Crop Genome Editing and Precision Breeding with CRISPR/Cas9

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Conventional Transgenic Approaches

Drawbacks:

Ø Random insertion of transgene



Fig. 2. Hawaiian papaya plot in 2011. Hawaiian papaya plot showing diseased, devastated, nontransformed trees in the foreground and healthy transgenic trees behind. [Photo courtesy of Dennis Gonsalves, Agricultural Research Service, U.S. Department of Agriculture, Hawaii]

- Ø Not suitable for gene targeting or precise gene mutation
- Ø Difficult to perform gene replacement or create allelic variation
- Introduction of undesirable DNA fragments (T-DNA, selection markers)
- Ø Extensive regulatory requirements
- Ø Public concerns over transgenic crops

New technology is much needed:

- **Ø** To precisely and efficiently manipulate genome for crop improvement
- Ø To reduce regulatory hurdles and public concerns

Genome Editing: Break and Repair DNA



Programmable Nucleases for Genome Editing



Program nuclease based on DNA binding specificity of zinc fingers and TAL effectors

Program nuclease according to RNA:DNA base pairing

CRISPR/Cas: A Bacterial Defense System

CRISPR: clustered regularly interspaced short palindromic repeats CAS: CRISPR-associated nuclease



These *Streptococcus pyogenes* bacteria use CRISPR/Cas9 system to battle viruses

(Science, Aug. 23, 2013)

2015 Breakthrough Prize



2nd Annual Breakthrough Prize Ceremony held at NASA's Ames Research Center in Moffett Field, CA, on November 9, 2014. The event was hosted by Breakthrough Prize founders Sergey Brin and Anne Wojcicki, Jack Ma and Cathy Zhang, Yuri and Julia Milner, Mark Zuckerberg and Priscilla Chan.

Engineering CRISPR/Cas9 for Plant Genome Editing



Plasmid vectors available via Addgene (www. addgene.org)

Design of gRNAs to Target Three Specific Sites of OsMPK5

* OsMPK5 encodes a stress-inducible MAP kinase which negatively regulates rice disease resistance

Mol Plant 6: 1975-1983 (2013)



Transgenic Rice Lines with Targeted Mutation of OsMPK5

Genome editing resulted in single base indels and frame-shift of *OsMPK5*

gRNA/Cas9 could be readily removed via segregation, resulting in transgene-free mutant lines



CRISPR/Cas9 Editing Specificity

Specificity/off-target determinants:

- 1. Cas9 protein (some variants are more specific)
- 2. gRNA/Cas9 concentration in the cell
- 3. gRNA/Cas9 exposure time/duration (transient vs. stable)
- 4. DNA sequences of genomic sites

Genome-wide prediction of specific gRNA spacers

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A Po	rtal of CRISPR-Cas9 Mediated Genome Editing	
Home Search Genome Browser Instruction Before searching, please read our instructions. Currently, C CRISPR-Cas9 mediated genome editing, will be displayed for regions longer than 30kb will not be accepted to maintain servi- results. The search function require your web browsers to sup Two RGE vectors developed by Yang's Lab are available via A Select species Chromosome From 10000 To 20000 Search by region Select one searching method then click search.	n Download More about RGE About us Class0 0 and Class1 0 gRNA spacer sequences, which are expected to be highly specific for the selected region or gene. All classes of gRNA spacers are available in the <u>Browser</u> . Search requests for er performance. Searches of bigger genes or longer regions may take more time to download the sport JavaScript (Latest version of Firefox is recommended). Addgene now. (http://www.addgene.org/Yinong Yang/) Select species Gene Locus Search by gene ID Browser JavaScript (Dense Dense	lu/crispr

CRISPR-PLANT is supported by Penn State and AGI

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Polycistronic tRNA-gRNA (PTG) Technology

Array gRNAs tandemly in a single polycistronic gene and utilize endogenous tRNA processing system for precise cleavage and production of numerous gRNAs *in vivo.* (*PNAS* 112: 3570-3575, 2015)



Multiplex Targeted Mutagenesis with PTG in Stable Transgenic Rice Plants

MPK1	gRNA4	gRNA3 🔑	gRNA4 site	gRNA3 site
WT	CGCGTGCCAACCATTT TATACCCCGGTGGGCCA CATC	CAGGCGACGCTGAG CCATGGCGGGAGGTTC		
#1	CGCGTGCCAACCATTT –ATACCCCGGTGGGCCA ·······CATC	CAGGCGACGCTGAaaCCA <mark>TGG</mark> CGGGAGGTTC	-1 bp	G->A, +1 bp
#10	CGCGTGCCAACCATTT -ATACCCCGGTGGGCCA·······CATC	CAGGCGACGCT CCA <mark>TGG</mark> CGGGAGGTTC	-1 bp	-3 bp
#11	CGCGTGCCAACCATTT -ATACCCCGGTGGGCCA·······CATC	CAGGCGACGCTGA- CCA <mark>TGG</mark> CGGGAGGTTC	-1 bp	-1 bp
MPK2	۰ ⁹	80		
	gRNA5	gRNA6	gRNA5 site	gRNA6 site
VV I #1		AT GCGCAGAC T CGTC AGG <mark>AGG T</mark> GGCAAT CAA	-1 bp	-12 hp
#10			-1 bp	-42 bp
#10 #11			11 bp	+1 bp
#11		ATGCGCAGACTCGTCIAGGAGGTGGCAATCAA	-11 bp	dd 1+
MPK5	ORNA1	CRNA2 20		
		911172 7	gRNA1 site	gRNA2 site
WT			 T 7 hn	11 hr
#1	CGCACGGCGGCCGGTA TACGACATCT	TACATUGUCAUGGAGCATUATGGACACCGACC	qu -/ p	+i pp

	11 1			1 00	
7	#10	CGCACGGCGGCCGGTATCTAC	CATCGCCACGGAGC tTCA <mark>TGG</mark> ACACCGACCT	-23 bp	+1 bp
i	#11	CGCACGGCGG <mark>CCG</mark> GTA	TCA <mark>TGG</mark> ACACCGACCT	delete 727 bp	

MPK6	gRNA8	gRNA7	gRNA8 site	gRNA7 site
WT	GGTGTGATCACCCTTT GATTGACCCGCACCCGC	CCATAT CGATGCCAAGCGGACAC		
#1	GGTGTGATCACCCTTTtACCCGCACCCGCCATTCGACA	CCATATTGCCAAGCGGACAC	+1bp, -5 bp	-3 bp
#10	GGTGTGATCACCCTTT -AT -GACCCGCACCCGCCATTCGACA/	A <mark>CCA</mark> TACCAAGCGGACAC	-2 bp	-6 bp
#11	GGTGTGATCACCCTTT -AGACCCGCACCCGCCATTCGACA/	ACCATATaCGATGCCAAGCGGACAC	-3 bp	+1 bp

Inheritance of *MPK1/MPK2/MPK5/MPK6* Quadruple Mutation in T1 Rice Lines

а.	PTGb9 T1	СК	b. MPK1	
MPK1 Bipi			WT CGCGTGCCAACCATTT - TATACCCCGGTGGGCCA CATCCAGGCGACGCTGAGCCATGGCGGGGGGGGGGGGGG	эр, -15bр эр, -3bр bp, -3bр bp, -3bр bp, -3bр 1c, -3bр bp, -3bр
MPK2		-	MPK2 after a	
LCOIN	====		WT TCCTCCTTCCCCTCC-TTGAGGCGACCGGGTTC GAATGCGCAGACTCGTC AGGAGGTGGCAATCAA 1-2 TCCTCCTTCTCCCCTCC GAGGCGACCGGGTTC GAATGCGCAGACTCGTC aa AGGAGGTGGCAATCAA -2bp, +2l 2-1 TCCTCCTTCTCCCCTCC t TTGAGGCGACCGGGTTC GAATGCGCAGACTCGTCt - AGGAGGTGGCAATCAA +1bp, +1 3-2 TCCTCCTTCTCCCCTCC t TTGAGGCGACCGGGTTC GAATGCGCAGACTCGTCc - AGGAGGTGGCAATCAA +1bp, +1 4-2aTCCTCCTTCTCCCTCC t TTGAGGCGACCGGGTTC GAATGCGCAGACTCGTCc - AGGAGGTGGCAATCAA +1bp, +1	bp bp bp op
MPK5 Kpnl			4-2bTCCTCCTT AGGCGACCGGGTTC GAATGCGCAGACTCGTCt - AGGAGGTGGCAATCAA -11bp, +1	bp
			MPK5	
			1-2 CGCACGGCGGCCGGTAtCCTGCTCTACGACATCTTC········TCTACATCGCCACGGAG c CT - CATGGACACCGACCT +1br 2-1 CGCACGGCGGCCGGTt CTCTACGACATCTTC··········TCTACATCG CT - CATGGACACCGACCT 1c/-4br	o, +1bp o, -8bp
Sacl			3-2 CGCACGGCGGCCGGTATCTACGACATCTTC·······TCTACATCGCT - CATGGACACCGACCT -5bp 4-2 CGCACGGCGGCCGGTATCTACGACATCTTC·······TCTACATCGCCACGGAG - CT t CATGGACACCGACCT -5bp), -8bp), +1bp
			<i>МРК</i> 6 а	
MPK6 Clal			WT GGTGTGATCACCCTTTGATTGACCCGCACCCGC ATTCGACAACCATAT- CGATGCCAAGCGGACAC 1-2aGGTGTGATCACC TTGACCCGCACCCGC ATTCGACAACCAT- c- CGATGCCAAGCGGACAC 1-2b ACCCGCACCCGC -6bp, 1c/- 2-1 GGTGTGATCACCCTTT - A ACCCGCACCCGC ATTCGACAACCATAT TGCCAAGCGGACAC 48bp, -21 9-1 GGTGTGATCACCCTTT - A ACCCGCACCCGC	1bp bp Ն
		-	4-2aGGTGTGATCACCCTTT - ACACCCGC···········ATTCGACAACCATATTGCCAAGCGGACAC -9bp, -3bp 4-2bGGTGTGATCACCCTTT - ACACCCGC············ATTCGACAACCATAT aCGATGCCAAGCGGACAC -9 bp, -3bp 4-2bGGTGTGATCACCCTTT - ACACCCGC·············ATTCGACAACCATAT aCGATGCCAAGCGGACAC -9 bp, +1bp	p op

(Yang lab, unpublished)

Broad Application of CRISPR-Cas9 Technology

Technical advantages for basic plant biology and crop breeding

- Targeted gene mutation (multiple or redundant genes)
- Site-specific integration and gene stacking
- Gene replacement via homologous recombination
- Site-directed mutagenesis to create allelic variation
- Ø Chromosomal engineering such as deletion or translocation
- Ø Modification and labeling of multiple genomic sites
- Transcriptional modulation of multiple genes and pathways
- Ø Epigenome editing such as methylation and demethylation
- Cisgenesis without introducing undesirable foreign DNA

Economic, regulatory and societal benefits:

- Ø Reduce costs for precise and efficient molecular breeding
- Ø Eliminate or significantly reduce regulatory requirements
- Ø Alleviate public concerns about GM crops

Simultaneous Mutation of Six MLO Alleles Confers Powdery Mildew Resistance



B. draminis B. graminis B. graminis B. graminis Cocolories per total no. of germinated spores (%) of germinated spores (%) for the first of the firs

Figure 2 Loss of *TaMLO* function confers resistance of bread wheat to powdery mildew disease. (a) Percentage of microcolonies formed from the total number of germinated spores of *Blumeria graminis* f. sp. *tritici* (*Bgt*) inoculated on the leaves of wild-type (WT) and various *tamlo* mutants. At least 2,000 germinated spores per genotype per experiment were examined 72 h after inoculation with virulent *Bgt* isolate E09. Values are the mean \pm s.d. of four independent experiments. ***P* < 0.01 (*t*-test). (b) Micrographs of microcolony formation of *Bgt* on the surfaces of leaves of the indicated genotypes 3 d postinoculation. Powdery mildew spores and

Nature Biotechnology 32: 947–951 (2014)



colonies were stained with Coomassie blue. Scale bars, 200 μm. (c) Macroscopic infection phenotypes of representative leaves of WT and the indicated *mlo* mutants 7 d after inoculation of detached leaves with *Bgt*. Scale bar, 1 cm. (d) Disease symptoms of wild-type (WT) and *tamlo-aabbdd* mutant plants. The photograph was taken 7 d after inoculation *in planta*. Scale bars, 2 cm.

Transgene-free Mutation of OsMPK5 to Enhance Rice Blast Resistance



Suitable for seed propagated crops

(Yang lab, unpublished)

MPK5 mutant



MPK1/MPK5 mutant



Transgene-free Mutation of AS1 for Potential Reduction of Acrylamide Levels in Potato









Transient expression

Callus formation w/o antibiotic selection

Regeneration



AS1 encodes asparagine synthase 1





Transgene-free, Anti-browning Mushroom to Extend Shelf Life and Facilitate Mechanical Harvesting



(Yang lab, unpublished)

Before 55 C treatment



4 hours after 55 C treatment





Near-term Applications for Crop Breeding

- 1. Targeted deletion of single or multiple genes for transgene-free, mutational breeding in various crop species.
- 2. Site-specific integration and precise gene stacking for transgenic or cisgenic breeding.
- 3. Multiplex editing to create allelic variation at quantitative trait loci to improve multiple agronomic traits (yield, quality, disease resistance and abiotic stress tolerance).

			Amino Acid Position				
Rice Variety	Resistant with AVR-Pita Fungus	Rice Type	6	148	158	176	918
Yashiro-mochi	Yes	Japonica	1	R	Н	D	Α
Tetep	Yes	Indica	1	R	н	D	Α
C101A51	No	Indica	1	R	Н	D	S
Tsuyuake	No	Japonica	S	S	Q	V	S
Table after Bry	an et al. (2000), The Plant Cell						

Genome editing in rice for S918A conversion in Pita

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