



RNA guided genome editing for target gene mutations in wheat

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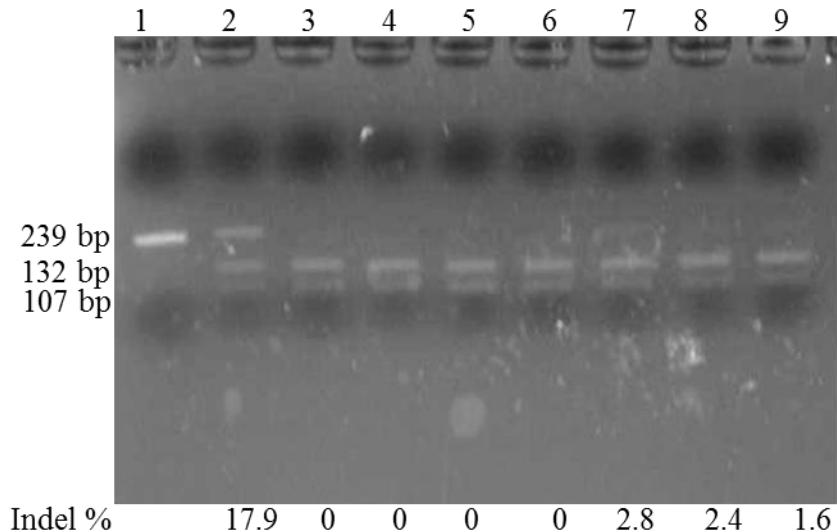


Figure S1 Sequence specificity analysis of CRISPR-Cas system by using different mutated cgRNAs. List of mutant cgRNA is given in Supplementary table 2. Normal and mutant cgRNAs (targeting protospacer 1 of *inox* gene) were co-expressed with Cas9 in suspension cells of *T. aestivum*. Targeted region was amplified, and digested with BsgI restriction enzyme (BsgI restriction site is present at cleavage position in *inox* protospacer1). BsgI could not digest the mutated DNA amplicon. Lane 1 undigested amplicon and lane 2-9 digested with BsgI. Lane 2, mutated with normal cgRNA; 3, wild type amplicon; 4-9, mutated with mutant cgRNA 1, 6, 9, 11, 12 and 13, respectively. Figure shows that mutations at 3' end of target binding region of cgRNA upto 12th bases completely abolished the cleavage activity. However mutations were detected in case of 5' end mutant cgRNA.

File S1

Partial sequence of (A) *inositol oxygenase (inox)* and (B) *phytoene desaturase (pds)* genes of wheat, and (C) *pds* gene of *Nicotiana benthamiana* used to decide the target for modification by CRISPR-Cas System. Targeted regions are shown in blue font and PAM in red. Primer used for amplification of gene after editing is shown in green.

(A)

Forward primer →

GCTCGACGGCGGCTTCACCGTGCCGGACTCCAACGCCTCGGCCACACCTT**CAGGGACTACGACGCGGAG**TCGGA BASE PAIRS
CGAGCTGCCGCCGAAGTGGCACGGCCTGAGGTTGCGGAAGCCGGTGTGGAAGTC CCTGATGCTGCGCCTCAGCCT 1 TO 75

Protospacer 1

GC₃GAAGAACGGTGGAGGAGTTCTACAGCGTAACCACATCAACC**AGACGTACGAGTTGTGCAGCGG**ATGCG BASE PAIRS
CGCCTTCTTGCCACCTCCTCAAGATGTCGCACTTGGTGTAGTTGGTCTGCATGCTCAAACACGTCGCCTACGC 76 TO 150

Protospacer 2

GGACGCATACGGCGGCTGG**CAAGACGGAGATGAGCATCTGG**AGTGCATCGAGCTGCTAACGAGTTCATCGA BASE PAIRS
CCTGCGTATGCCGCCGACCTGTTCTGCCTACTCGTAGACCCTCACGTAGCTGACGAGTTGCTCAAGTAGCT 151 TO 225

CGACAGTGACCCGACCTGGACATGCCGAGATCGAGCACCTCCTCAAACCGCCGAGGCCATCCGCAAGGACTA BASE PAIRS
GCTGTCACTGGGCTGGACCTGTACGGCGTCTAGCTCGTGGAGGAG**GT**TTGGCGCTCCGGTAGGCGTTCTGAT 226 TO 300

← Reverse primer

Yellow highlighted region is the site for BsgI used for digestion of amplified DNA.

(B)

Forward primer

GCTGAGCTTGGTATTAGTGATCGCTTGCAATGGAAGGAACACTCCATGATATTTGCCATGCCAAACAAACCAGGA BASE PAIRS
CGACTCGAACATAATCACTAGCGAACGTTACCTCCTGTGAGGTACTATAAACGGTACGGTTGTTGGTCCT 1 TO 75

Protospacer 1

Protospacer 2

GAATACAGCCGTTTGATTTCAGAGACTTGCCGGCGCCCTTAAATGGAGTGTGGGCCATACTGAAAAACAAT BASE PAIRS
CTTATGTCGGCAAAACTAAAAGGTCTCTGAAACGGCCGCGGAATTACCTCACACCCGGTATGACTTTGTTA 76 TO 150

GAAATGCTTACTTGGCCGGAGAAGGTGAAG BASE PAIRS
CTTTACGAATGAACCGGCCTTCCACTTC 151 TO 180

Reverse primer

(C)

Forward primer

GAATTGGTTTTGCACCTGCAGAAGAGTGGATAAAATCGCAGTGACTCTGAAATTATTGATGCTACAATGAAGGAA BASE PAIRS
CTTAACCAAAAACGTGGACGTCTTCACCTATTAGCGTCACTGAGACTTTAAACTACGATGTTACTTCCTT 1 TO 75

Protospacer 1

CTAGCAAAGCTTTCCCTGATGAAATTTCGGCAGATCAGAGCAAAGCAAAATATTGAAGTATCATGTTGTCAA BASE PAIRS
GATCGTTCGAAAAGGGACTACTTAAAGCCGTAGTCTCGTTCTGTTTATAACTTCATAGTACAACAGTTT 76 TO 150

ACTCCAAGGTCTGTTATAAAACTGTGCCAGGTTGTGAACCCTGCCGCCCTGCAAAGATCCCCTATAGAGGGG BASE PAIRS
TGAGGTTCCAGACAAATATTGACACGGTCCAACACTTGGGACGGCCGGGAACGTTCTAGGGATATCTCCCC 151 TO 225

Reverse primer

File S2

Chimeric guide RNA (cgRNA) for targeting (A) *inositol oxygenase (inox)* and (B) *phytoene desaturase (pds)* genes of wheat, and (C) *pds* gene of *Nicotiana benthamiana*. (i) cgRNA for protospacer 1, (ii) cgRNA for protospacer 2 and (iii) cgRNA for targeting both protospacer 1 and 2. Target region is given in blue font and guide RNA scaffold in red font. Restriction site SpeI (highlighted in yellow) was used for ligation of the two cgRNAs.

(A)

(i)

NNNNNAGACGTACGAGTTGTGCAGGTTTAGAGCTAGAAATAGCAAGTAAAATAAGGCTA
GTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTNNNNNNNN

(ii)

NNNNNCAAGACGGAGATGAGCATCTGTTTAGAGCTAGAAATAGCAAGTAAAATAAGGCTA
GTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTNNNNNN

(iii)

NNNNNAGACGTACGAGTTGTGCAGGTTTAGAGCTAGAAATAGCAAGTAAAATAAGGCTA
GTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTACTAGTNNNNCAAGACGGAG
ATGAGCATCTGTTTAGAGCTAGAAATAGCAAGTAAAATAAGGCTAGTCGGTTATCAACTT
GAAAAAGTGGCACCGAGTCGGTGCTTTNNNNNN

(B)

(i)

NNNNNTTGCATGCCAACAAACCGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTA
GTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTNNNNNNNN

(ii)

NNNNNGCGCCCTAAATGGAGTGTGTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTA
GTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTNNNNNN

(C)

(i)

NNNNNGCTTTCCCTGATGAAATTGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTA
GTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTNNNNNNNN

(ii)

NNNNNATCATGTTGTCAAAACTCCAGTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTA
GTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTNNNNNN

Table S1 Plant expression vectors used in the study.

Vector	Detail	Target gene
pCas9	Expression of FLAG tag and NLS containing Cas9 protein.	NA
pTpds1	Expression of crRNA targeting protospacer 1 of <i>Nicotiana benthamiana</i> <i>phytoene desaturase</i> (<i>pds</i>) gene	<i>N. benthamiana pds</i> gene
pTpds2	Expression of crRNA targeting protospacer 2 of <i>N. benthamiana pds</i> gene	<i>N. benthamiana pds</i> gene
pCtpds1	Co-expression of Cas9 and crRNA targeting protospacer 1 of <i>N. benthamiana pds</i> gene	<i>N. benthamiana pds</i> gene
pCtpds2	Co-expression of Cas9 and crRNA targeting protospacer 2 of <i>N. benthamiana pds</i> gene	<i>N. benthamiana pds</i> gene
pCinox1	Co-expression of Cas9 and crRNA targeting protospacer 1 of <i>T. aestivum inositol oxygenase (inox)</i> gene	<i>T. aestivum inox</i> gene
pCinox2	Co-expression of Cas9 and crRNA targeting protospacer 2 of <i>T. aestivum inox</i> gene	<i>T. aestivum inox</i> gene
pCwpds1	Co-expression of Cas9 and crRNA targeting protospacer 1 of <i>T. aestivum pds</i> gene	<i>T. aestivum pds</i> gene
pCwpds2	Co-expression of Cas9 and crRNA targeting protospacer 2 of <i>T. aestivum pds</i> gene	<i>T. aestivum pds</i> gene
pCinox12	Co-expression of Cas9 and duplex crRNAs targeting protospacer 1 and 2 of <i>T. aestivum pds</i> gene	<i>T. aestivum pds</i> gene
pCpin1	Co-expression of Cas9 and duplex crRNAs targeting protospacer 1 of both <i>inox</i> and <i>pds</i> gene of <i>T. aestivum</i> .	<i>T. aestivum inox</i> and <i>pds</i> gene

Table S2 Specificity analysis of cgRNA. Table shows average mutation percentage at targeted locus with different mutant cgRNA.

	Sequence	Average mutation (%)
Normal cgRNA	AGACGTACGAGTTTGCA	17.9
Mutant cgRNA	1 AGACGTACGAGTTTGCA A	0
	2 AGACGTACGAGTTTGCA G	0
	3 AGACGTACGAGTTTGCA C	0
	4 AGACGTACGAGTTTGCA T	0
	5 AGACGTACGAGTTGCAG TTT	0
	6 AGACGTACTAGTTGCAG	0
	7 AGACGTACGAGTTGCAG AA	0
	8 AGACGTACGAGTTGCAG CTAG	0
	9 AGACGTACAAGTTA TGCAG	0
	10 AGACGTACGAGT GGGTGCAG	0
	11 TGACGTACGAGTTGCAG	2.8
	12 CAACGTACGAGTTGCAG	2.4
	13 CAGCGTACGAGTTGCAG	1.6
	14 AGACAGTCGAGTTGCAG	0
	15 AGACTGCA GAGTTGCAG	0