

Supplementary material

CRISPR/Cas9-Mediated Resistance to Wheat Dwarf Virus in Hexaploid Wheat (*Triticum aestivum* L.)

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Table S1 PCR Primers used and their applications

| Primer name | Primer sequence (5'-3') | Application |
|--------------------|--|---|
| gWDV-LIR-F1 | actcgTATGCTCTACCTGCGTGG | To clone WDV LIR-sgRNA |
| gWDV-LIR-R1 | aaacCCACGCAGGGTAGAGCATAc | |
| gWDV-CP-F1 | actcgACAAGGACTCCCCGAGGTA | To clone WDV CP/MP-sgRNA |
| gWDV-CP-R1 | aaacTACCTCGGGAGTCCTTGTtc | |
| TaCas9-F1 | GGTCTGGAGGATGCCCTTCT | PCR detection for Cas9 |
| TaCas9-R1 | GGCTATCGTGGACCTCCTGT | |
| WDV-Rep-F | TGGTCTCATGGCAAATGAGTG | PCR detection for Rep of WDV |
| WDV-Rep-R | TCCATCACCAATCCCAATGCC | |
| WDV-Rep-Q4-F | TGAGTGGGGAACATTCGTGG | RT-qPCR for WDV accumulation |
| WDV-Rep-Q4-R | GAAATAGATGGCGTGCCGTG | |
| LIR-Q1-F | AAAACCCACGCAGGGTAGAG | RT-qPCR for sgRNA-LIR expression |
| LIR-Q1-R | CATCGGCTAGCGAAAGGGAA | |
| CP-Q2-F | GCGCGTGGCTTATAAACTGG | RT-qPCR for sgRNA-CP/MP expression |
| CP-Q2-R | ACTATTTTGGGCCACACCGA | |
| GAPDH-Q-F | ACTTCCAGGGTGACAACAGG | RT-qPCR for GAPDH expression |
| GAPDH-Q-R | GTGCTGTATCCCCACTCGTT | |
| WDV-CP-Det-F | TGTCCGATGCATCAGCTCCGT | Amplifying WDV probe for northern blot |
| WDV-CP-Det-R | TAACACGCGTGCGTATAGGCA | |
| CP-Hi-F2 | GGAGTGAGTACGGTGTGCAGGACCGAGG AAATTGGTTACG | Hi-TOM sequencing for CP/MP target site |
| CP-Hi-R2 | GAGTTGGATGCTGGATGGCGGCCTTACCC TGAGCAAAA | |
| LIR-Hi-F1 | GGAGTGAGTACGGTGTGCAACAGCAGCG ATGTAGAGG | Hi-TOM sequencing for LIR target site |
| LIR-Hi-R1 | GAGTTGGATGCTGGATGGGGACACATTGC ATTTGCAGTG | |
| WDV-554-F | TGTGTTTGCATCGGAGTCAACC | Mutation analysis in LIR target site |
| WDV-554-R | GCCCACACGATTTCGCTACG | |
| WDV-773-F | GTAGGCGTTGCTTGGCTTGC | Mutation analysis in CP/MP target site |
| WDV-773-R | TAATGTGCGCTATCTTGCCGTC | |

(A)



WT L69-6-1 L69-7-1 L69-10-1

(B)



WT C41-2-1 C41-6-1 C41-8-1 C41-9-1 C41-10-1

Figure S1. Symptoms in the transgenic T₂ lines and control plants at 30 dpi. WT, wild-type plant.

| Line | Total ratio | | Indels | Ratio | |
|-----------------------------|-------------|--------|---|-------|--------|
| V _{CP} -line41-6 | 1 | 48.34% | C A G A T T A A A T G G T G A C C A A C A A G G A C T C C C G A G G T A A G G G T A A G C G G A A G A T G G A A G | WT | |
| | | | C A G A T T A A A T G G T G A C C A A C A A G G A C T C - - - - - G T A A G G T A A G C G G A A G A T G G A A G | -5 | 41.08% |
| | | | C A G A T T A A A T G G T G A C C A A C A A G G A C - - - - - A G G T A A G G T A A G C G G A A G A T G G A A G | -5 | 7.26% |
| | | | C A G A T T A A A T G G T G A C C A A C A A G G A C T C C C G - - G T A A G G T A A G C G G A A G A T G G A A G | -2 | 9.91% |
| | | | C A G A T T A A A T G G T G A C C A A C A A G G A C T C C C G - G G T A A G G T A A G C G G A A G A T G G A A G | -1 | 2.75% |
| | | | C A G A T T A A A T G G T G A C C A A C A A G G A C T C C C G - G G T A A G G T A A G C G G A A G A T G G A A G | -1 | 2.23% |
| V _{LIR} -line69-10 | 5 | 39.33% | G G T G T G C C A G A A A A C T C T A T G C T C T A C C T G C G T G G A G G T G T G A A T T C T G C A C A C T G | WT | |
| | | | G G T G T G C C A G A A A A C T C T A T G C T C T A C C T G C - T G G A G G T G T G A A T T C T G C A C A C T G | -1 | 28.62% |
| | | | G G T G T G C C A G A A A A C T C T A T G C T C T A C C T G C - T G G A G G T G T G A A T T C T G C A C A C T G | -1 | 39.33% |

Figure S2. Hi-TOM sequencing analysis of sgRNA-Cas9-induced mutations in T2 progenies of lines C41-6 and L69-10. WT, Wild-type control, PAM is in red and gRNAs in purple. Black dashes denote nucleotide deletions. -/+ indicates deletion/insertion of nucleotides.