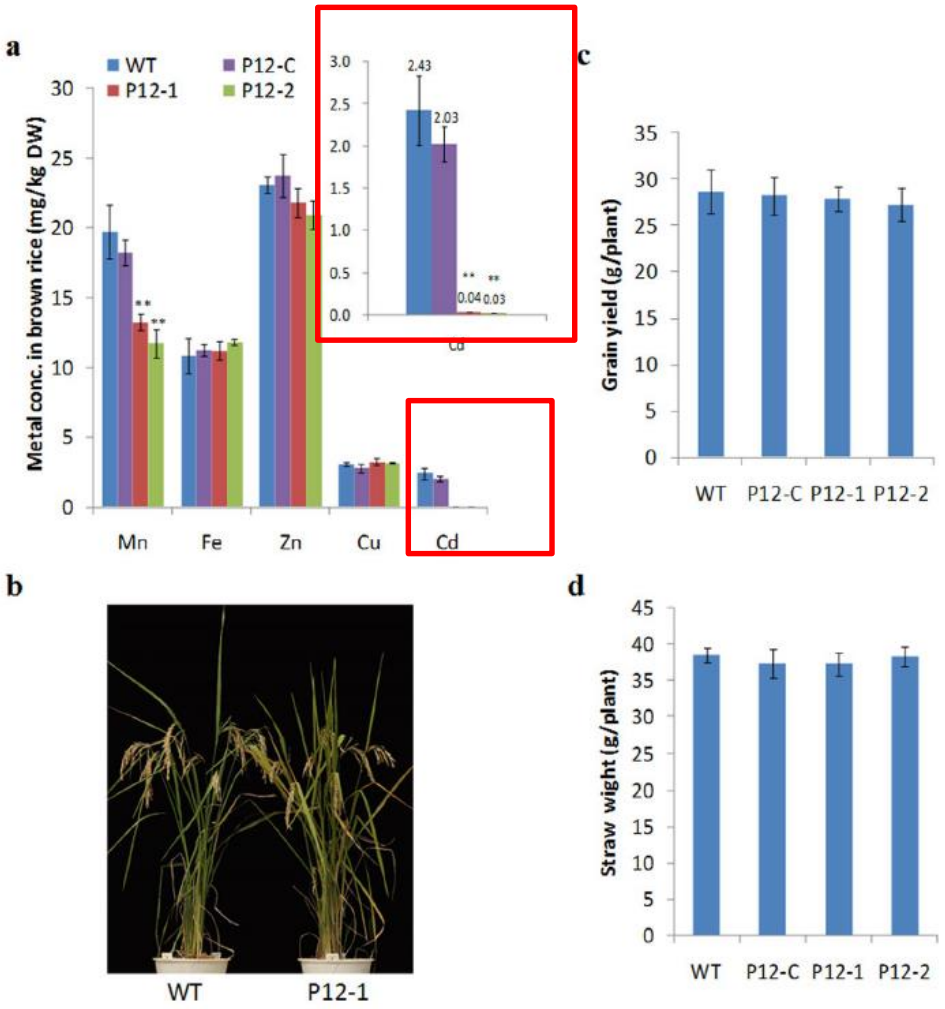


図 2　DNA マーカーを利用した効率的な低カドミウム品種の育成方法（概略図）
コシヒカリ環 1 号用の判別マーカーを使うことで、低カドミウム遺伝子の導入の有無が確認出来ます。遺伝背景を交配親（例えば品種 A）に戻すことによって見た目や味は元の A 品種のままで、カドミウム吸収の少ない品種が完成します。

https://www.naro.affrc.go.jp/archive/niaes/sinfo/result/result31/result31_42.html

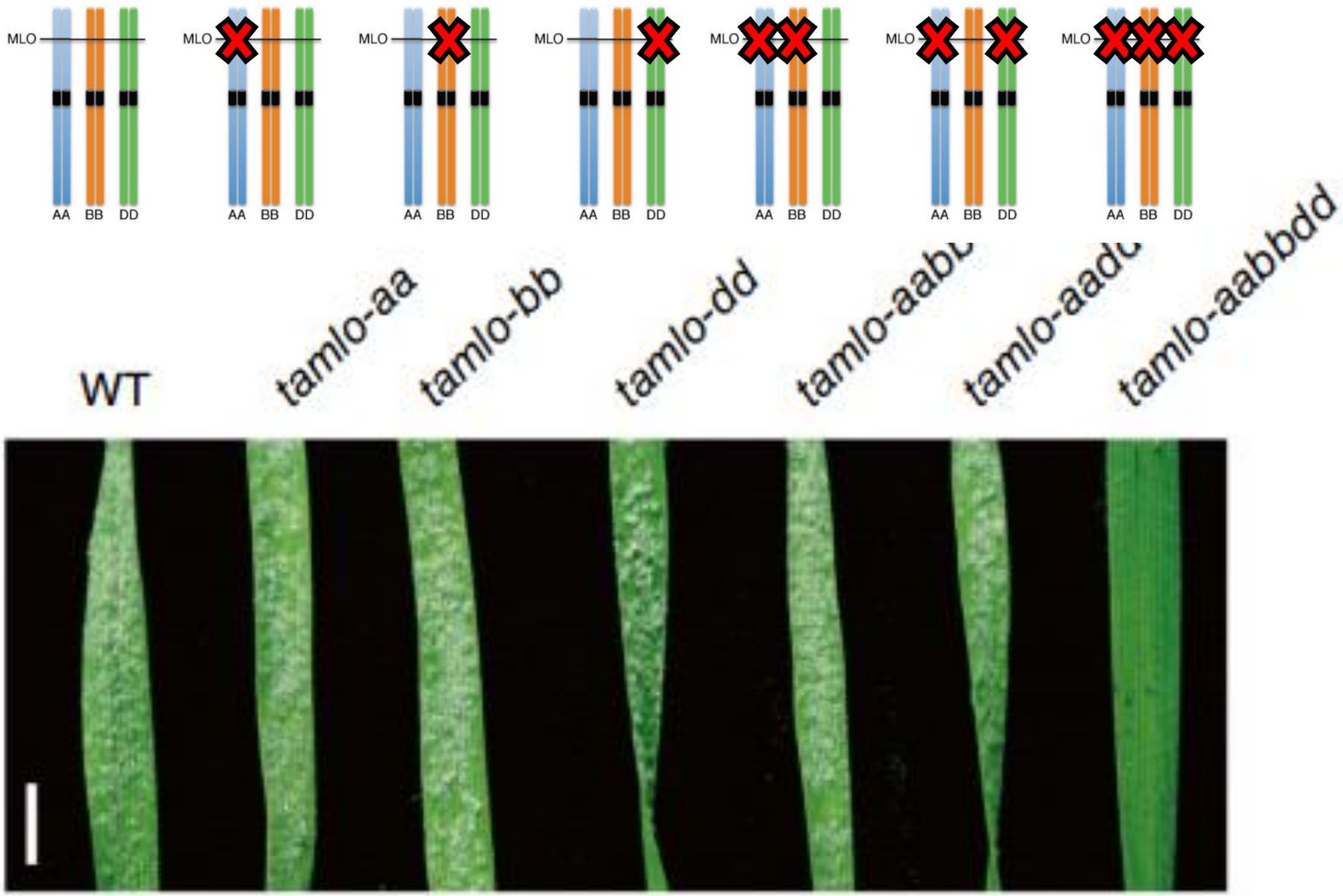
Generation of low cadmium rice by CRISPR/Cas9



利用基因編輯突變水稻*Nramp5*基因大幅抑制鎘的吸收

Tang et al. 2017

Loss of TaMLO function confers resistance of bread wheat to powdery mildew disease



Nature Biotechnol. (2014)32

Japan Launches World's First Genome-Edited Tomato

March 24, 2021

Photo Source: Sanatech Seed Co.

https://www.isaaa.org/kc/cropbiotechupdate/article/default.asp?ID=18668

Notification to MAFF and MHLW

Notification has completed on December 11, 2020

Environmental safety information (To MAFF)

For cultivation

Food safety information (To MHLW)

For food

Feed safety information (To MAFF)

For feed

Source: Dr. Ezura, Univ. Tsukuba

Labelling of the gene edited tomato

- **This tomato has been improved by gene editing technology**
- **Notifications to MAFF and MHLW have been completed**

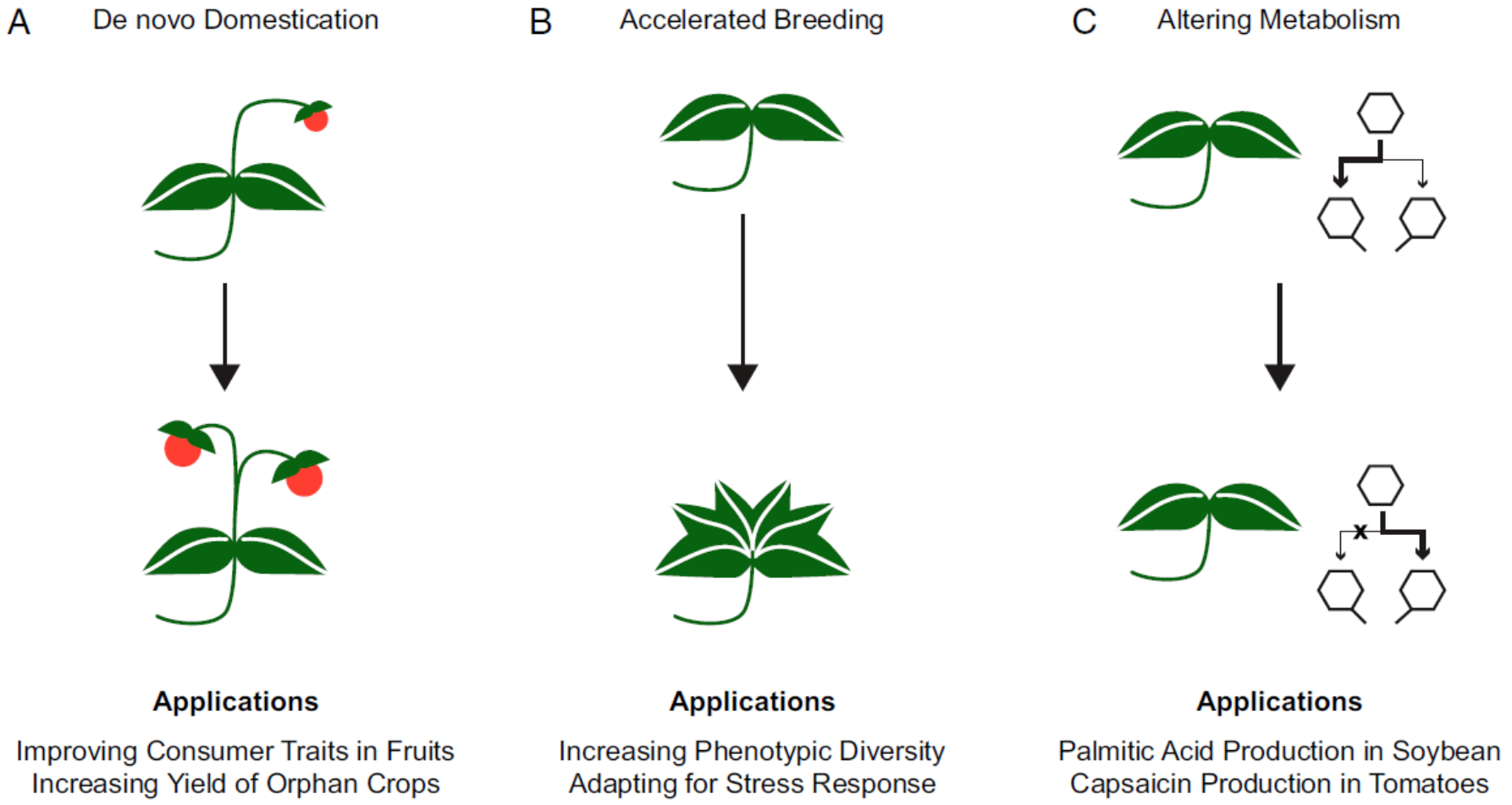
sanatechseed

Source: Dr. Ezura, Univ. Tsukuba

https://japan-forward.com/a-new-era-for-food-the-potential-benefits-of-gene-edited-foods/

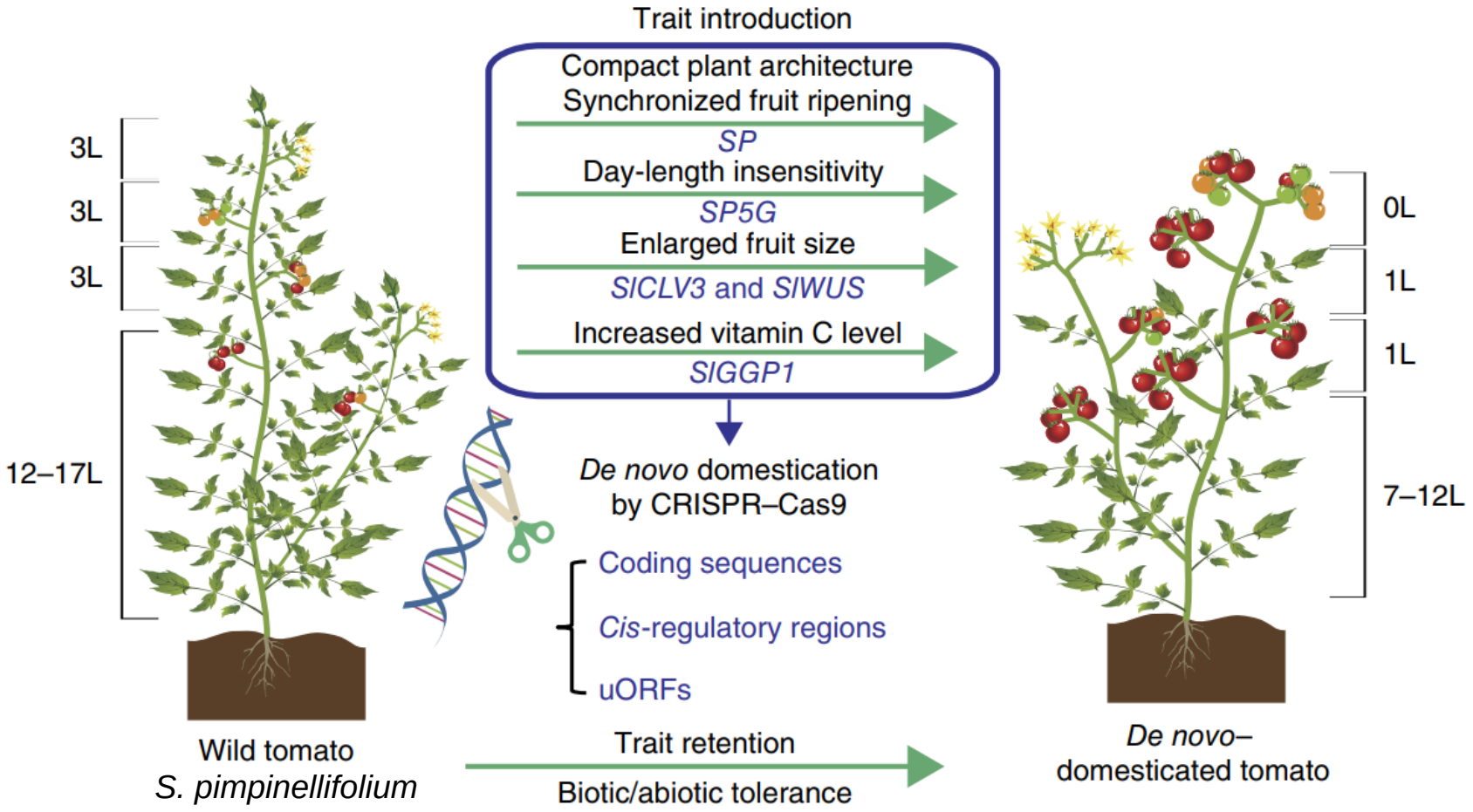
https://japan-forward.com/a-new-era-for-food-the-potential-benefits-of-gene-edited-foods/

Future applications for innovative plant design



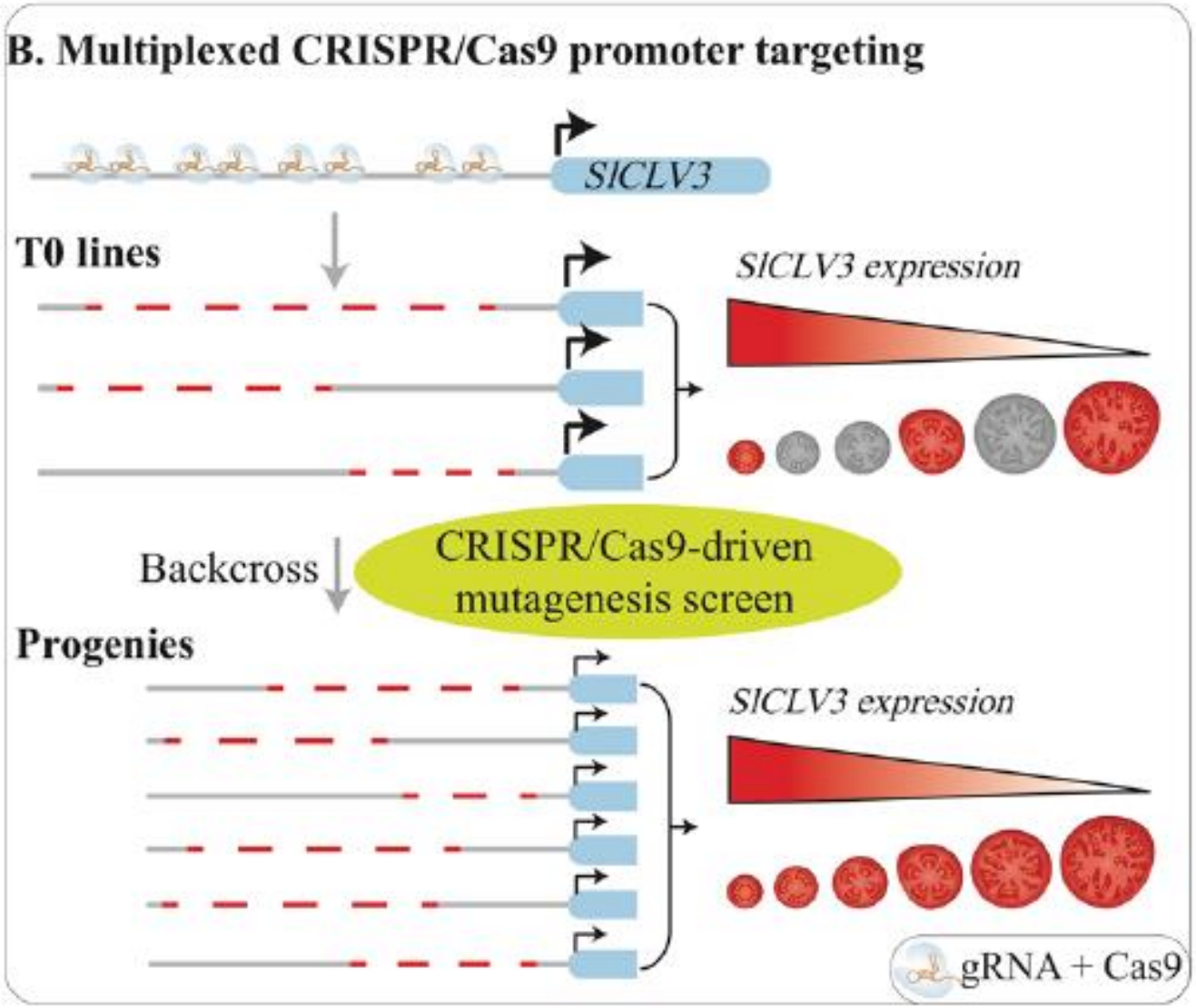
Nastia and Voytas (2021) PNAS

Domestication of wild tomato is accelerated by genome editing



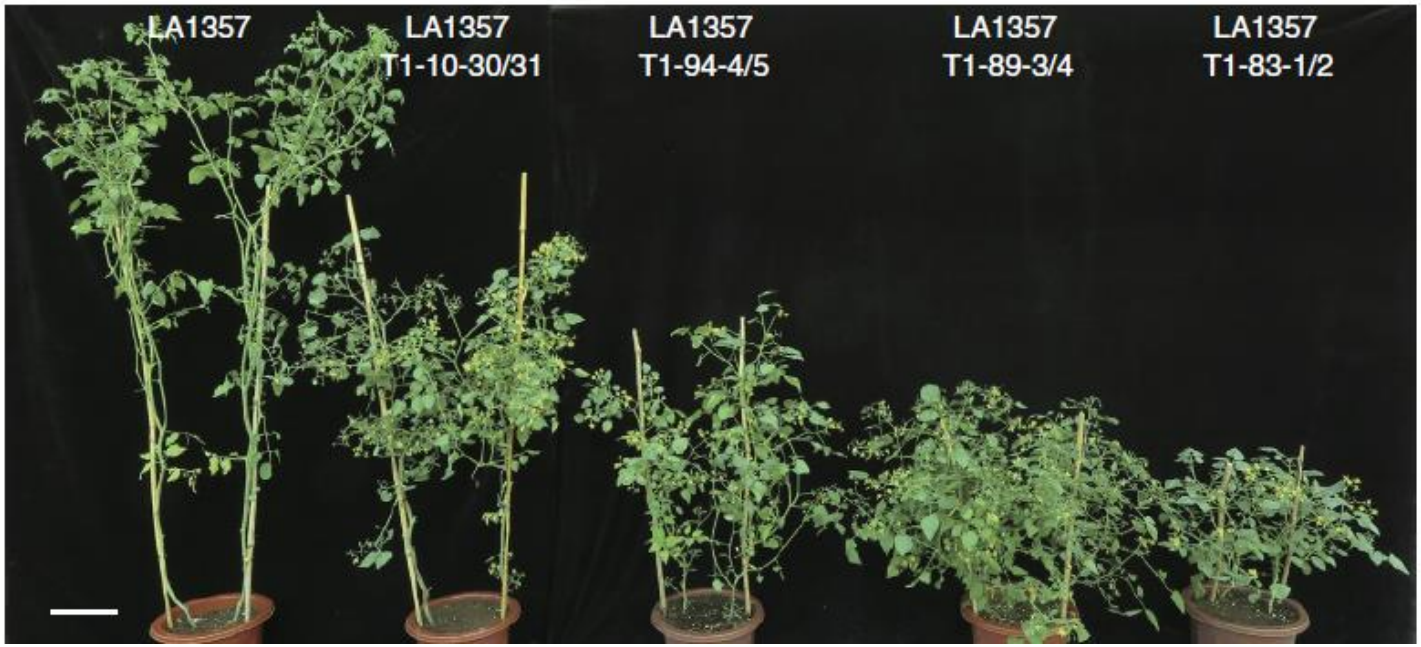
Li et al. (2018) Nat Biotechnol

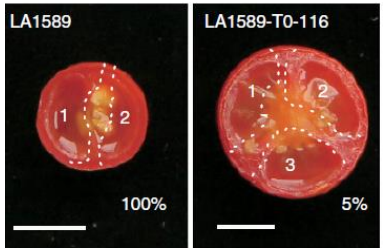
Recent progress in CRISPR/Cas-mediated cis-engineering in plants

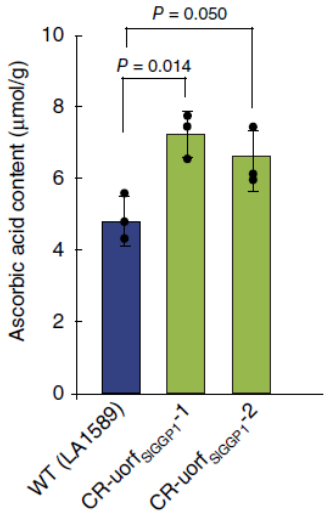


Horticulture Research (2020) 7:36

Domestication of wild tomato is accelerated by genome editing







Li et al. (2018) Nat Biotechnol

Take home messages

基因編輯可加速育種、補強傳統育種之不足

- 簡單、高效、精準、低成本
- 同時編輯多個基因、多倍體育種利器
- 克服遺傳累贅
- 微調基因表達，創造新數量性狀
- 無轉基因

https://newsletter.sinica.edu.tw/15761/

https://food.ltn.com.tw/article/8691

Thanks for your attention