



# The CRISPR/Cas9 rEvolution

Breedtech

Leonardo Caproni

[I.Caproni@santannapisa.it](mailto:I.Caproni@santannapisa.it)

 [@cap\\_leonardo](https://twitter.com/cap_leonardo)

# Question we will try to answer these two hours

1. What is genome editing?
2. What is CRISPR/Cas9 technology? From where does it come from?
3. How does CRISPR/Cas9 work?
4. Are there possible downsides of the system?
5. What are the potential applications in plant science?
6. How can we apply this technology to plants?
7. Application of CRISPR/Cas9 technology in real world...
8. CRISPR/Cas9 perspectives...

# GENOME EDITING

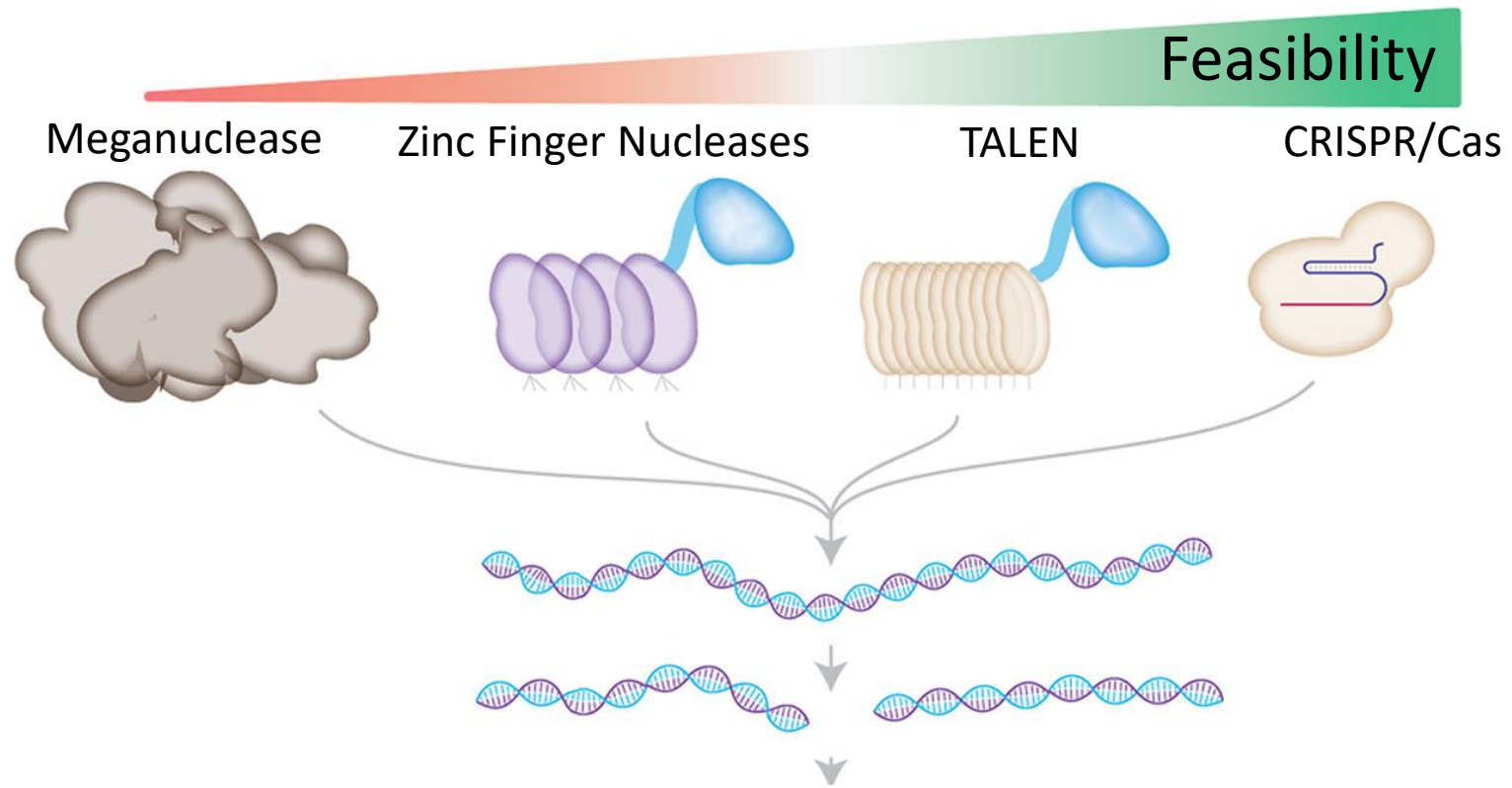
- Oligonucleotide Directed Mutagenesis (**ODM**)
- Homing Endonucleases: e.g. **Meganucleases**
- Zinc Finger Nucleases (**ZFN**)
- Transcription Activator Like Effector Nucleases (**TALEN**)
- **CRIPR-Cas**

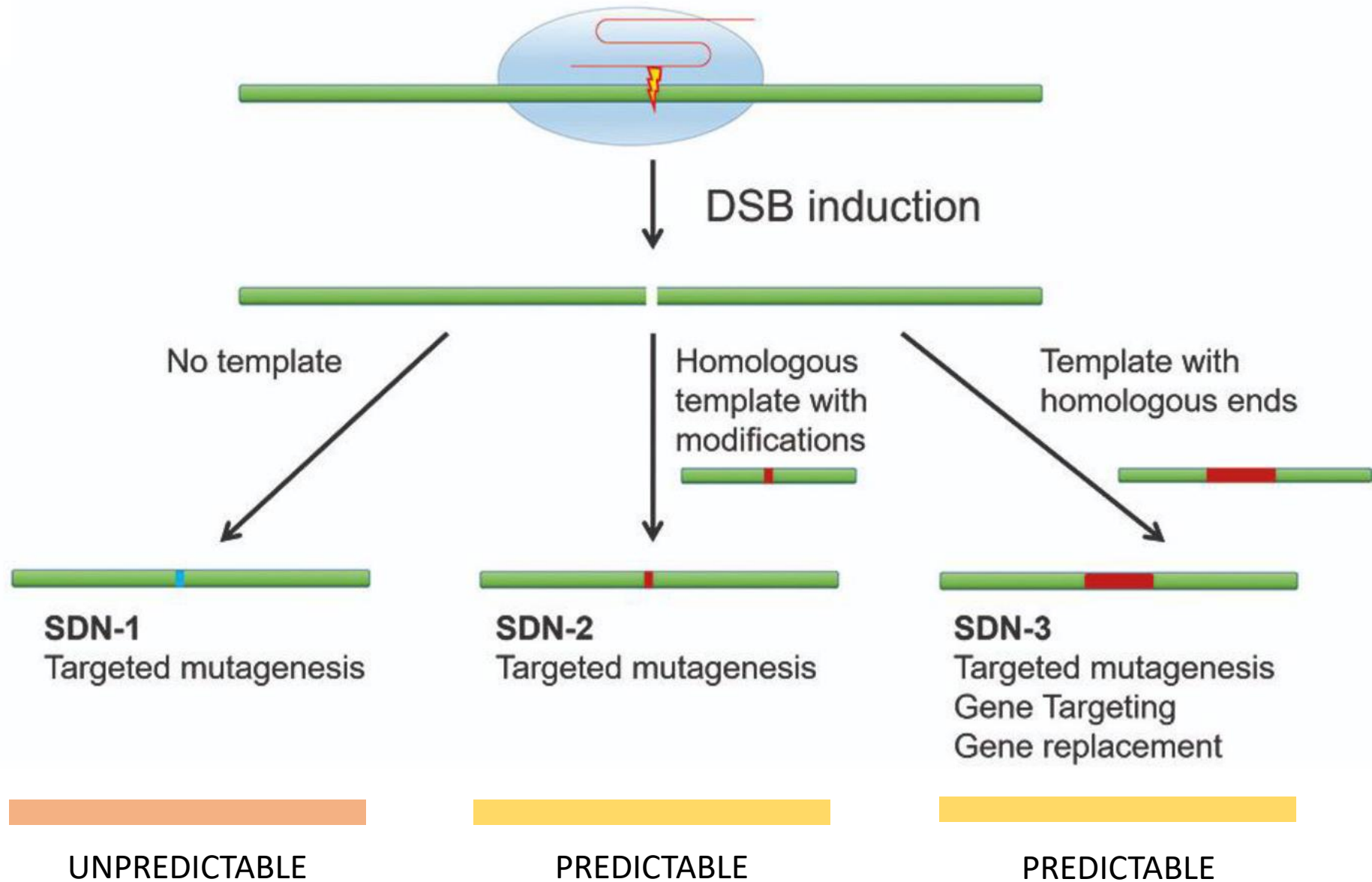
**What do they all have in common?**

Precise DNA targeting



GGTAGATGCGATGCTAGCCAGATGGTGCAGAATGCTGGGGCACGAAGTGTAGGCAGTGTGTAGA  
GGTAGATGCGATGCTAGCCAGATGGTGCAGA-TGCTGGGGCACGAAGTGTAGGCAGTGTGTAGA





What is CRISPR/Cas9 technology?  
From where does it come from?

# The Discovery of CRISPR loci: we need to go back 30 years ago

CTGCAGTCTG	CTCTCCATCC	TACAGTTCTT	CATATCCGCC	GCAAAGCACT	CGATGTGCAG	60
GGCTGCGAGT	ATTCCGAGCA	ACTAACTCAA	CGACCTACTC	GCTTCTCAAA	CTGGGTTACC	120
TATAGTAGCG	TTTGCAAGTC	ATTGCACACT	CGATCGACCG	CTATCGTGCG	ATTGGCTGTG	180
TCACCAGTTG	CAAACGCTAC	TATAGACAGT	GCCAGTCTAA	GAGTGTCATT	GGAGCCCAGA	240
TCTGAAAAAC	TGAAGAATAA	TCACAGACCA	AAGAAACAGA	CCCAAGCCAT	AGCAGATTAA	300
AATAATTCGA	GTAAGTCCG	TTCCAGATGT	TGATGGTAAG	TGAATATTCC	CAACCACTCC	360
TCTGCCAATG	GCTTCTTTT	CCTGGACGCC	TTCAGTAGTC	ACATTCTGTC	TTCTGCTTG	420
ACCACCACCG	AGAGCTACCA	ACACGACCCC	GATAATTGCG	GTCAGGACGA	GAATATAACC	480
CAGAGTGTGT	CGTTAGATAG	ATAGCACCGA	CAGTAATGAT	TCCCCGCGAG	ATCGTATAGA	540
TGAGGACTGT	TACTGCGACT	ACTCGCTTGT	CCATGTCATA	AGTAGAACGA	CAGTTAGTTT	600
AATTTTATC	ATTTTGAGGA	ATTGGTGTAT	CGCGCGTCCC	GGTGTCTCG	GAAGTCCGT	660
ACGTGGGTCT	TGACCTGAAT	TTCCGTCGAC	CCCCCGGGG	GTTGGGGGT	ATTG	714
GGGGTCGACG	GAAACT GTT	GAGTGGGAGT	AGTGTGTAGG	AGGCTGTATA	CCCTCGAATC	780
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	GAACAGGATG	GCGAACCGGT	GTCTGCACCA	843
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	CACGACAATC	AAGTCTGGTT	GCATGGCGAC	908
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	CTGTGCCTCC	AGCGGCCGTC	AGACAGTCGC	974
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	AAGAAGCCGC	TGCCGCTCCT	CGATGACGGG	1040
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	GACAAGACTC	GCGACGAAGC	CGAGTCGAAA	1106
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	CTCTTTATCC	CTCCTGCCCG	AATGTCTACG	1172
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	GAACCCACTG	GTGAAGAAAA	AGTTGTAGAG	1238
GTTACAGACG	AATCCCTAGTT	GGGTTGAAGC	ACGACAATCA	AGTCTGGTTA	CATGGCGACA	1305
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	TTCCACAACG	TGGGGGAGGG	CGAAATTAGC	1371
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	TCCCCTGGG	GATGTCGGGA	GTGCCGGGCG	1436
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	CCCCGGCCCGT	TGCCCCCAC	GGCAATCGTC	1500
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	CGTCTGTGTT	ATTCTGTGCG	TCTGCCGCGA	1564
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	ATTGCCTGTA	CCCGTCGTGT	AATCAACTCG	1629
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	GAGATGTGCG	ACCGCGGCGA	AATGAGCAGT	1694
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	GCGACATGGG	GACCGTCGAG	AACGCGCTCT	1761
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	CGAGGGTCCC	GGTGTGAGA	GGACCGGGAC	1828
GTTACAGTCTG	AACCCTAGTT	GGGTTGAAGC	TCGTAATCT	GGGAAGGCGT	CAGTCTCGGC	1897
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	CTCGCCATCG	CCGCGAACTC	GGTCTCTCTC	1963
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	AAGCCTTGAG	AGTGTCTGTT	GGTATGATGA	2028
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	AAGTAGACCG	CGTCTAGTTA	CGACAGCTGC	2092
GTTACAGACG	AACCCTAGTT	GGGTTGAAGC	ACGATGATCT	CGCCAGTCTG	CAGCGTTACA	2156
GTTACAAACG	AATCTTTTCT	CGTGAGGACT	TCCGAAACTA	ACCTCTTCCC	GGAAGTCTG	2216

Studying halophilic bacteria



Sequencing parts of their genomes  
Finds loci with particular architecture

identical sequences alternating  
with variable sequences

Short Regularly Spaced Repeats  
(SRSR)



# Short Regularly Spaced Repeats (SRSR)

Biological significance of a family of regularly spaced repeats in the genomes of Archaea, Bacteria and mitochondria

**Table 1.** Main features of the SRSRs.

Organism	SRSR size (bp)	Spacing (bp)	Number of clusters	SRSR units per cluster	Reference
<b>Archaea</b>					
<i>H. volcanii</i>	30	ND	$\geq 2$	ND	Mojica <i>et al.</i> (1995) <i>Mol Microbiol</i> <b>9</b> : 13–21
<i>H. mediterranei</i>	30	33–39	3	21/ ND / ND	Mojica <i>et al.</i> (1995) <i>Mol Microbiol</i> <b>9</b> : 13–21
<i>M. jannaschii</i>	28–30	31–51	$7^A + 6^B + 1^C$	4–25	Bult <i>et al.</i> (1996) <i>Science</i> <b>273</b> : 1058–1073 and this work
<i>M. thermoautotrophicum</i>	30	34–38	2	124/47	This work
<i>A. fulgidus</i>	$37^A/30^B$	$\approx 37$	$1^A + 2^B$	$42^A/48^B/60^B$	This work
<i>S. solfataricus</i>	25	$\approx 40$	$\geq 2$	94/102	Sensen <i>et al.</i> (1998) <i>Extremophiles</i> <b>2</b> : 305–312
<i>P. abyssii</i>	$29^A/30^B$	26–43	$1^A + 2^B$	$7^A/22^B/27^B$	This work
<i>P. horikoshii</i>	29	34–58	3	18/26/66	Kawarabayasi <i>et al.</i> (1998) <i>DNA Res</i> <b>5</b> : 55–76
<i>A. permix</i>	$24^A/23^B$	37–52	$2^A + 1^B$	$19^A/27^A/42^B$	Kawarabayasi <i>et al.</i> (1999) <i>DNA Res</i> <b>6</b> : 83–101
<b>Bacteria</b>					
<i>T. maritima</i>	30	39–40	8	2–40	Nelson <i>et al.</i> (1999) <i>Nature</i> <b>399</b> : 323–329
<i>A. aeolicus</i>	29	36–38	1	6	This work
<i>E. coli</i>	29	32–33	3	2/7/13	Nakata <i>et al.</i> (1989) <i>J Bacteriol</i> <b>171</b> : 3553–3556 and this work
<i>S. typhi</i>	29	32	$\geq 1$	6	This work
<i>C. jejuni</i>	36	30	1	5	This work
<i>Y. pestis</i>	28	32–33	2	6/9	This work
<i>C. difficile</i>	29	36–38	$4^A + 2^B$	5–17	This work
<i>M. tuberculosis</i>	36	38–40	1	Variable	Hermans <i>et al.</i> (1991) <i>Infect Immun</i> <b>59</b> : 2695–705
<i>Calothrix sp.</i>	37	35–41	$> 1$	5	Masepohl <i>et al.</i> (1996) <i>Biochim Biophys Acta</i> <b>1307</b> : 20–36
<i>Anabaena sp.</i>	37	32–43	$> 1$	17	Masepohl <i>et al.</i> (1996) <i>Biochim Biophys Acta</i> <b>1307</b> : 20–36
<b>Mitochondria</b>					
<i>V. faba</i>	40	20–35	1	6	Flamand <i>et al.</i> (1992) <i>Plant Mol Biol</i> <b>19</b> : 913–923

A,B, Types of SRSRs distinct (more than 3 bp differences) within the same microorganism. ND, Not determined.



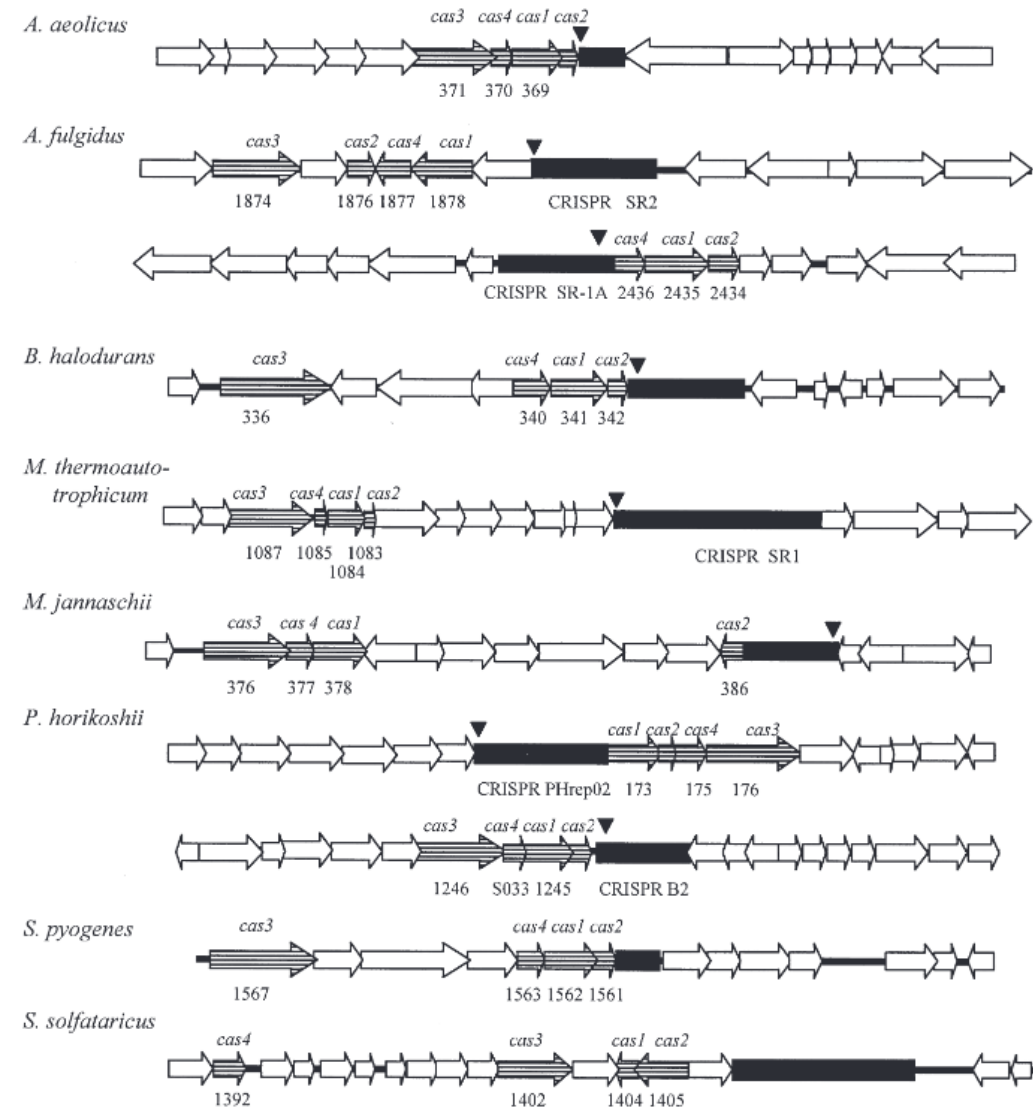
# Identification of genes that are associated with DNA repeats in prokaryotes

## ~~Short Regularly Spaced Repeats (SRSR)~~



from 21 to 37 bp, interspaced by similarly sized non-repetitive sequences. To appreciate their characteristic structure, we will refer to this family as the clustered regularly interspaced short palindromic repeats (CRISPR). In most species with two or more CRISPR loci, these loci were flanked on one side by

Jansen et al. 2002, *Mol Microbiol*



## Q: What are CRISPR loci? What is their function?...

**Table 5.** Features of the sequences most similar to CRISPR spacers from *S. pyogenes*

Spacer	Gene	Prophage <sup>a</sup>	Activity	Alignment <sup>b</sup>
4-1	<i>spyM3_1239</i>	315.4	Unknown	gctgtgacattgcgggatgtaatcaaagtaaaaa       gctgtgacattgcggaatgtaatcaaagcaaaaa
4-2	<i>spyM3_0941</i>	315.2	Capside protein	taaagcaaacctagcagaagcagaaaatgac       taaagcgaacctagtagaagcagaaaacgac
4-3	<i>spyM18_0741</i>	$\Phi_{\text{speC}}$	Methyltransferase	ctgatgtaattggtgattttcgtgatatgcttt       ctgatgtaattggtgattttcgtgatatgcctt
7-1	<i>spyM3_1215</i>	315.4	Endopeptidase	gcgctggttgattttcttcttgctgtttt       gcgctggttgattttcttcttgctgtttt
7-2	<i>speM</i>	$\Phi_{\text{speLM}}$	Exotoxin	tatatgaacataactcaatttgtaaaaa       tatatgaacataactcaatttgtaaaaa
7-3	<i>spyM18_0742</i>	$\Phi_{\text{speC}}$	Methyltransferase	aggaatatccgcaataattaattgcgctct       aggaatatccgcaataattaattgcgctct
7-4	<i>hylP</i>	315.3	Hyaluronidase	agtgcgaggaaaaattaggtgcgcttggc       agtgcgaggaaaaattaggtgcgcttggc
7-5	<i>spyM3_1347</i>	315.5	Unknown	aaatttgtttagcaggtaaaccgtgcttt       aaatttgtttagcaggtaaaccgtgcttt

<sup>a</sup>Prophages 315.2-5 are integrated into *S. pyogenes* MGAS315.  $\Phi_{\text{speC}}$  and  $\Phi_{\text{speLM}}$  are integrated into *S. pyogenes* MGAS8232.

<sup>b</sup>CRISPR-spacer sequence (top line) and best-match homologous sequence (bottom line).

When the **viral sequence** is present in the bacterial genome, **resistance can be observed**



CRISPR is postulated for the first time as an:  
**Acquired Resistance Against Viruses**

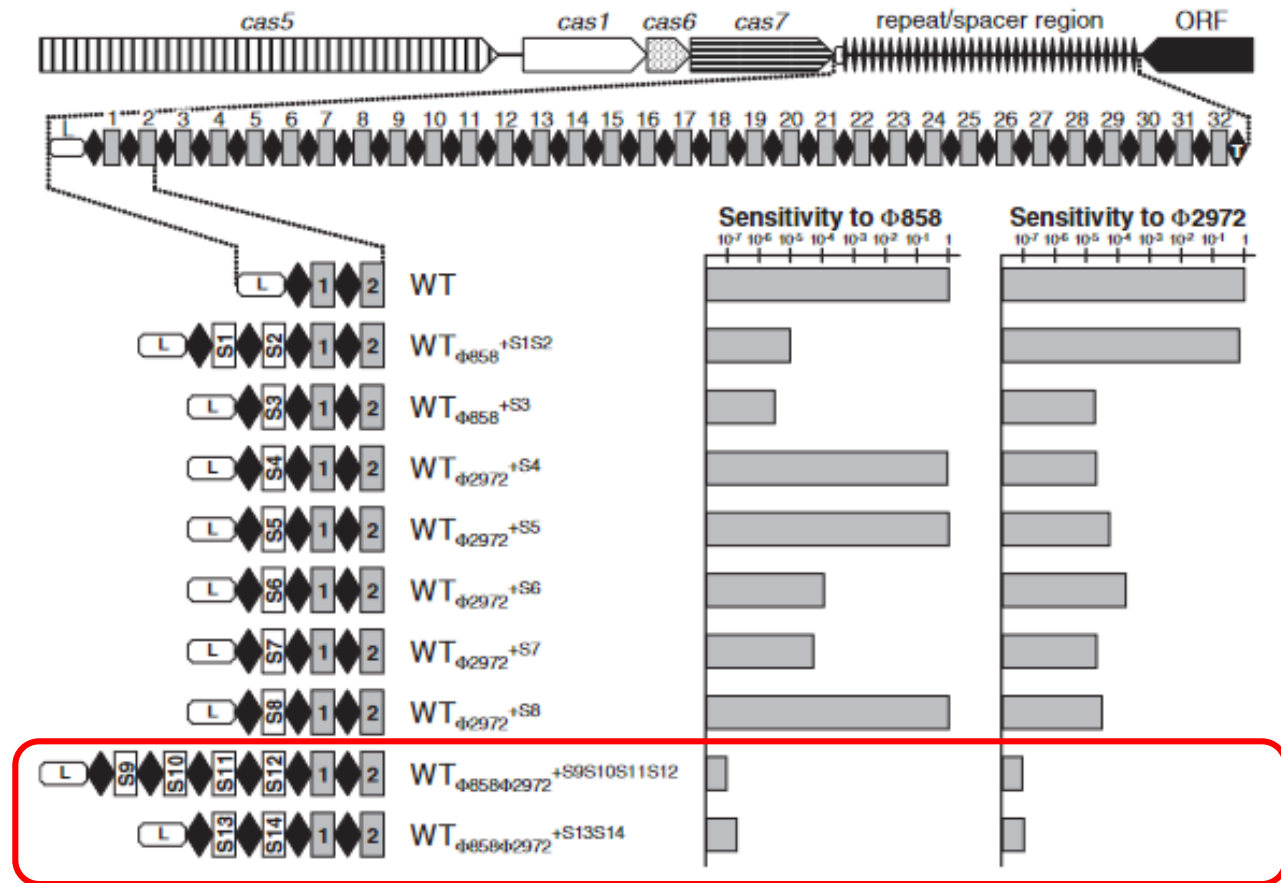
CRISPR loci have extrachromosomal origin  
and are components of an adaptive immune  
system



When plasmids containing CRISPR loci are cloned  
into a strain *S. thermophilus*, resistance can be  
induced

For the first time  
**bacterial immunity is engineered**

## Breakthrough



Barrangou et al. 2007, *Science*

# Engineering the CRISPR locus of *S. thermophilus* fundamental functions of the adaptive immune system



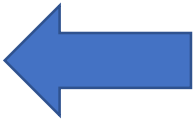
When some Cas elements are not cloned, the system stops working



No **Cas9** (here called cas5)

=

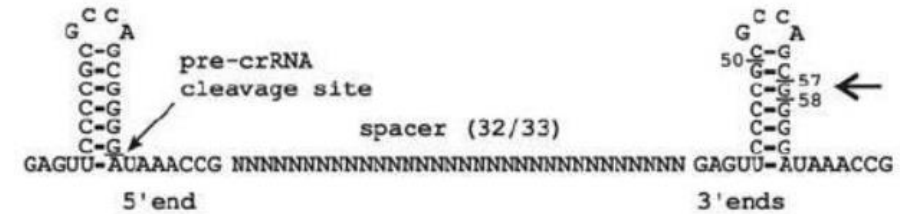
high sensitivity to bacteriophages



Barrangou et al. 2007, *Science*

## 1- The CRISPR RNA (crRNA) is processed by Cas proteins into shorter fragments

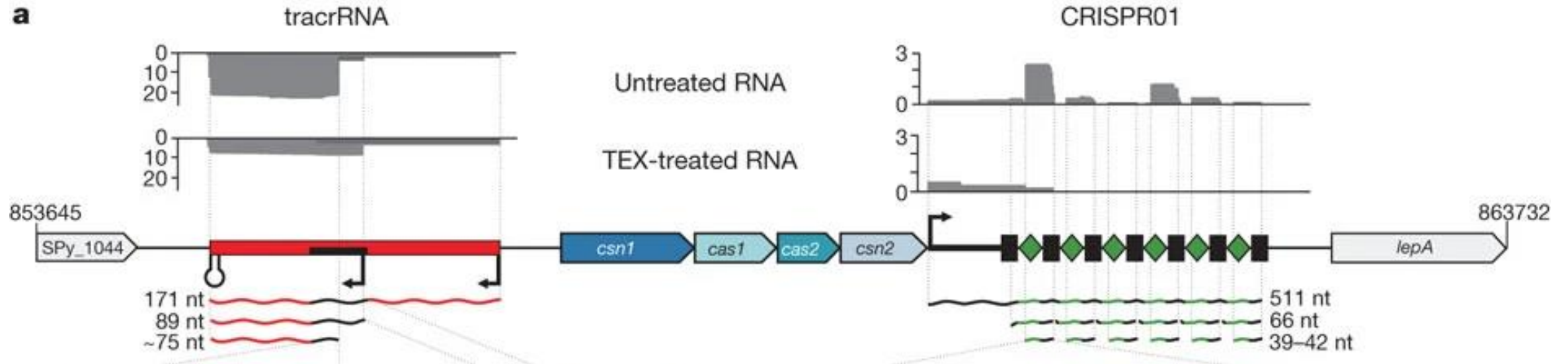
CRISPR loci are transcribed and then processed into 50 b fragments where the spacer sequence is specific, and the flanking sequences are conserved (by a complex termed *Cascade*)



RNA66	AUAAACCG	CTTTCGCAGACGCGCGCGCATACGCTCACGCA	GAGUUCCCCG	sp1
RNA31	AUAAACCG	CAGCCGAAGCCAAAGGTGATGCCGAACACGCT	GAGUUCCCCG	sp2
RNA8	AUAAACCG	GGCTCCCTGTCTGGTTGTAATTGATAATGTTGA	GAGUUCCCCGCGCCAGCGG	sp3
RNA16	AUAAACCG	TTTGGATCGGGTCTGGAAATTCTGAGCGGTCGC	GAGUUCCCCGCGCCAGCG	sp4
RNA35	AUAAACCG	CGAATCGCGCATACCCTGCGCGTCGCCGCTGC	GAGUUCCCCGCGC	sp5
RNA1	AUAAACCG	TCAGCTTTATAAATCCGGAGATACGGAAACTA	GAGUUCCCCG	sp6
RNA52	AUAAACCG	GACTCACCCCGAAAGAGATTGCCAGCCAGCTT	GAGUUCCC	sp7
RNA62	AUAAACCG	CTGCTGGAGCTGGCTGCAAGGCAAGCCGCCC		sp8
	5'handle		3'handle	

Brouns et al. 2008, *Science*

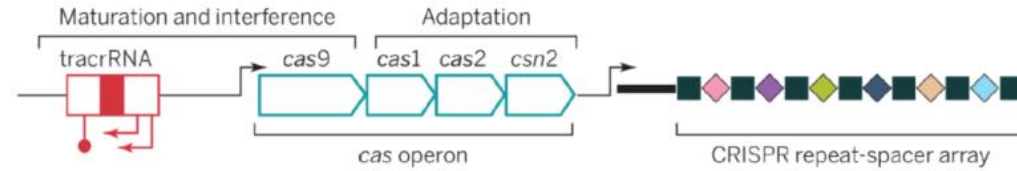
# CRISPR loci produce crRNAs and tracrRNAs, required for acquired immunity



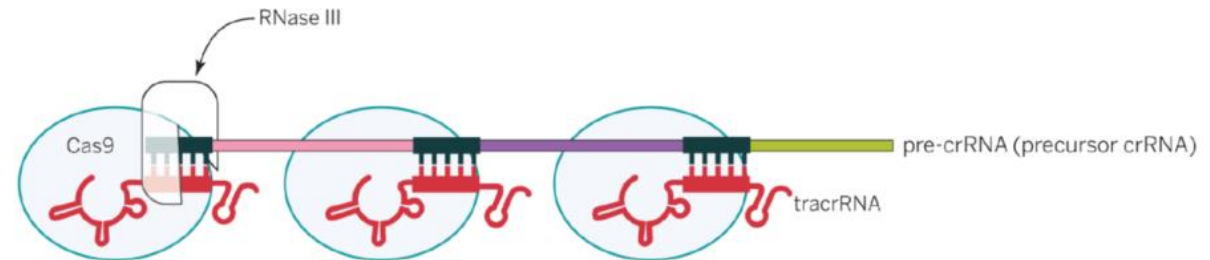


# Summary of the CRIPR/Cas9 system

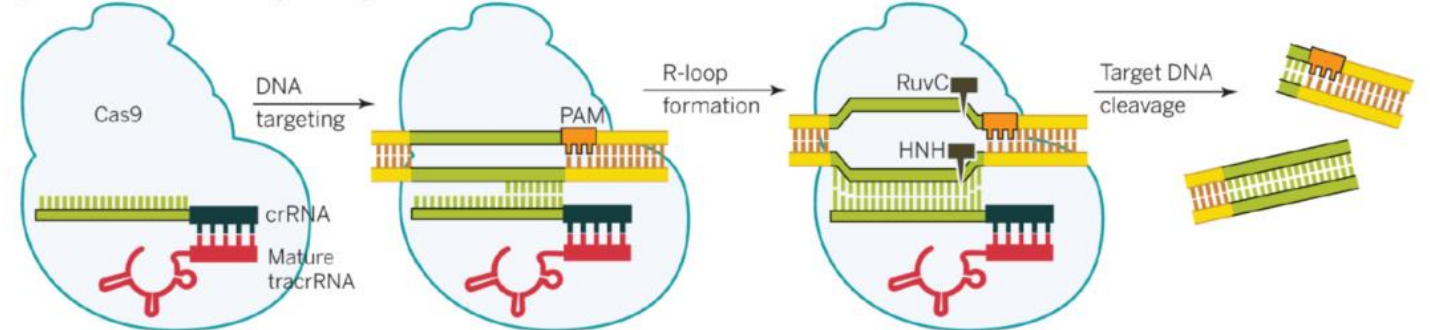
## A Genomic CRISPR locus



## B tracrRNA:crRNA co-maturation and Cas9 co-complex formation

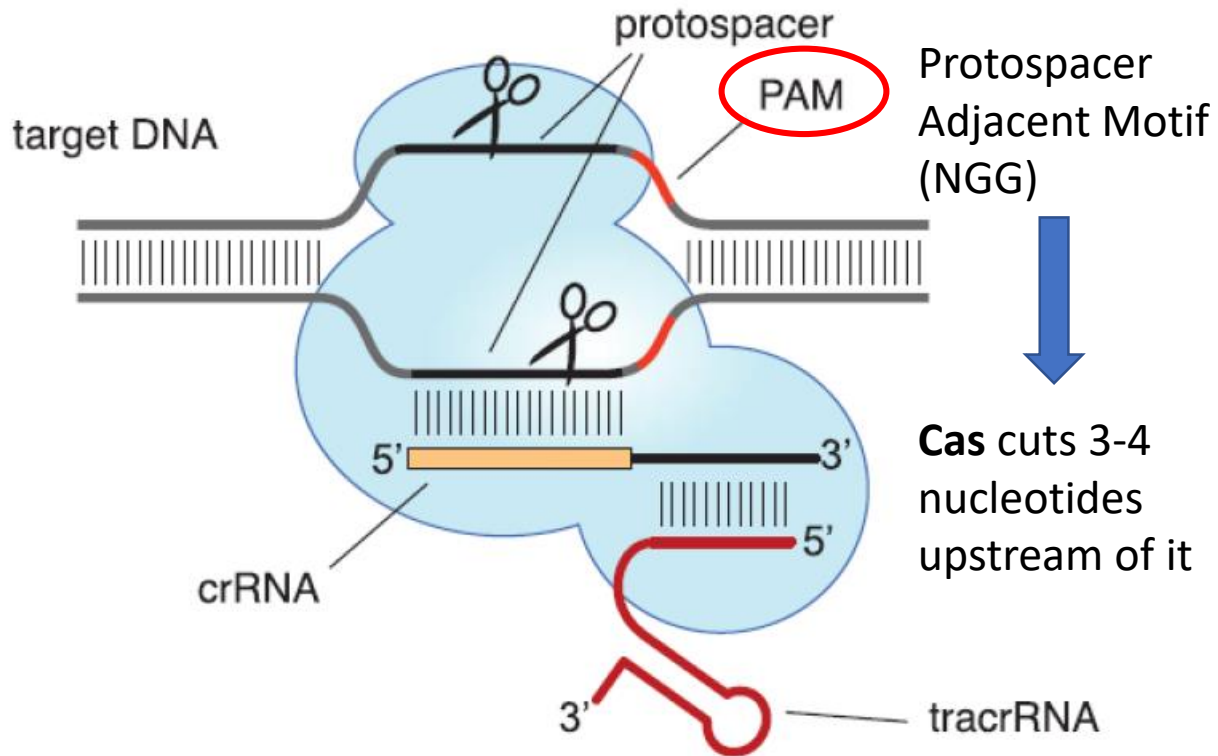


## C RNA-guided cleavage of target DNA

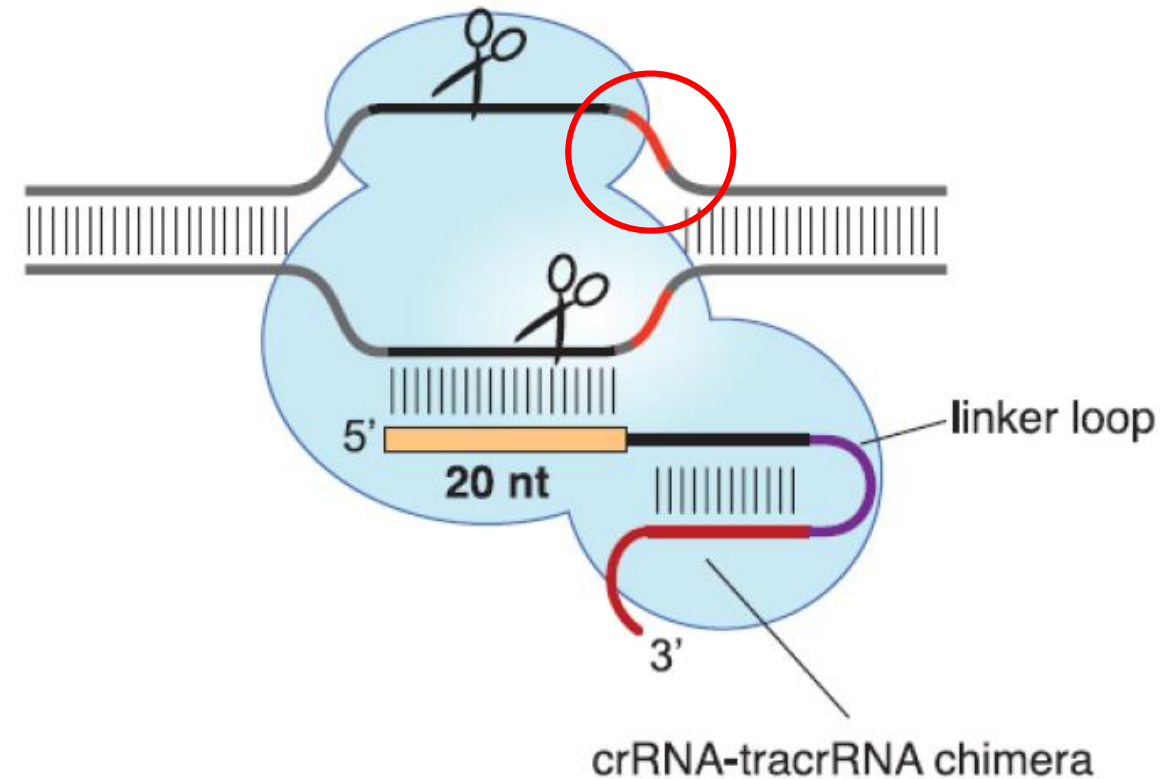




## Cas9 programmed by crRNA:tracrRNA duplex



## Cas9 programmed by single chimeric RNA



.... the CRISPR/cas9 system is programmable!

## RESEARCH ARTICLE

# A Programmable Dual-RNA–Guided DNA Endonuclease in Adaptive Bacterial Immunity

Martin Jinek,<sup>1,2\*</sup> Krzysztof Chylinski,<sup>3,4\*</sup> Ines Fonfara,<sup>4</sup> Michael Hauer,<sup>2†</sup>  
Jennifer A. Doudna,<sup>1,2,5,6‡</sup> Emmanuelle Charpentier<sup>4‡</sup>

Clustered regularly interspaced short palindromic repeats (CRISPR)/CRISPR-associated (Cas) systems provide bacteria and archaea with adaptive immunity against viruses and plasmids by using CRISPR RNAs (crRNAs) to guide the silencing of invading nucleic acids. We show here that in a subset of these systems, the mature crRNA that is base-paired to trans-activating crRNA (tracrRNA) forms a two-RNA structure that directs the CRISPR-associated protein Cas9 to introduce double-stranded (ds) breaks in target DNA. At sites complementary to the crRNA-guide sequence, the Cas9 HNH nuclease domain cleaves the complementary strand, whereas the Cas9 RuvC-like domain cleaves the noncomplementary strand. The dual-tracrRNA:crRNA, when engineered as a single RNA chimera, also directs sequence-specific Cas9 dsDNA cleavage. Our study reveals a family of endonucleases that use dual-RNAs for site-specific DNA cleavage and highlights the potential to exploit the system for RNA-programmable genome editing.

n. of citations may 7<sup>th</sup> 2022 = 13,658

## THE NOBEL PRIZE IN CHEMISTRY 2020

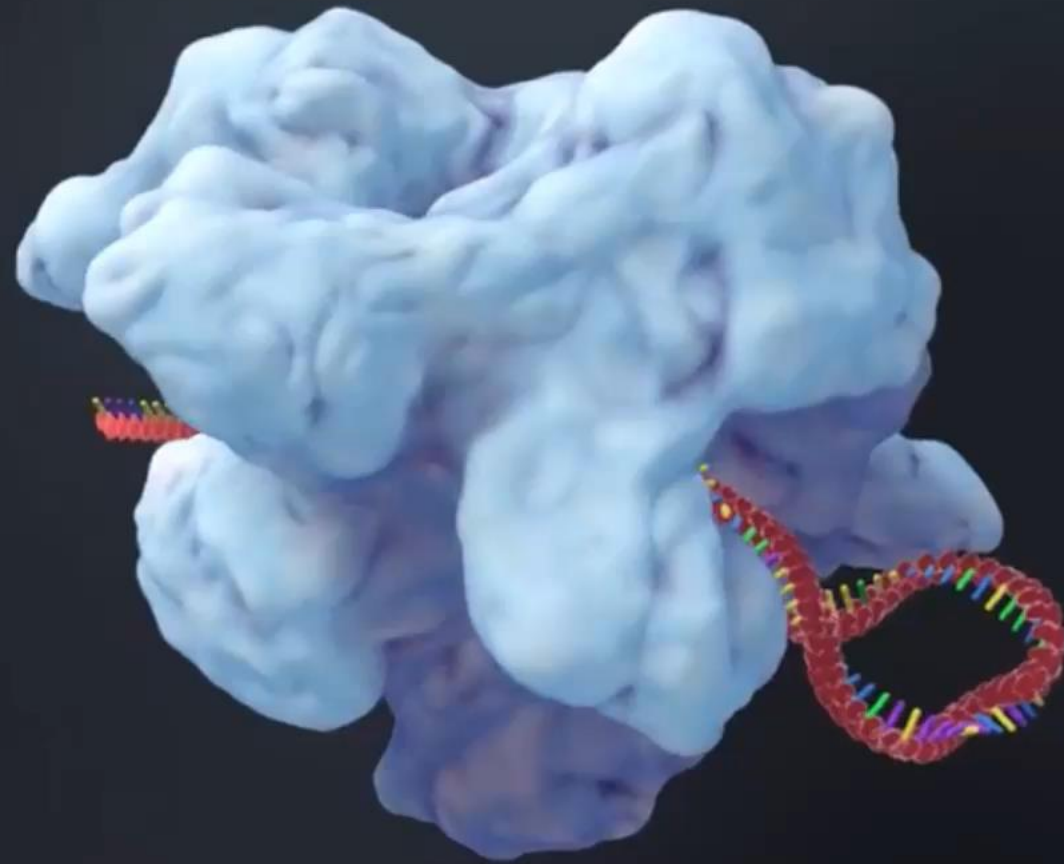


Emmanuelle  
Charpentier

Jennifer A.  
Doudna

"for the development of a method  
for genome editing"

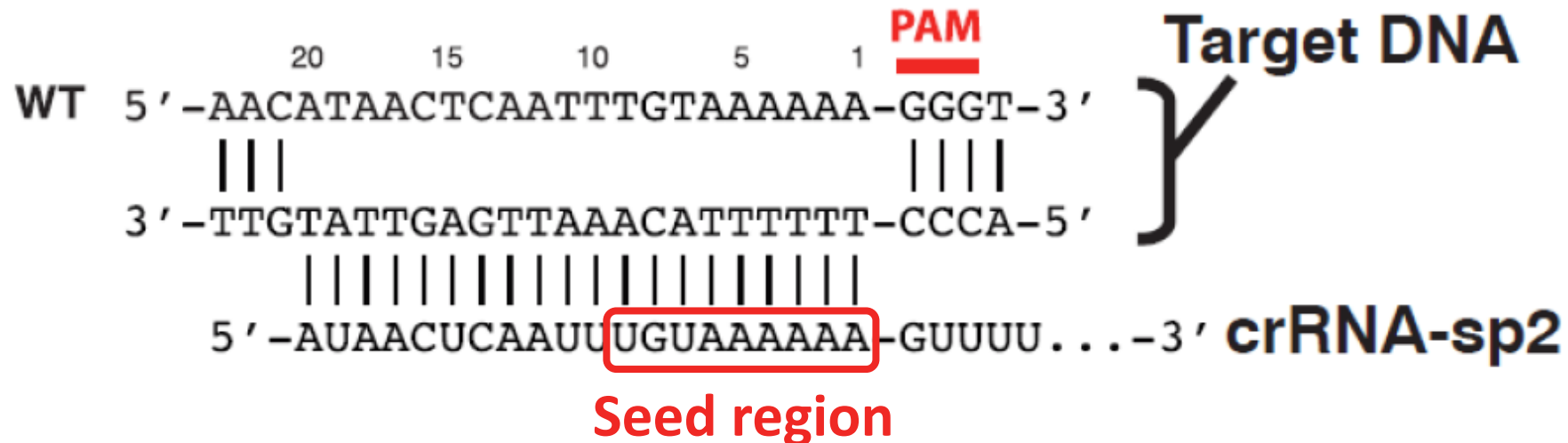
THE ROYAL SWEDISH ACADEMY OF SCIENCES



# Precision of the system: off-targets

- Off-target:

“unintended cleavage and mutation at untargeted genomic sites showing a similar but not an identical sequence to the target site”





The *seed* region of the gRNA is fundamental for target recognition and Cas9 cleavage



### mismatched targets

22	5' -A <b>G</b> CATAACTCAATTTGTAAAAAA-3'	Targets are recognized
10	5' -AACATAACTCAAT <b>C</b> TGTAAAAAA-3'	
7	5' -AACATAACTCAATTTG <b>A</b> AAAAAA-3'	
6	5' -AACATAACTCAATTTGT <b>T</b> AAAAA-3'	Targets are NOT recognized
5	5' -AACATAACTCAATTTGTAT <b>T</b> AAAA-3'	
4	5' -AACATAACTCAATTTGTAA <b>T</b> AAA-3'	
3	5' -AACATAACTCAATTTGTAAAT <b>T</b> AA-3'	

**Seed region =**  
8-10 bases at the 3' end of  
the gRNA targeting region

# The best strategy to avoid off-targets is good design of sgRNAs

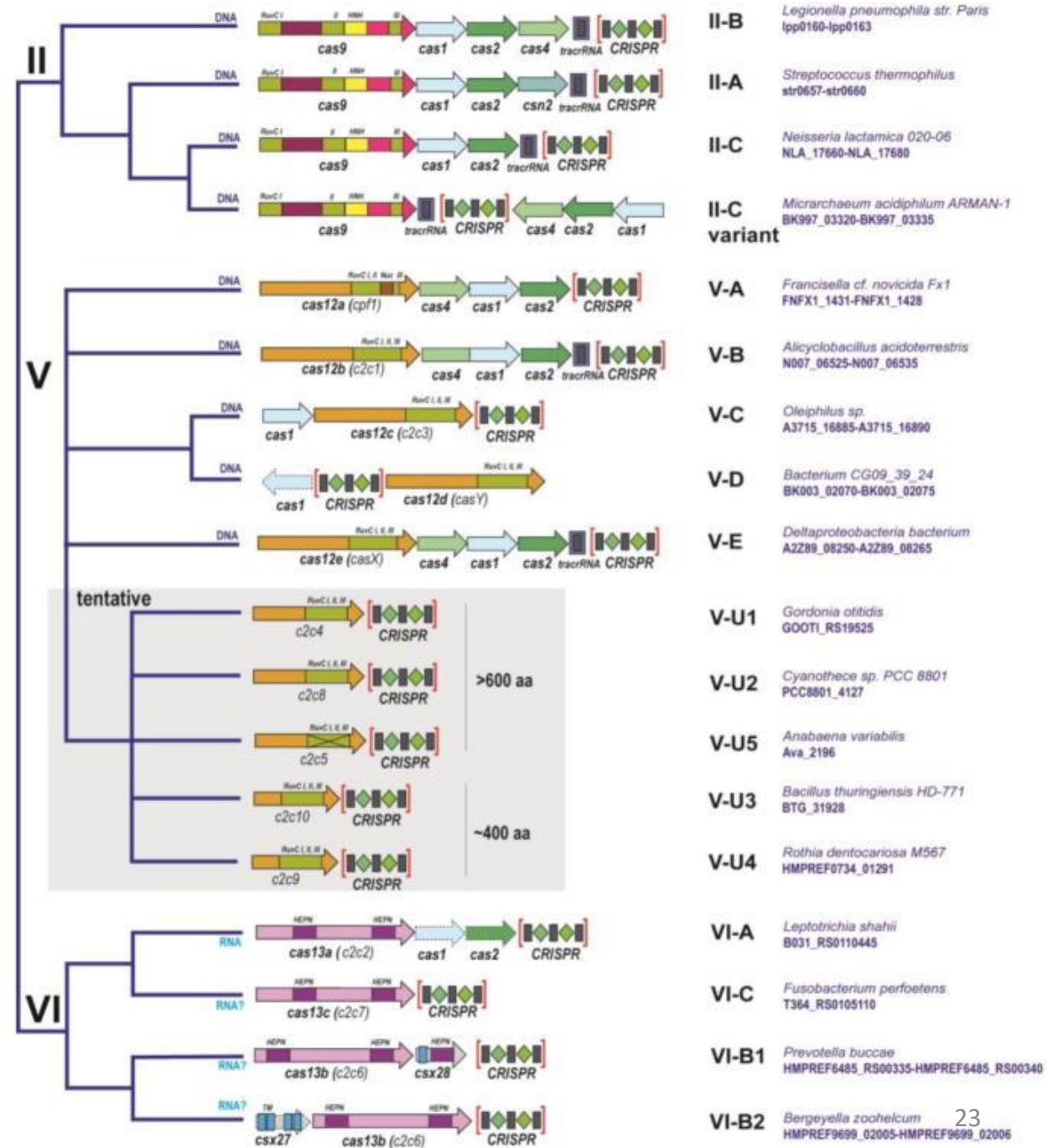
Online tool	Website	References
Cas-Offinder	<a href="http://www.rgenome.net/cas-offinder/">http://www.rgenome.net/cas-offinder/</a>	Bae et al. (2014)
Chop-Chop	<a href="http://chopchop.cbu.uib.no/index.php">http://chopchop.cbu.uib.no/index.php</a>	Labun et al. (2016)
CRISPOR	<a href="http://crispor.tefor.net/">http://crispor.tefor.net/</a>	Haeussler et al. (2016)
E-CRISP	<a href="http://www.e-crisp.org/E-CRISP/">http://www.e-crisp.org/E-CRISP/</a>	Heigwer et al. (2014)
CRISPR-P 2.0	<a href="http://crispr.hzau.edu.cn/CRISPR2/">http://crispr.hzau.edu.cn/CRISPR2/</a>	Liu et al. (2017)
CCTop	<a href="https://crispr.cos.uni-heidelberg.de/">https://crispr.cos.uni-heidelberg.de/</a>	Stemmer et al. (2015)
Benchling	<a href="https://benchling.com/crispr">https://benchling.com/crispr</a>	<a href="http://www.benchling.com">http://www.benchling.com</a>
CRISPR-GE	<a href="http://skl.scau.edu.cn/">http://skl.scau.edu.cn/</a>	Xie et al. (2017)

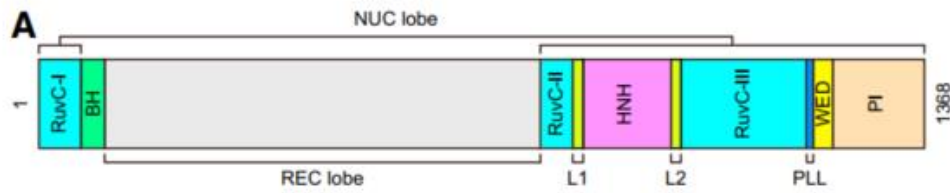
# Cas9 is the most versatile and easy-to-use programmable nuclease

	Zinc Finger Nuclease	TALEN	Cas9	Meganuclease
Recognition site	Typically 9-18 bp per ZFN monomer	Typically 14-20 bp per TALEN monomer	20bp guide RNA sequence+ 3bp PAM	14-40 bp
Specificity	Small number of positional mismatches tolerated	Small number of positional mismatches tolerated	Positional and multiple consecutive mismatches tolerated (not in seed region though)	Small number of positional mismatches tolerated
Targeting constraints	Difficult to target non-G rich sequences	5' targeted base must be a T for each TALEN monomer	Targeted sequence must precede a PAM	
Dimerization required	Yes	Yes	No	No
Ease of engineering	difficult	Moderate (complex cloning methods)	easy	difficult
Ease of multiplexing	Low	Low	High	Low

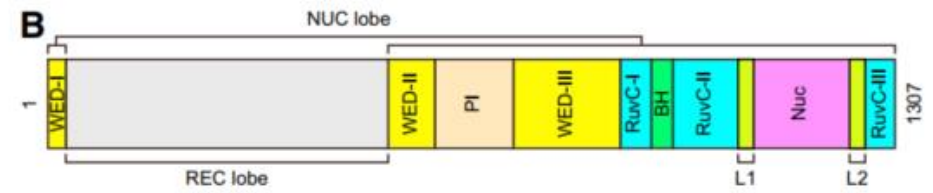
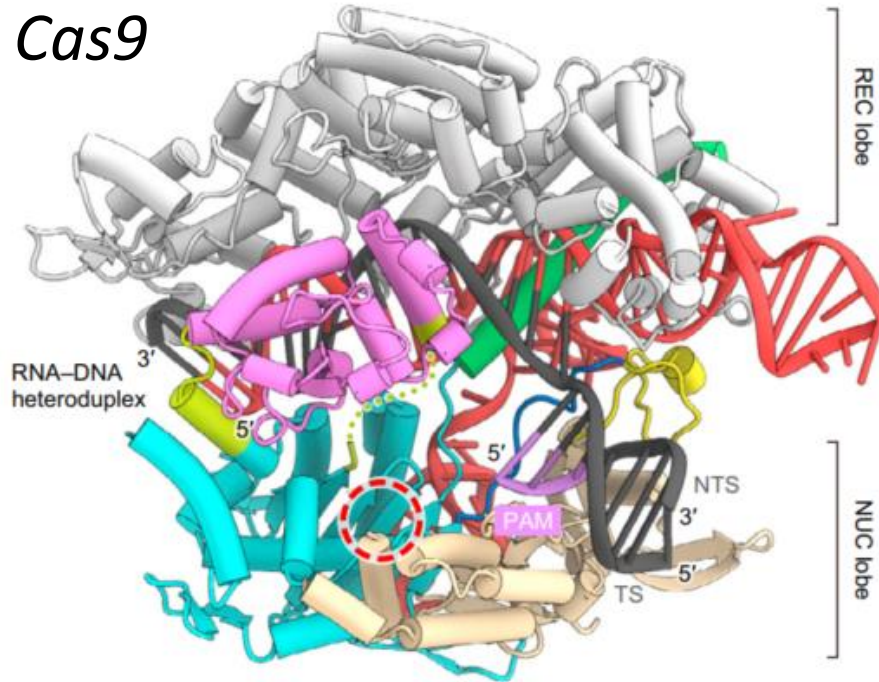


Cas9 is not alone



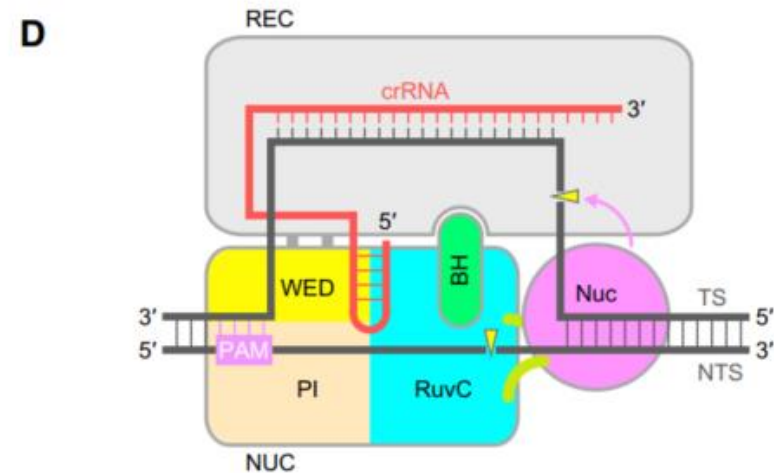
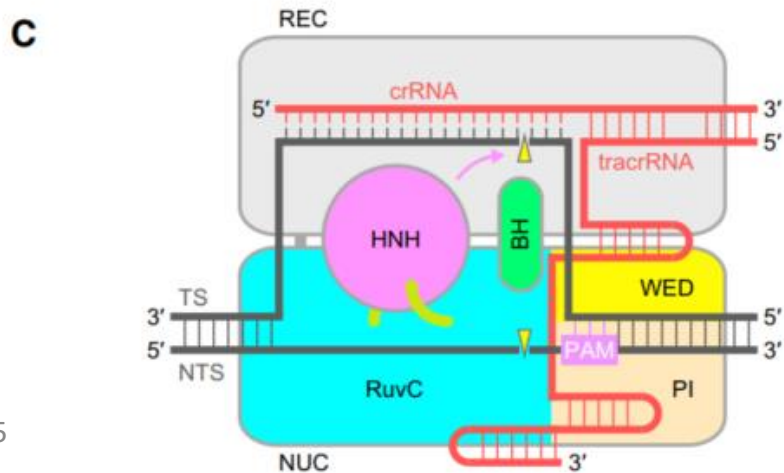
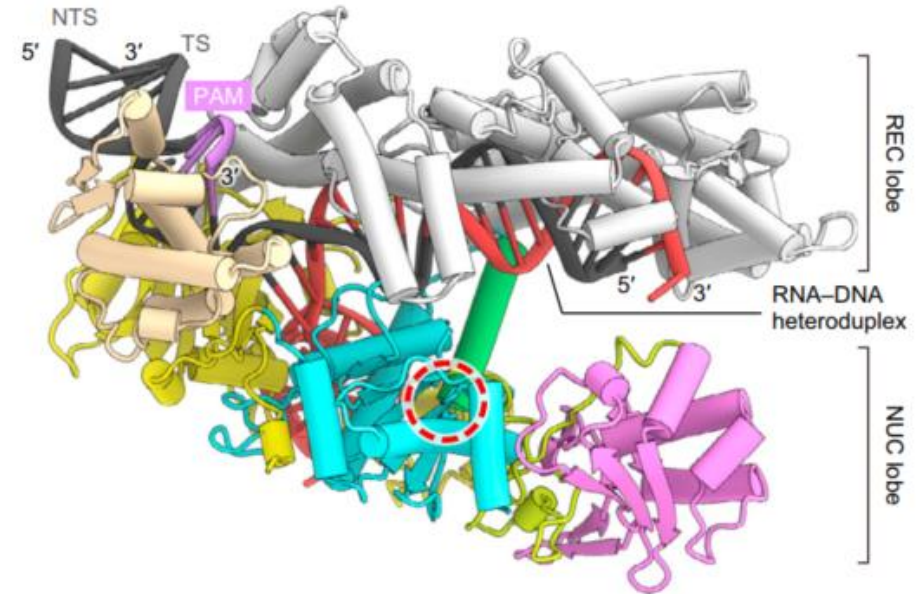


*Cas9*





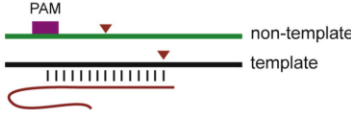
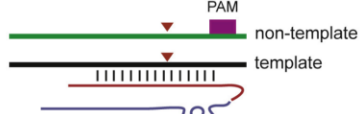
*CPF1 (Cas12a)*

Yamano et al. 2016, *Cell*



# Cas12a vs. Cas9

Bijoya et al. 2020, *Biomed J*  
(review)


	Cas12a	Cas9
Size of protein	~1300 amino acids	~1000-1600 amino acids
RNA	 crRNA Single RNA molecule	 crRNA tracrRNA Two RNA molecules
Nuclease sites	Single nuclease site RuvC-Nuc	2 nuclease domains HNH and RuvC
Type of cut	 PAM non-template template Staggered ends	 PAM non-template template Blunt ends
PAM requirements	Recognises 5' T-rich PAM sequences of 3-4 nt	Recognises 3' G-rich PAM sequences of 3-5 nt
precrRNA processing	possesses intrinsic RNase activity to process precr-RNA	requires host RNase III and tracrRNA

# The CRISPR/Cas9 rEvolution

## PART II

Leonardo Caproni

[I.Caproni@santannapisa.it](mailto:I.Caproni@santannapisa.it)


 [@cap\\_leonardo](https://twitter.com/cap_leonardo)

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2. What is CRISPR/Cas9 technology? From where does it come from?
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5. What are the potential applications in plant science?
6. How can we apply this technology to plants?
7. Application of CRISPR/Cas9 technology in real world...
8. CRISPR/Cas9 perspectives...

# Applications of CRISPR/Cas9 platforms for genome editing in plant

For REVERSE GENETICS approaches alternative to:

- **Random mutagenesis** (undesirable mutations + large scale screening is costly... and tedious)
  - Antisense RNA or virus-induced **gene silencing**
  - **RNA interference**
- 
- Can interrupt functions of specific genes by repressing the corresponding mRNAs

CRISPR/Cas9 provides a more efficient platform to perform:

- **Gene knock-out**
- **Gene Knock-in**
- **Disruption of cis-regulatory elements**
- **Suppression of virus infection**

# Delivery of CRISPR/Cas9 into plant cells



Direct delivery

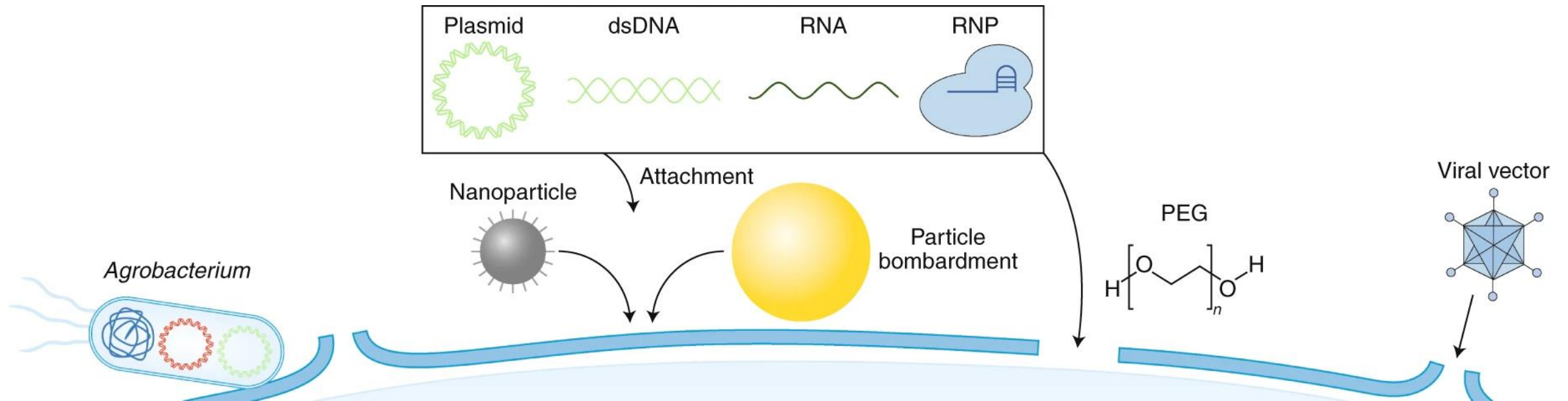


*Agrobacterium tumefaciens*-  
mediated transformation

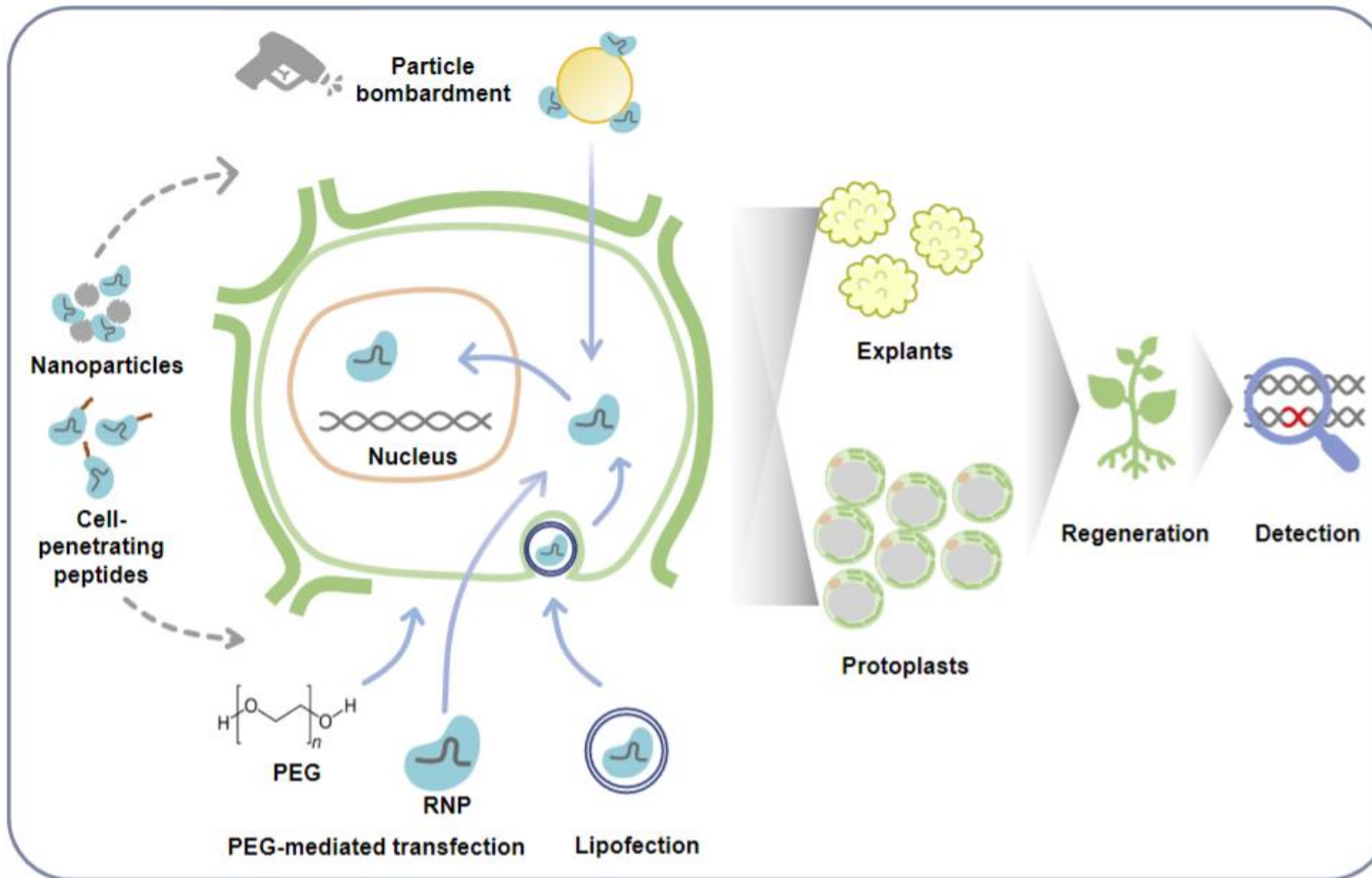


# Applications of CRISPR technology in plant cells

Outside the plant cell, CRISPR reagents can be delivered as **plasmids**, **dsDNA**, **RNA** and **ribonucleoprotein** (RNP) through **PEG-mediated transformation** (polyethylene glycol), particle bombardment or nanoparticles. Plasmids can also be delivered by *Agrobacterium tumefaciens* and viral vectors.



# Direct delivery: all about it



CRISPR reagents can be delivered into plant cells as RNPs.

- **Particle bombardment** can be used to deliver **plasmids** (or **RNPs**) into explants.
- **PEG-mediated transfection** and lipofection can be used to deliver plasmids (or RNPs) into protoplasts.
- **Nanoparticles** and **cell-penetrating peptides** are emerging methods for RNP delivery. Transformed cells and tissues are used for plant regeneration and edit detection.

# What is *Agrobacterium tumefaciens*?

- It causes crown gall disease
- The infection process is associated with presence of the so-called *Ti* plasmid
- During the process, a part of the plasmid (T-DNA) is integrated in the host genome (random position)
- T-DNA carries information of multiple genes (eucaryotic promoter) .
- The expression of the newly acquired genes causes the tumor

2  
Signal molecules  
recognized by the  
receptors

4  
Activated Vir  
proteins process  
the ss T-DNA

5  
Formation of the  
immature T-complex

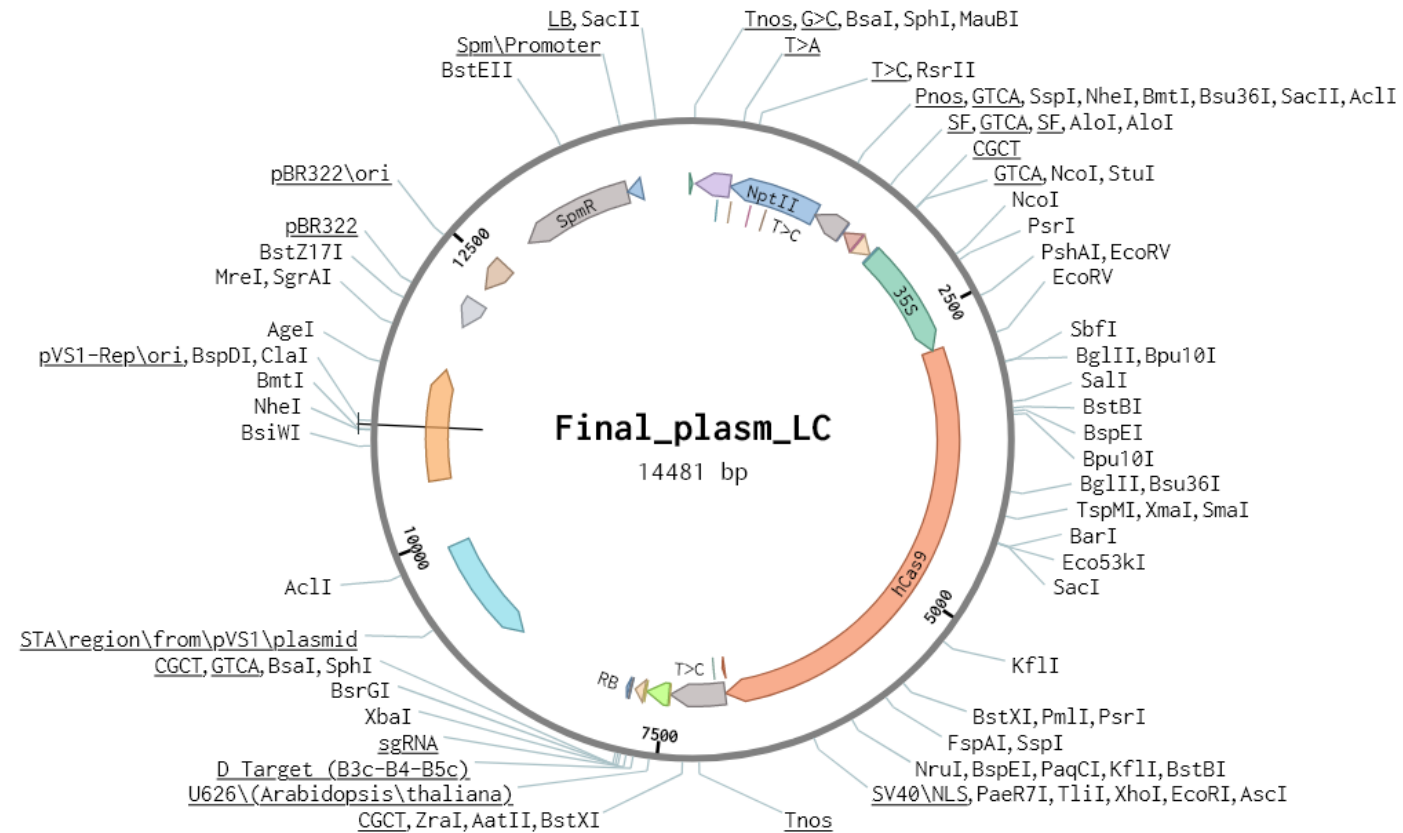
Pacurar et al.  
*Plant Pathol*





# *Agrobacterium tumefaciens*-mediated transformation

- *Agrobacterium tumefaciens* has been extensively used as 'platform' for transformation
- Principle based on the modification of the Ti plasmid
- There are several systems, a quite common one is the so-called **binary system** (it can be cloned in both *E. coli* and *A. tumefaciens*)
- The final plasmid will carry *vir* genes and the artificial T-DNA

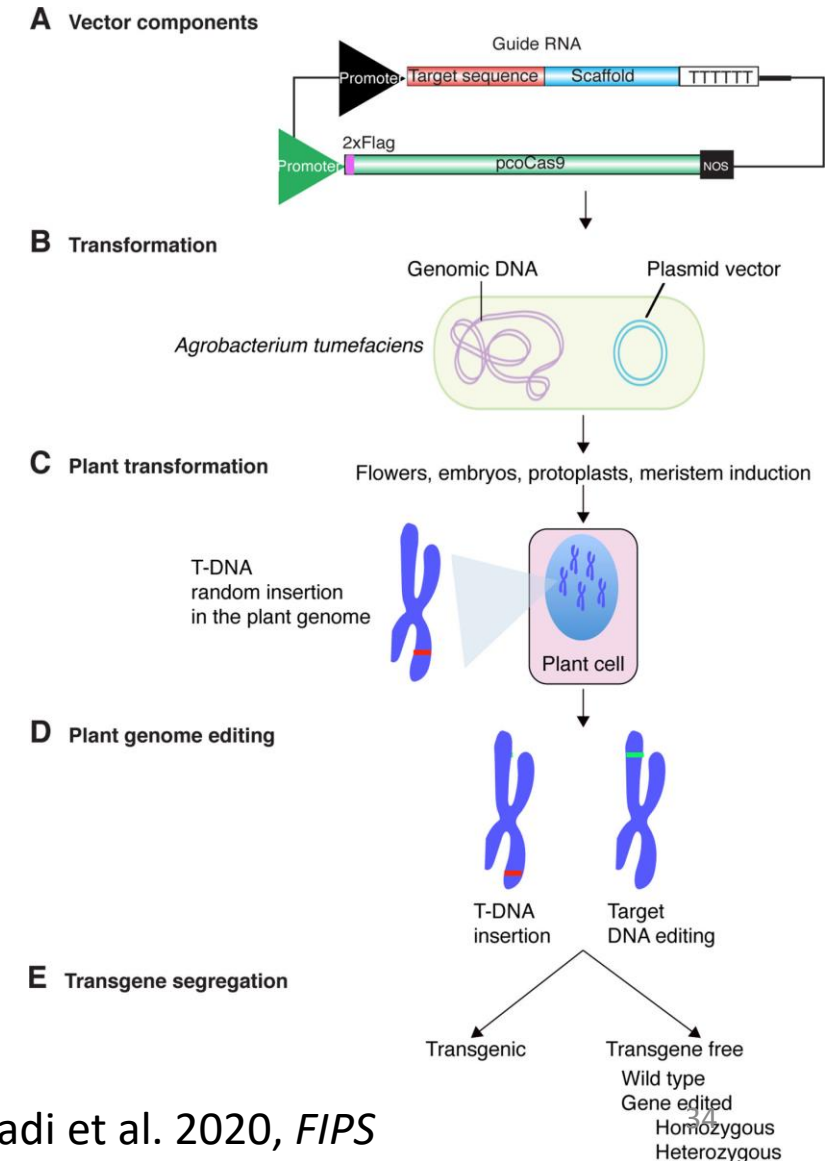


# *Agrobacterium tumefaciens*-mediated CRISPR-Cas

- A. Assemble a plasmid containing all the information you want to carry into the plant cells.
- B. *A. tumefaciens* is transformed with the plasmid vector carrying the cassette for Cas9 protein and guide RNAs
- C. *A. tumefaciens* is used to **transform ovules in flowers, embryos, explants, meristematic cells** or **protoplast**. The integration is random.
- D. Expression of Cas9 protein and guide RNAs lead to editing of the target DNA; insertion site and target site are likely not linked.
- E. The insertion and the edited DNA can be separated through Mendelian segregation.

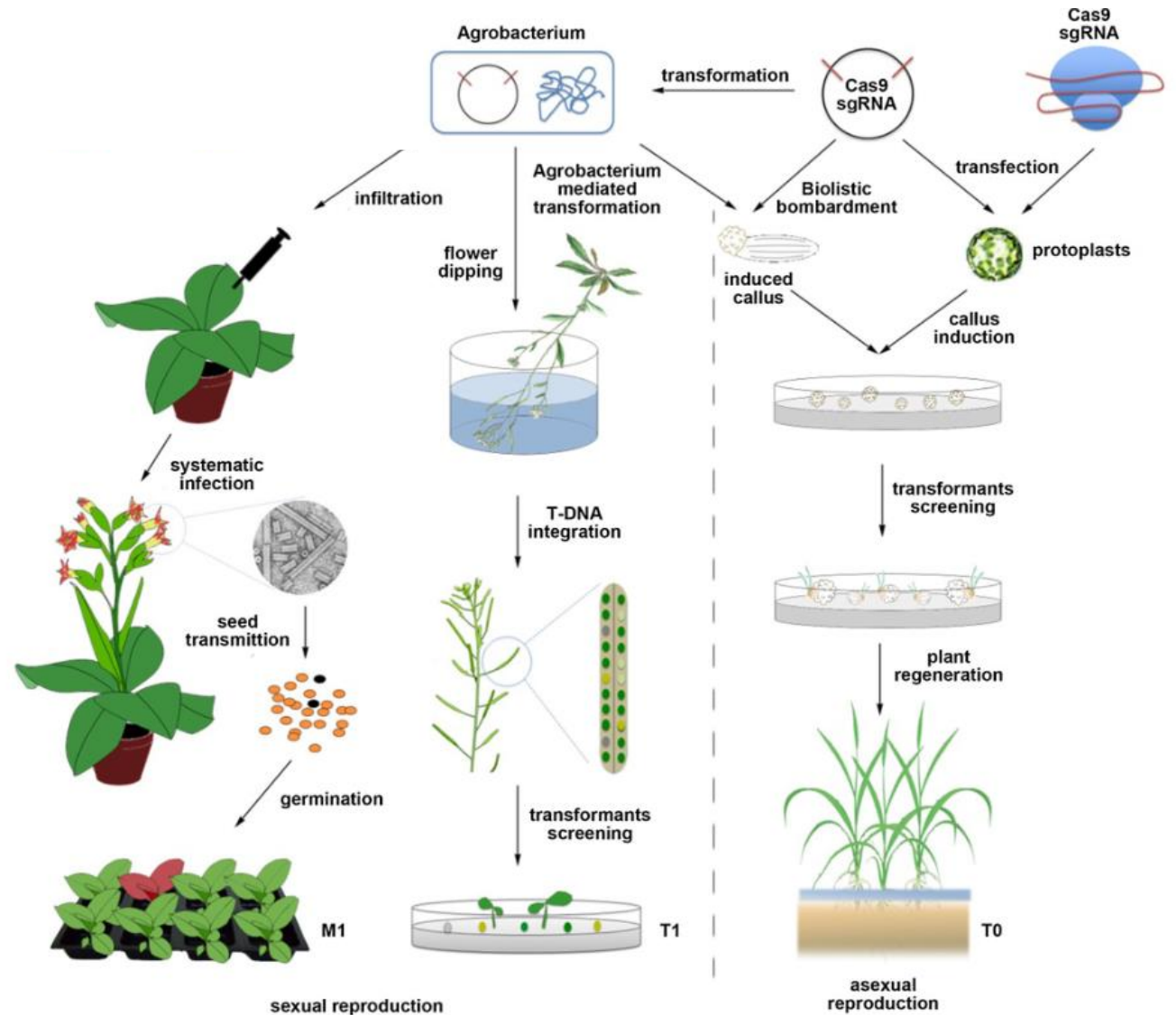
Actually, *A. tumefaciens* is not the one only option, the same principles can be applied using *Rhizobium rhizogenes*

8/18/2025



El-Mounadi et al. 2020, *FIPS*

# Brief recap on the most common approaches



# ...producing 'edited' plants is complex

## **Several limiting factors**

1. Many species (or genotypes within species) are recalcitrant to in vitro culture
2. The efficiency of most approaches is still low
3. Policy-makers are behind





# Edited organisms are reaching the table



Non-browning mushrooms



Low phytate maize



Powdery mildew resistant  
tomato



Altered starch quality in potato  
(low acrylamide)



High oleic soybean

# Stunning application of CRISPR/Cas technology in plant science

LETTER

nature  
biotechnology

## *De novo* domestication of wild tomato using genome editing

Agustin Zsögön<sup>1,7</sup> , Tomáš Čermák<sup>2,6,7</sup>, Emmanuel Rezende Naves<sup>1</sup>, Marcela Morato Notini<sup>3</sup>, Kai H Edel<sup>4</sup>, Stefan Weinl<sup>4</sup>, Luciano Freschi<sup>5</sup>, Daniel F Voytas<sup>2</sup>, Jörg Kudla<sup>4</sup>  & Lázaro Eustáquio Pereira Peres<sup>3</sup> 

# So... what is domestication?

**definition:** a sustained multi-generational relationship in which humans assume a significant degree of control over the reproduction and care of another group of organisms to secure a more predictable supply of resources from that group

**500 *Angiospermae*** species (250.000)

**20** animal species (5.000)

*e.g.* domestication and evolution of a species under domestication did not generally lead to the creation of new species.  
(exception : *Triticum aestivum*)

P. Gepts, 2004; *Plant Breeding Reviews*

## Results of interaction of 3 factors

Plants or Animals



- Morphology
- Behaviour
- Genetics

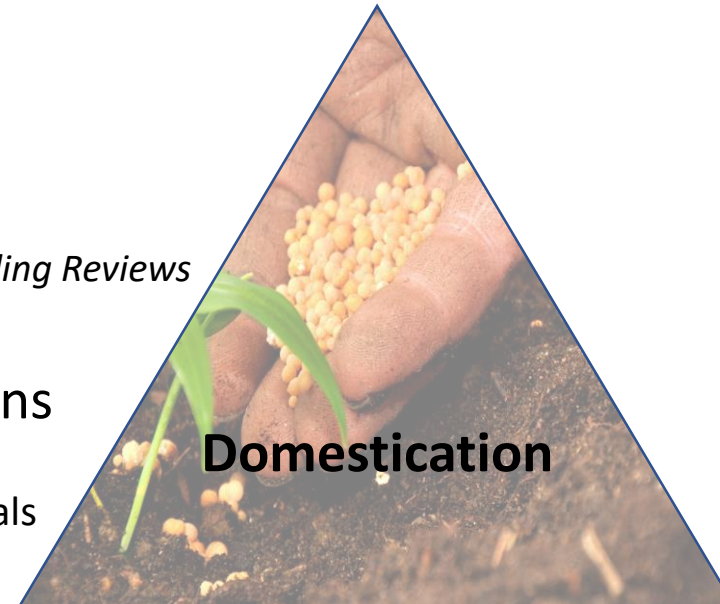
Humans

Cultural development:

- Knowledge of plants and animals
- Technology

Environment

- Climate shift
- Seasonality
- Diversity of environmental niches



# Domestication of crops made agriculture possible

- Domestication is the genetic modification of a wild species to create a new form that is altered to meet human needs
- The process by which humans actively interfere with nature and direct evolution
- In the beginning, an unconscious process of selection
- Humans change the conditions in which cultivated species live and reproduce -> species adapt and evolve as a consequence
- Results in a continuum of increasing **codependance** between people and crops/livestock





# Timeline for crop domestication

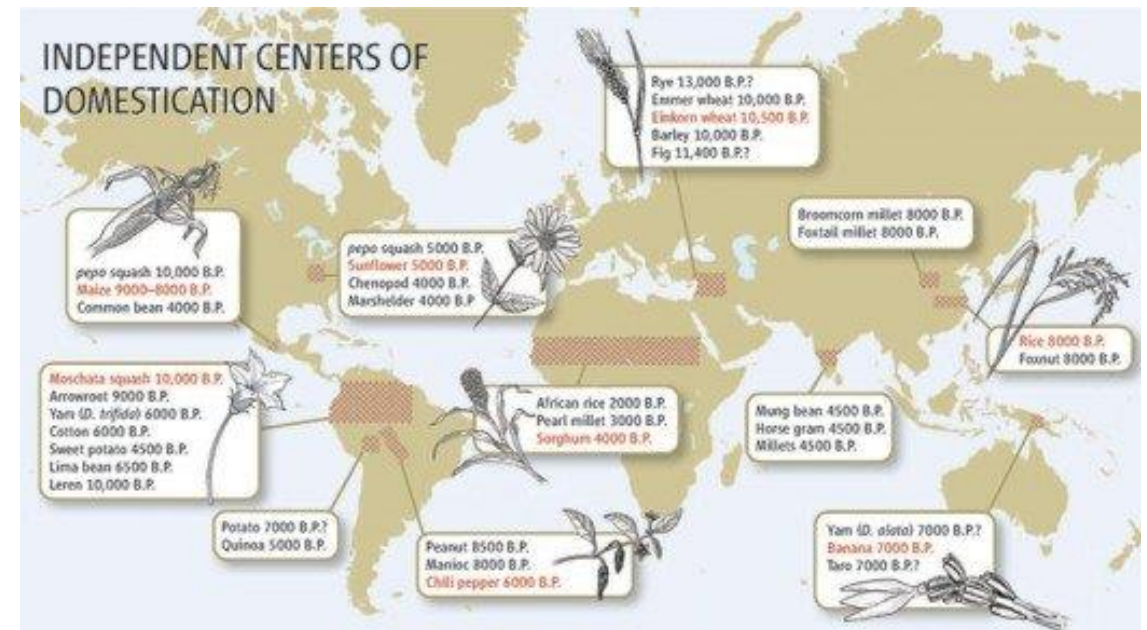
**Table 1.2.** Time frame of domestication and early spread of agriculture

Location	Crop <sup>z</sup>	Age (years BP)	Source
<b>DOMESTICATION CENTERS</b>			
Mesoamerica	Squash	10,000	Smith 1997
	Maize	6,200	Piperno and Flannery 2001
Fertile Crescent	Einkorn wheat	9,400-9,000	Willcox 1998
	Lentil <sup>y</sup>	9,500-9,000	Willcox 1998
	Flax <sup>y</sup>	9,200-8,500	Willcox 1998
	Goat <sup>x</sup>	10,000	Zeder and Hesse 2000
	Pig <sup>x</sup>	10,000	Giuffra et al. 2000
China	Rice	9,000-8,000	Zhao 1998
Eastern United States	Squash	4,300	Asch 1995, cited by Hart et al. 2002
	Sunflower	4,300	Crites 1993
<b>SPREAD FROM DOMESTICATION CENTERS</b>			
Lowland Mesoamerica and Central America	Cassava, <i>Dioscorea</i> yam, arrowroot, maize	7,000-5,000	Piperno et al. 2000 Pope et al. 2001
Eastern North America	Maize	1,100	Smith 1989
Europe	Einkorn wheat	9,000-5,000	Hart et al. 2002 Ammerman and Cavalli-Sforza 1984

<sup>z</sup> Only the earliest domesticated crop remains are listed

<sup>y</sup> Uncertainty as to the domestication status

<sup>x</sup> Additional centers of domestication for the goat (in the Indian subcontinent) and the pig (in Eastern Asia) have been postulated



# Domestication of plants: traits

In particular:

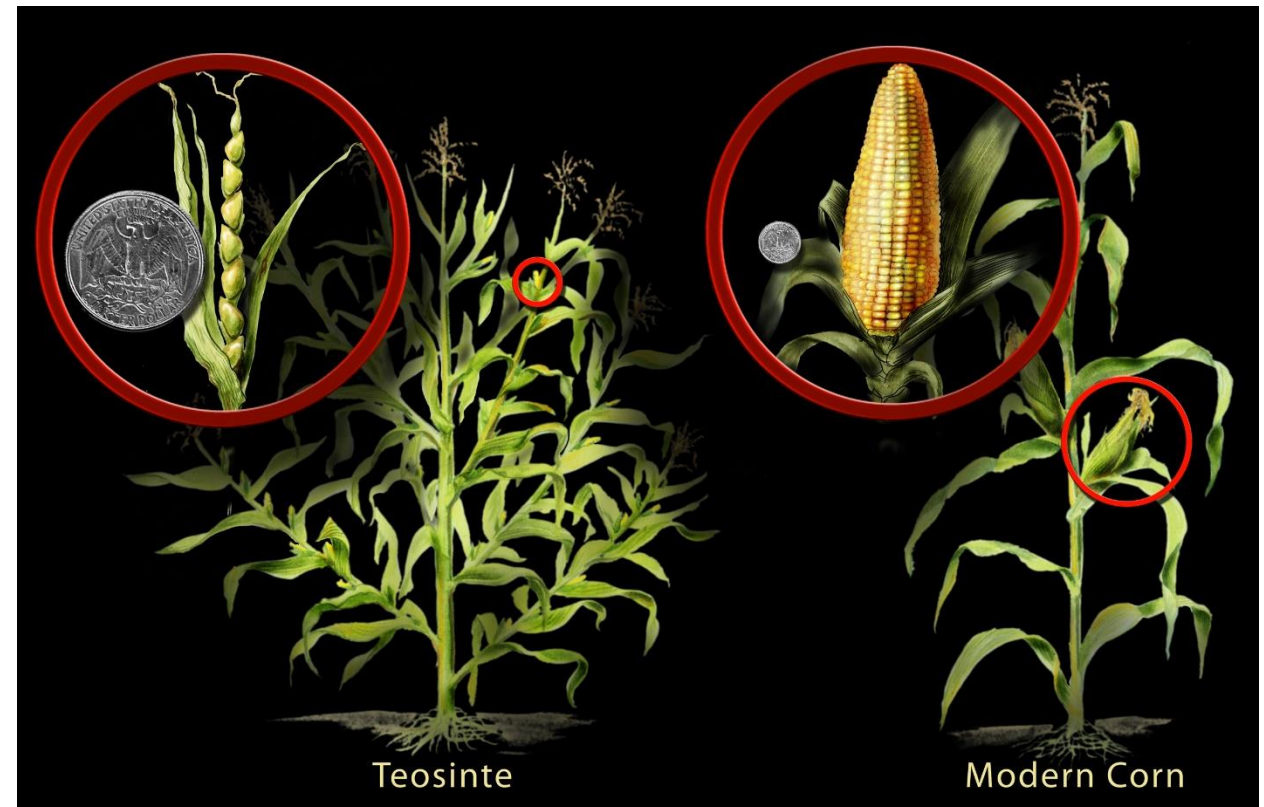
- **No seeds dispersal**
- **No seed dormancy**

} These are taxonomic traits

... also:

- Compact habitus
- Bigger edible parts
- Increased fertility
- Increased inbreeding
- Photoperiod-independent behaviour
- Less toxic compounds
- Colours

So called Domestication Syndrome (Hammer 1984)

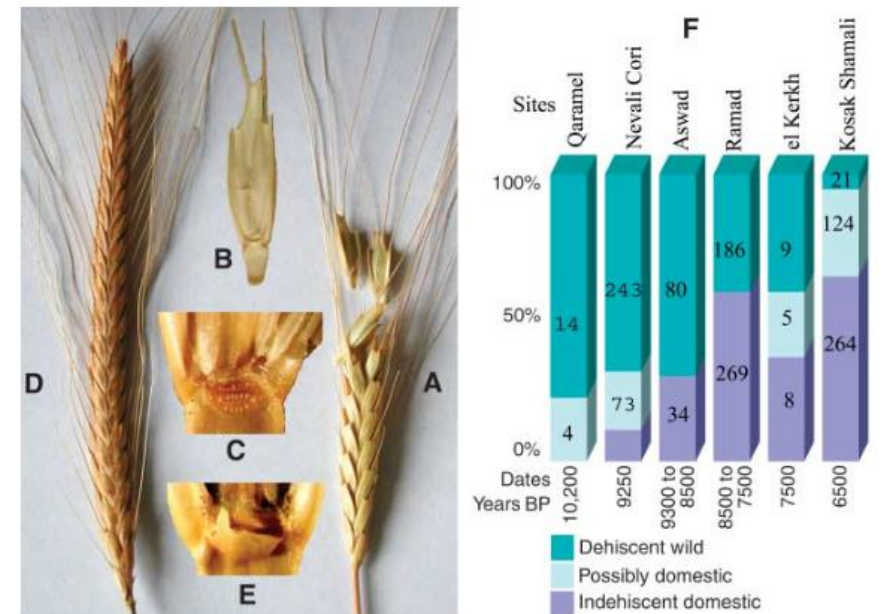




# Domestication traits of crops

## Seed shattering

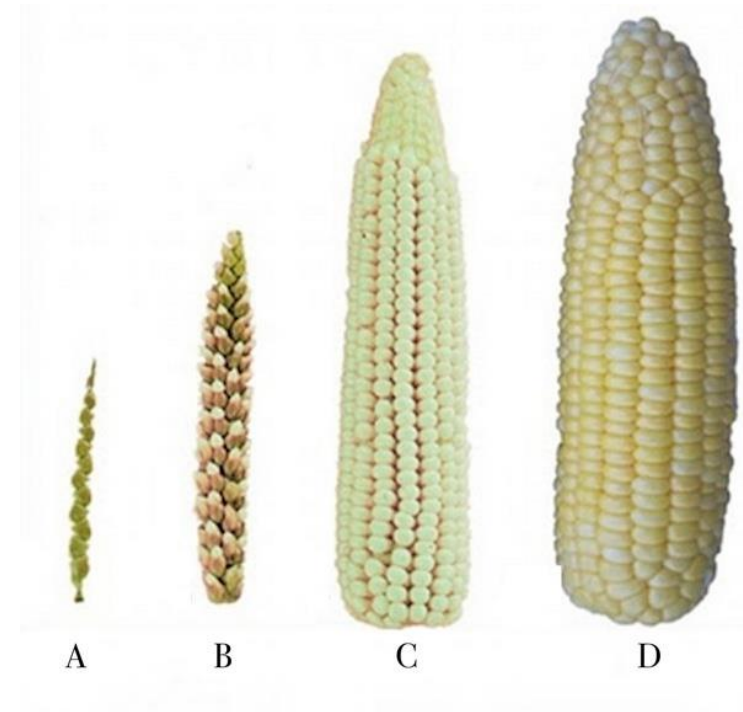
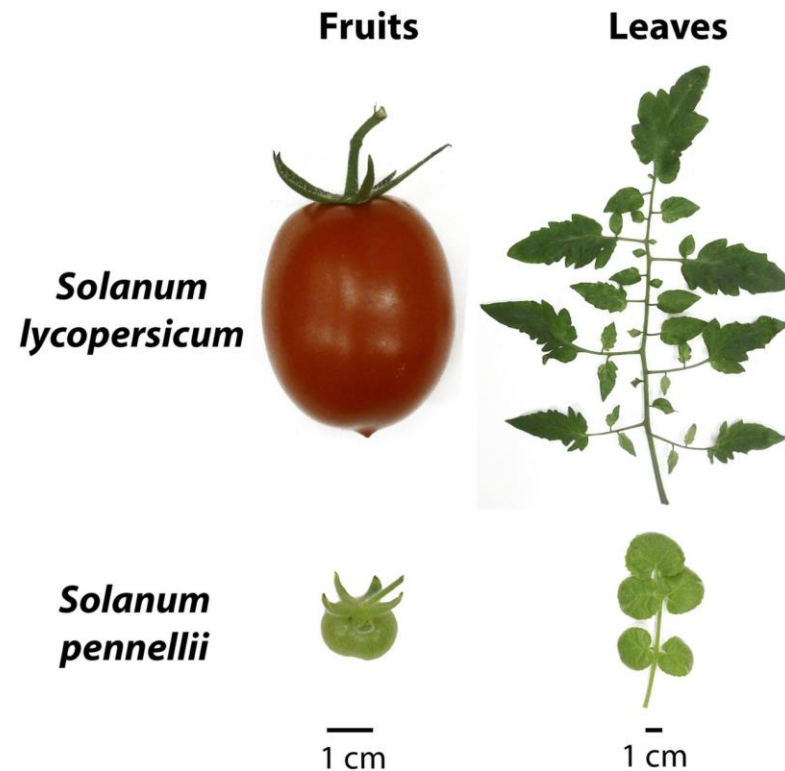
- The tendency to disperse seeds; favoured in the wild (e.g. epizoochory), bad for harvesting
- Very few genes involved



**Fig. 1.** Modern examples of dehiscent wild einkorn wheat ear (A) and spikelet (B). Detail of spikelet with smooth wild abscission scar (C), indehiscent domestic ear (D), and detail of spikelet with jagged break (E) are shown. The bar chart (F) gives relative frequencies of subfossil finds with the absolute figures. Records from Aswad and Ramad (6) are of barley; the other four sites are of wheat. For full data of both studies, see table S1.

## Fruit size

- More energy diverted towards fruit bodies than what would be necessary for survival alone



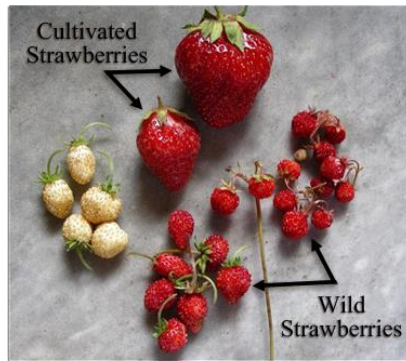
Maize Vs teosinte

## Change in photoperiod sensitivity

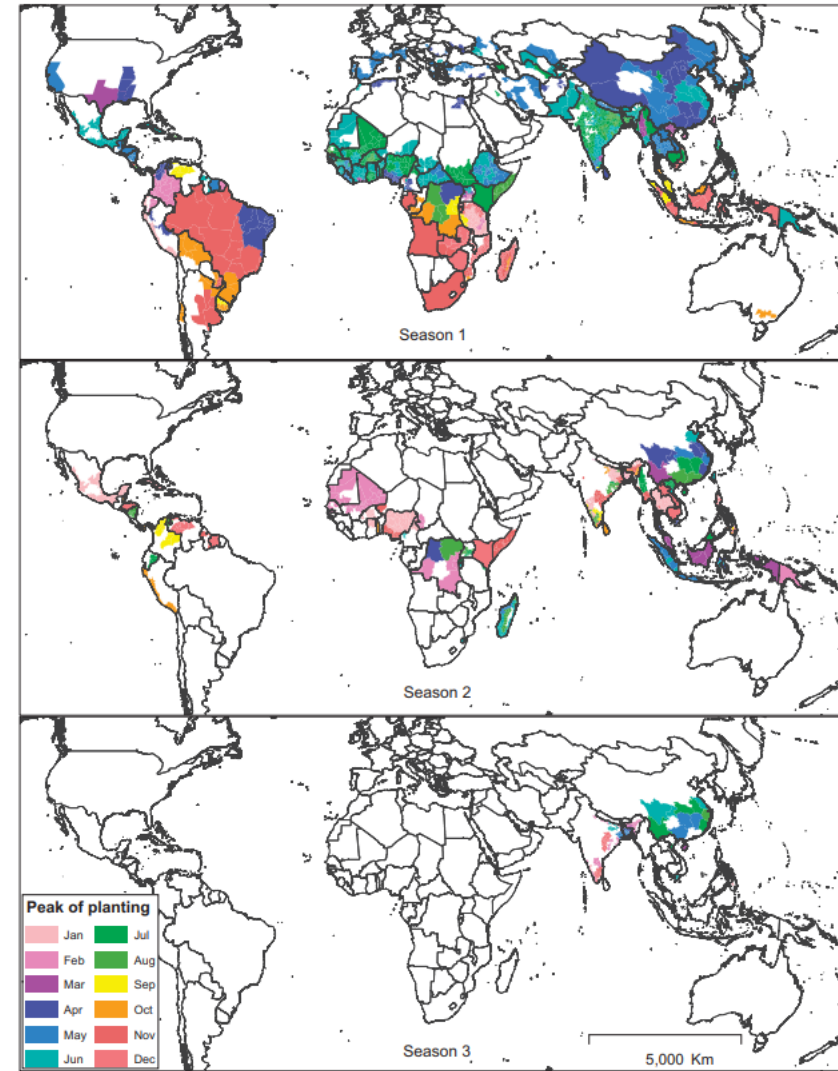
- Alteration of seasonality
- Diffusion across different latitudes

## Changes in sexual reproduction

- Induced sterility
- Lack of normal pollinating organs



Wild banana



**Figure 2.** Peak rice planting months by season. Season 1 refers to the main rice-growing season, that is, the season with the highest rice production. Season 2 has the second highest rice production and Season 3 the least.



## Increased apical dominance

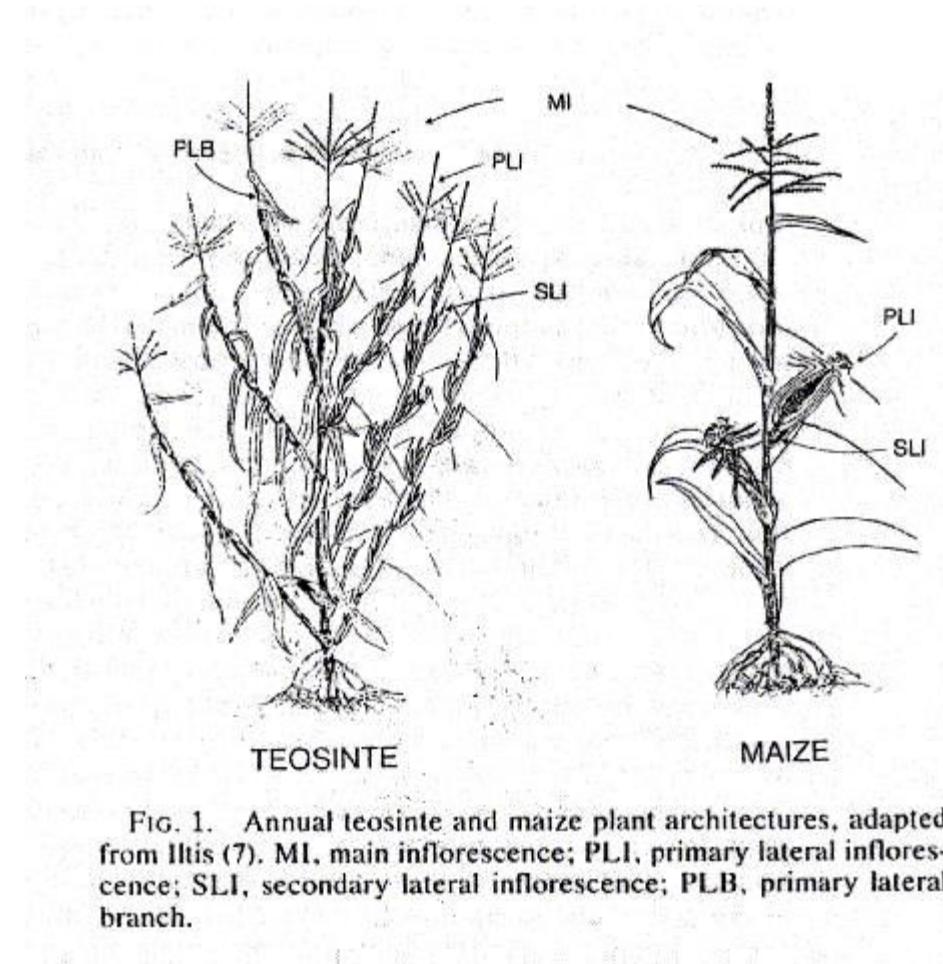
- more resources in the main stem of the plant and a corresponding suppression of axillary branches

## Determined growth

- reduction of vegetative growth in favor of fruiting bodies
- Switch from perenniality to annuality

## Loss of seed dormancy

- Seeds immediately ready to produce plants



# The idea behind this work

nature  
biotechnology

*De novo* domestication of wild tomato using genome editing

Agustin Zsögön<sup>1,7</sup> , Tomáš Čermák<sup>2,6,7</sup>, Emmanuel Rezende Naves<sup>1</sup>, Marcela Morato Notini<sup>3</sup>, Kai H Edel<sup>4</sup>, Stefan Weinl<sup>4</sup>, Luciano Freschi<sup>5</sup>, Daniel F Voytas<sup>2</sup>, Jörg Kudla<sup>4</sup>  & Lázaro Eustáquio Pereira Peres<sup>3</sup> 

## 1. Identify a wild species

- *Solanum pimpinellifolium*

## 2. Identify a suite of key loci that have shaped morphology and agronomic potential

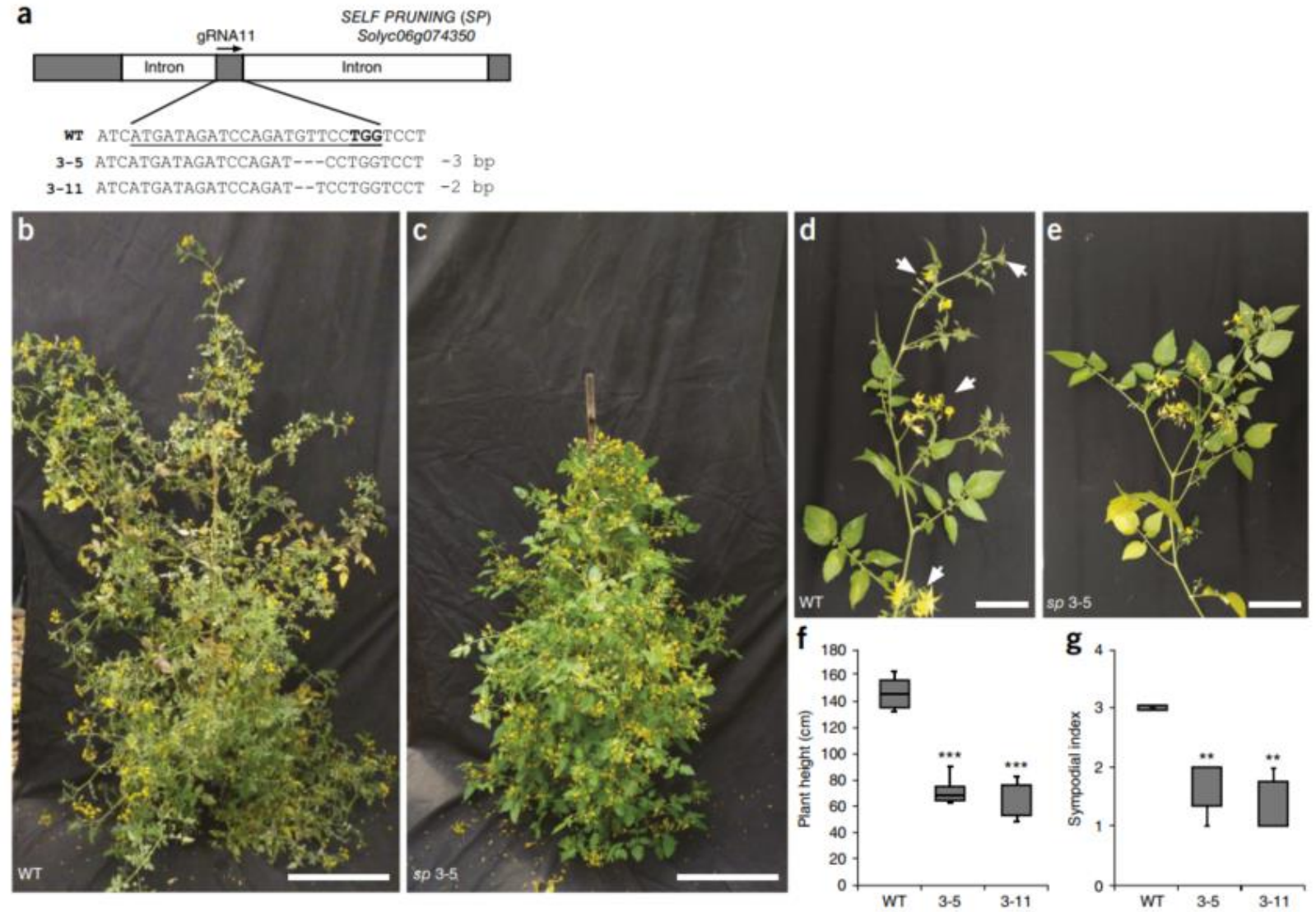
- Growth habit
- Fruit shape and size
- Fruit number
- Nutritional value

} Forward Genetics

## 3. Target this set of genes using multiplex CRISPR-Cas9 approach to generate loss-of-function alleles

# Growth habit

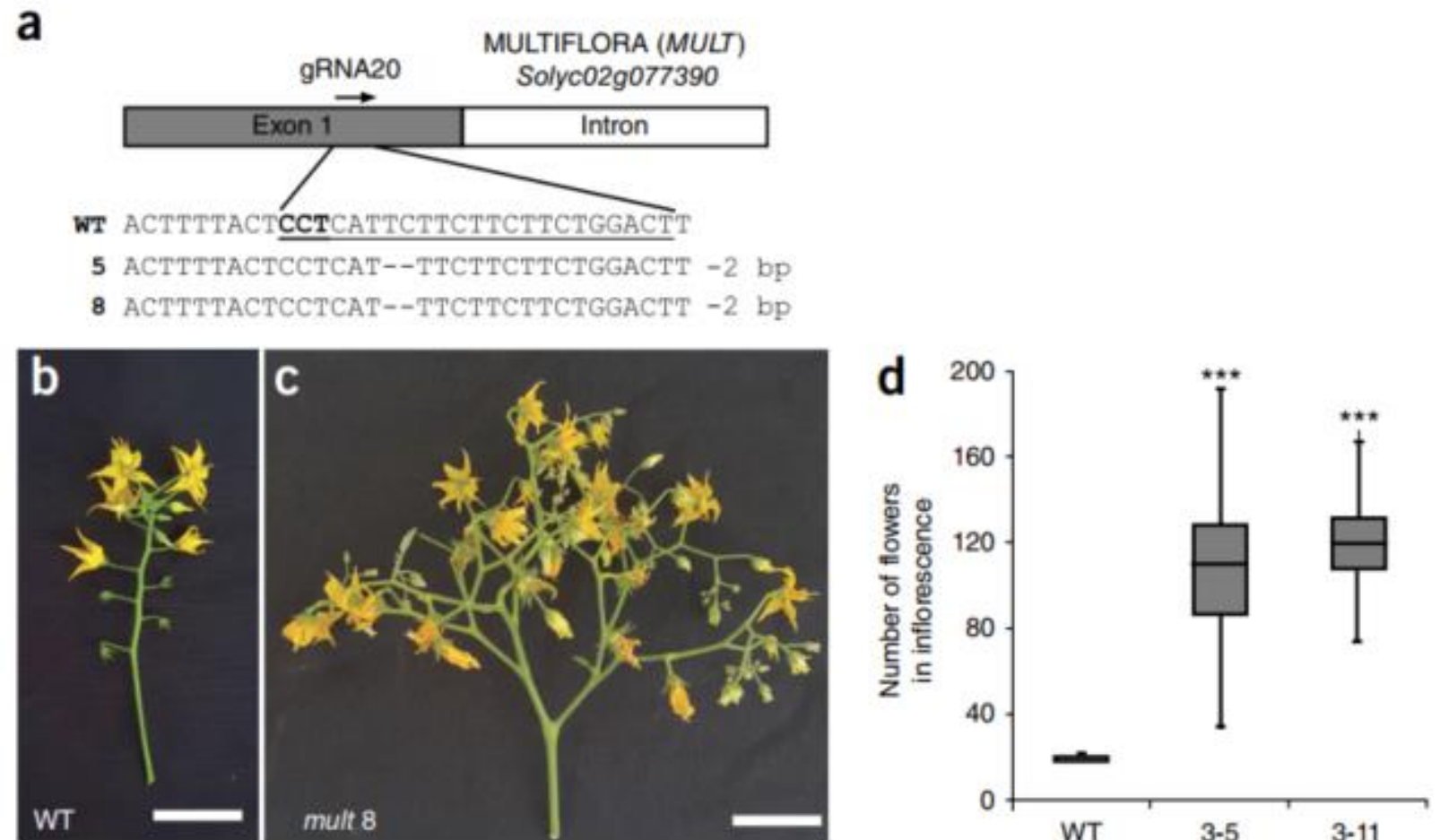
- Two events of missense mutation
- Displayed WT vs T2 plant
- Reduced plant height
- Reduced sympodial index (sympodial unit 3 leaves + flower)





# Fertility

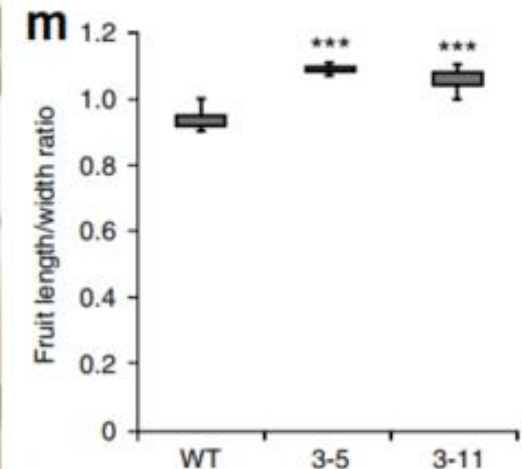
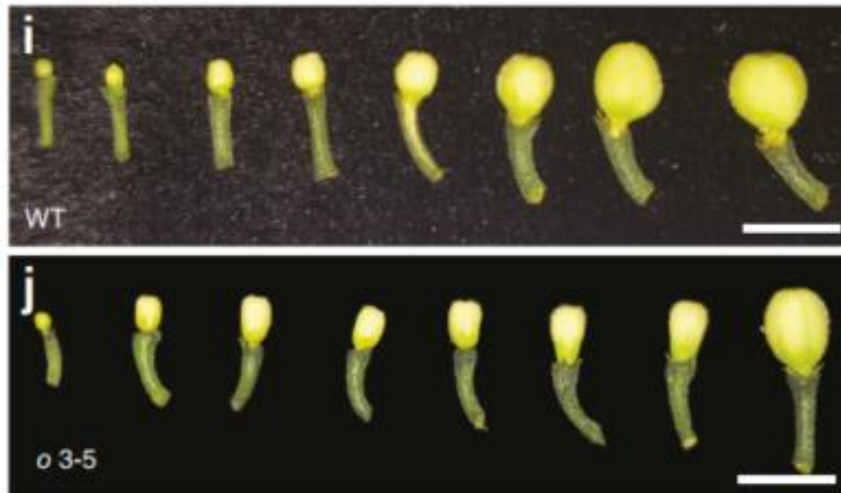
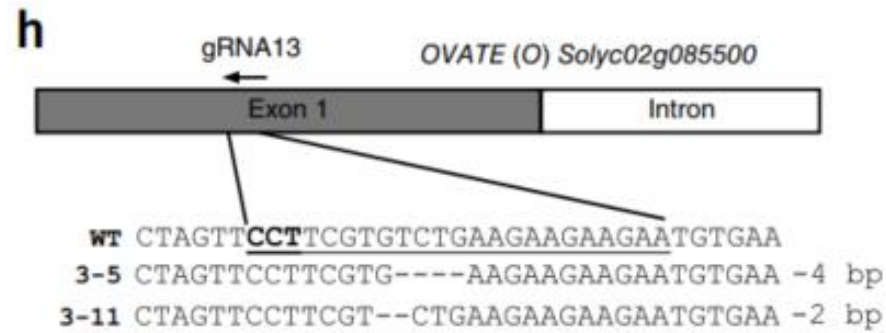
- Two events of missense mutation (identical)
- Displayed WT vs T2 plant
- Increased number of flowers per inflorescence in both events (n=6).



Zsögön et al. 2018, *Nature biotech*

# Fruit Shape

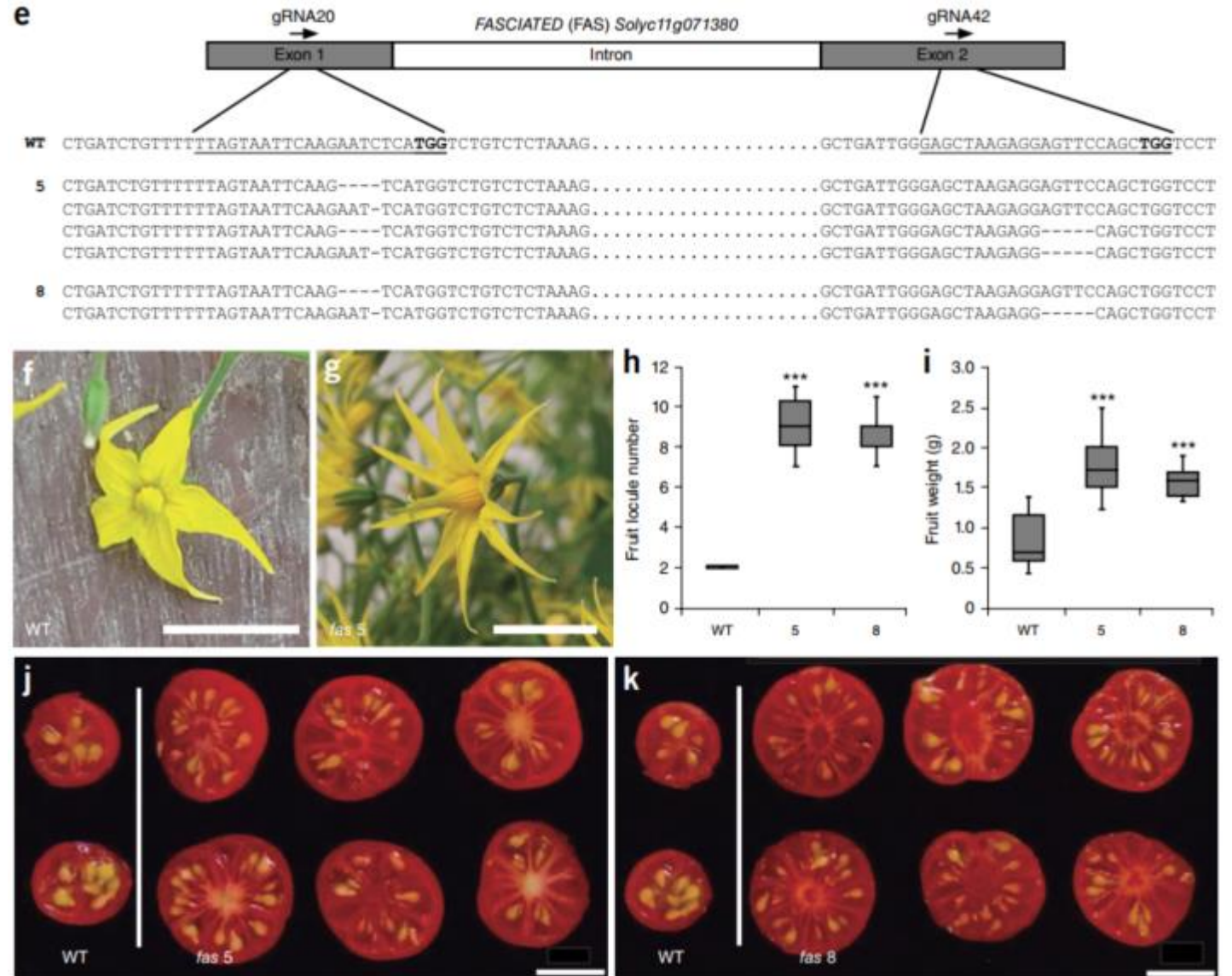
- Two events of missense mutation
- Displayed WT vs T2 plant
- Altered fruit length/width ratio; transformed individuals show oval fruit shape (n=90)



Zsögön et al. 2018, *Nature biotech*

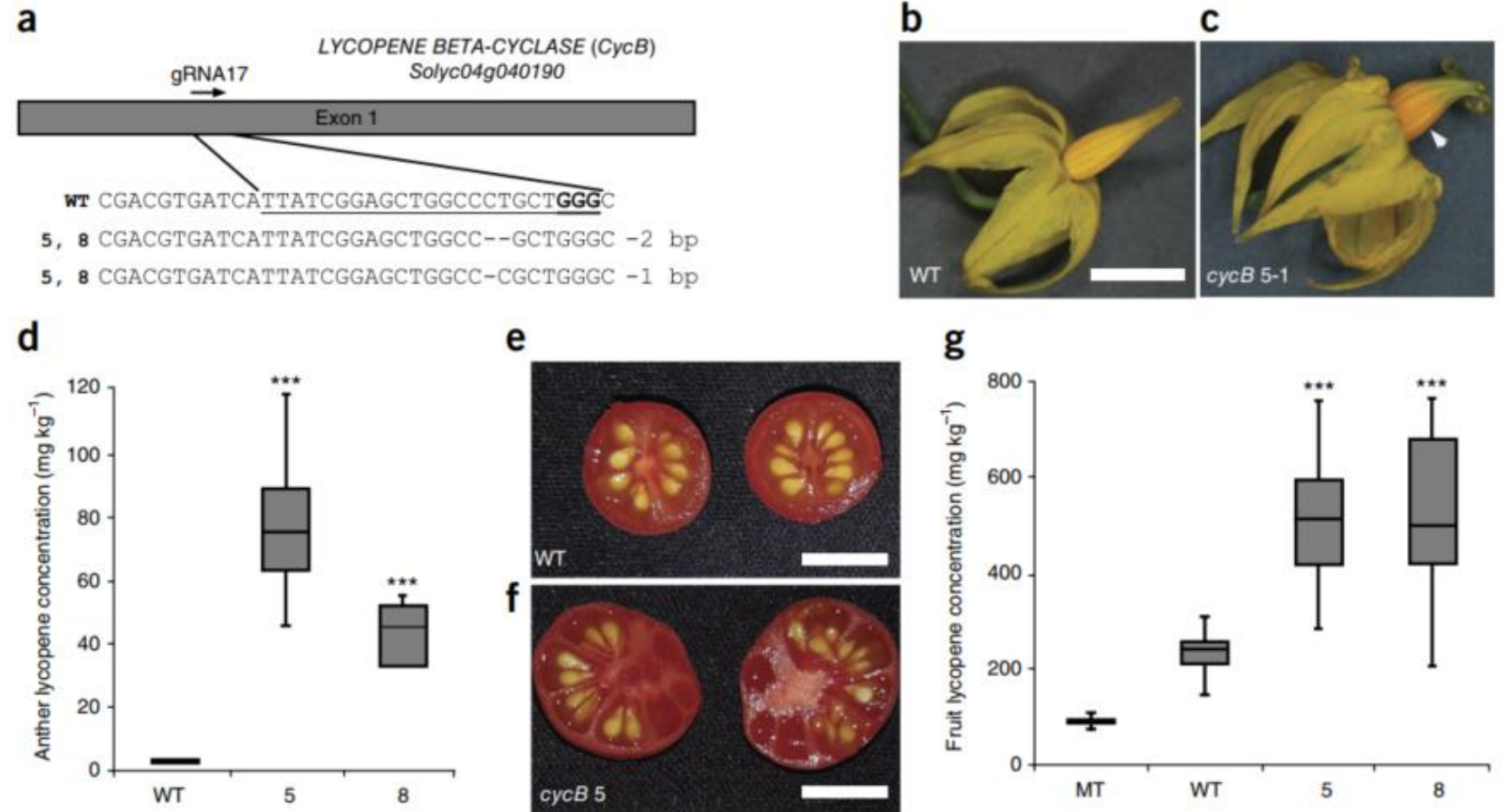
# Fruit size

- Events of missense mutation, gRNAs target two loci of the *fas* in CLV3; in T1 we observe **biallelic deletion in exon 1** while **heterozygous in exon 2**;
- Displayed WT vs T1 plant
- Increased number of locules per fruit (n=60)
- Increased fruit weight (n=90)



# Colour

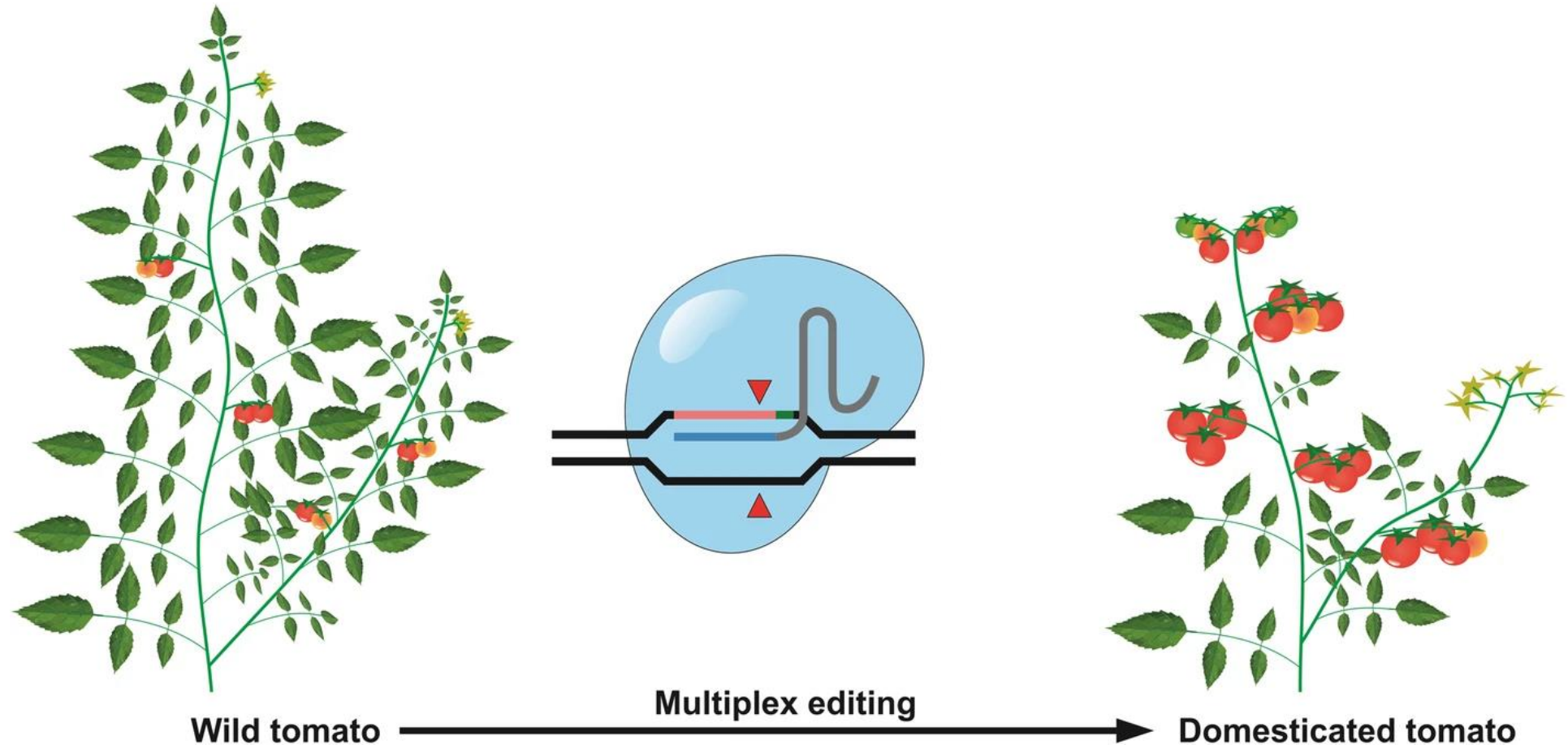
- Two events of missense mutation
- Displayed WT vs T1 plant
- Increased number of locules per fruit (n=60)
- Increased fruit weight (n=90)



Zsögön et al. 2018, *Nature biotech*



# *De novo* domestication of tomato



# The impact of CRIPR/Cas9 technology: a broader picture

Table 2 | Ongoing clinical trials using CRISPR technologies to engineer immunotherapies for the treatment of human cancers

Target and method	Cell type	Phase	Clinical trial identifier
PD1 KO	Autologous TILs	I	NCT03081715 (REF. <sup>332</sup> )
PD1 KO	Autologous TILs	I	NCT02793856 (REF. <sup>286</sup> )
PD1 KO	Autologous EBV CTLs	I/II	NCT03044743 (REF. <sup>333</sup> )
PD1 KO	Autologous TILs	I	NCT04417764 (REF. <sup>334</sup> )
PD1 and TCR KO	Allogeneic mesothelin-targeting CAR T cells	I	NCT03545815 (REF. <sup>335</sup> )
Edited endogenous HPK1	Autologous CD19-targeting CAR T cells	I	NCT04037566 (REF. <sup>336</sup> )
Endogenous CD5 KO	Allogeneic CD5-targeting CAR T cells	Early phase I	NCT04767308 (REF. <sup>337</sup> )
Endogenous TCR and $\beta_2m$ KO	Allogeneic CD19-targeting CAR T cells	I	NCT03166878 (REF. <sup>338</sup> )
Insert CAR, endogenous TCR and MHC-I KO	Allogeneic CD70-targeting CAR T cells	1	NCT04502446 (REF. <sup>339</sup> )
Insert CAR, endogenous TCR and MHC-I KO	Allogeneic BCMA-targeting CAR T cells	I	NCT04244656 (REF. <sup>340</sup> )
Insert CAR, PD1 and endogenous TCR KO	Allogeneic CD19-targeting CAR T cells	I	NCT04637763 (REF. <sup>341</sup> )
Insert CAR, endogenous TCR and MHC-I KO	Allogeneic CD70-targeting CAR T cells	I	NCT04438083 (REF. <sup>342</sup> )
Insert CAR, CD52 KO	Allogeneic CD19-targeting CAR T cells	I	NCT04557436 (REF. <sup>343</sup> )
CISH KO	Autologous CD19-targeting CAR T cells	I/II	NCT04426669 (REF. <sup>344</sup> )

$\beta_2m$ ,  $\beta_2$ -microglobulin; BCMA, B cell maturation protein (also known as TNFRSF17); CAR, chimeric antigen receptor; CISH, cytokine-inducible SH2-containing protein; CTL, cytotoxic T lymphocyte; EBV, Epstein-Barr virus; HPK1, haematopoietic progenitor kinase 1; KO, knockout; MHC-I, major histocompatibility complex class I; PD1, programmed cell death protein 1; TCR, T cell receptor; TIL, tumour-infiltrating lymphocyte.



# EC and the CRISPR/Cas9

On **25th of July 2018**, the **Court of Justice of the European Union** ruled that the regulatory framework for genetic engineering should be extended to the so-called **New Breeding Technologies** including recently developed methods of genome editing known as new genetic technologies (NGTs). The judgement claimed to be based on the **precautionary principle**.

**Little incentive for private research**

# Recommended readings

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- A. Zsögön, et al., **De novo domestication of wild tomato using genome editing**. *Nat. Biotechnol.* (2018) <https://doi.org/10.1038/nbt.4272>.


INSTITUTE  
OF PLANT  
SCIENCES



**Sant'Anna**  
School of Advanced Studies – Pisa

Leonardo Caproni

[I.Caproni@santannapisa.it](mailto:I.Caproni@santannapisa.it)

 [@cap\\_leonardo](https://twitter.com/cap_leonardo)

Thanks for you attention

