Supplemental Table S1. Ascorbate and glutathione redox states in Col-0 and *dhar* mutants.

Data show 100 x (reduced form/total) and are means of three biological replicates. No significant differences were observed in *dhar* mutants compared to Col-0 at $P < 0.05$.

	Ascorbate	Glutathione
Col-0	87 ± 1.25	91 ± 1.23
dhar1	86 ± 0.61	88 ± 1.07
dhar2	88 ± 1.65	90 ± 0.51
dhar3	89 ± 4.34	86 ± 1.18
dhar1 dhar2	86 ± 1.36	90 ± 2.34
dhar1 dhar3	85 ± 3.11	90 ± 2.09
dhar2 dhar3	86 ± 1.51	91 ± 1.43
dhar1 dhar2 dhar3	83 ± 1.53	88 ± 0.31

Supplemental Table S2. Ascorbate and glutathione redox states in Col-0, *cat2* and *cat2 dhar* mutants

Data show 100 x (reduced form/total) and are means of three biological replicates. *Indicates significant difference compared to Col-0 while $^{+}$indicates significant difference of *cat2 dhar* mutants compared to *cat2* at $P < 0.05$.

	Ascorbate	Glutathione
Col-0	89 ± 0.92	91 ± 2.67
cat2	85 ± 2.14	64 ± 0.82*
cat2 dhar1	84 ± 1.54*	59 ± 3.45*
cat2 dhar2	79 ± 1.21*	50 ± 2.21$^{*/+}$
cat2 dhar3	84 ± 2.05	61 ± 2.39*
cat2 dhar1 dhar2	82 ± 2.52	79 ± 2.02$^{*/+}$
cat2 dhar1 dhar3	82 ± 1.37*	58 ± 4.31*
cat2 dhar2 dhar3	84 ± 3.21	58 ± 2.93*
cat2 dhar1 dhar2 dhar3	80 ± 0.71*	86 ± 1.44^{+}

Supplemental Table S3. T2 segregation of DHAR-complemented lines growing in vitro on agar.

Transformed plants were identified *in vitro* based on their resistance (R) or sensitivity (S) to hygromycin.

Lines	Total	Hygromycin R	Hygromycin S	χ^2 ($P < 0.05$)
dhar1-1	120	86	34	0.40
dhar1-2	116	88	28	0.83
dhar2-1	117	85	32	0.56
dhar2-2	120	85	35	0.29
dhar3-1	129	88	41	0.08
dhar3-2	114	92	22	0.16

Supplemental Table S4. T2 segregation of lesion phenotypes in complemented lines growing in soil.

Data show numbers of plants showing either the *cat2* lesion phenotype or the *cat2 dhar1 dhar2 dhar3* phenotype in two independent experiments performed on plants growing in soil.

Expt 1		Phenotype		
Lines	Total	*cat2*	quadruple mutant	χ^2 ($P < 0.05$)
dhar1-1	44	33	11	1.00
dhar1-2	56	43	13	0.76
dhar2-1	47	36	11	0.80
dhar2-2	50	38	12	0.87
dhar3-1	46	35	11	0.86
dhar3-2	48	36	12	1.00

Expt 2		Phenotype		
Lines	Total	*cat2*	quadruple mutant	χ^2 ($P < 0.05$)
dhar1-1	47	35	12	0.93
dhar1-2	52	41	11	0.52
dhar2-1	57	43	14	0.94
dhar2-2	39	29	10	0.93
dhar3-1	51	39	12	0.81
dhar3-2	45	33	12	0.80

Supplemental Table S5. Glutathione redox states in Col-0 and *dhar* mutants after treatment with 3-amino-1,2,4-triazole.

Data show 100 x (reduced form/total) and are means of three biological replicates. *Indicates significant difference compared to Col-0 at $P < 0.05$.

Col-0	41 ± 3.61
dhar1	41 ± 5.00
dhar2	36 ± 6.28
dhar3	27 ± 6.40
dhar1 dhar2	66 ± 0.87*
dhar1 dhar3	54 ± 5.77
dhar2 dhar3	39 ± 2.97
dhar1 dhar2 dhar3	84 ± 2.75*

Supplemental Table S6. DNA primer sequences used in this study.

Oligonucleotide	Sequence	Technique
For_CAT2	5’-CCCAGAGGTACCTCTTCTTCTCCCATG-3’	Genotyping
Rev_CAT2	5’-TCAGGGAACTTCATCCCATCGC-3’	Genotyping
For_DHAR1	5’-TTAGGTCCGTTCAGCCAAC-3’	Genotyping
Rev_DHAR1	5’-AAGCTCTCAGGGACAGACCAG-3’	Genotyping
For_DHAR2	5’-AATGGGTGGCTGATTCTGAC-3’	Genotyping
Rev_DHAR2	5’-GATCCACATCACGCATTCAC-3’	Genotyping
For_DHAR3	5’-GTTACTGACAATGGAGGAGAAG-3’	Genotyping
Rev_DHAR3	5’-GTGCCAAGGACAAATCTGC-3’	Genotyping
Lb1	5’-TGGACCGCTTGCTGCAACTCTC-3’	Genotyping
LB_Sail	5’-GAAATGGATAAATAGCCTTGCTTCC-3’	Genotyping
For_Actin2	5’-TTCCCTCAGCACATTCCAGCAG-3’	RT-PCR
Rev_Actin2	5’-TTAACATTGCAAAGAGTTTCAAGG-3’	RT-PCR
For_CAT2	5’-GTGCTGACTTTCTCCGAGCT-3’	RT-PCR
Rev_CAT2	5’-CCTGAACCATCCATGTGCCT-3’	RT-PCR
For_DHAR1	5’-TGGCTCTGGAAATCTGTG-3’	RT-PCR
Rev_DHAR1	5’-AGCAAGGCATGTTCAGATCC-3’	RT-PCR
For_DHAR2	5’-AATGGGTGGCTGATTCTGAC-3’	RT-PCR
Rev_DHAR2	5’-CCGCAACCACAATCTCTTTC-3’	RT-PCR
For_DHAR3	5’-GTTACTGACAATGGAGGAGAAG-3’	RT-PCR
Rev_DHAR3	5’-GTGCCAAGGACAAATCTGC-3’	RT-PCR
For_Actin2	5’-CTGTACGGTAACATTGTGCTCAG -3’	RT-qPCR
Rev_Actin2	5’-CCGATCCAGACACTGTACTTCC -3’	RT-qPCR
For_RCE1	5’-CTGTTCACGGAACCCAATTC-3’	RT-qPCR
Rev_RCE1	5’-GGAAAAAGGTCTGACCGACA-3’	RT-qPCR
For_PR1	5’-AGGCTAACTACAACTACGCTGCG-3’	RT-qPCR
Rev_PR1	5’-GCTTCTCGTTCACATAATTCCCAC-3’	RT-qPCR

For_PR2	5’-TCAAGGAGCTTAGCCTCACC-3’	RT-qPCR
Rev_PR2	5’-CGCCTAGCATCCCGTAGC-3’	RT-qPCR
For_ICS1	5’-TTGGTGGCGAGGAGAGTG-3’	RT-qPCR
Rev_ICS1	5’-CTTCCAGCTACTATCCCTGTCC-3’	RT-qPCR
Amplification with stop codon		
For_SalI_DHAR1	5’-GCGCGTCGACAAATGGCTCTGGAAATCTGTGTG-3’	Cloning
Rev_DHAR1_stop_NotI	5’-TTTTGCGGCCGCTTTCAAGGGTTAACCTTGGGAG-3’	Cloning
For_SalI_DHAR2	5’-ACGCGTCGACGTATGGCTCTAGATATCTGCGTGAAGG-3’	Cloning
Rev_DHAR2_stop_NotI	5’-ATTTGCGGCCGCTTTCACGCATTCACCTTCG-3’	Cloning
For_SalI_DHAR3	5’-ACGCGTCGACGTATGATAAGCCTTAGGTTTCAACCAAGC-3’	Cloning
Rev_DHAR3_stop_NotI	5’-ATTTGCGGCCGCTTTTAACCCATAACCTTTGGTCTCC-3’	Cloning
Amplification without stop codon		
For_SalI_DHAR1	5’-GCGCGTCGACAAATGGCTCTGGAAATCTGTGTG-3’	Cloning
Rev_DHAR1_NotI	5’-TTTTGCGGCCGCTTAGGGTTAACCTTGGGAG-3’	Cloning
For_SalI_DHAR2	5’-ACGCGTCGACGTATGGCTCTAGATATCTGCGTGAAGG-3’	Cloning
Rev_DHAR2_NotI	5’-ATTTGCGGCCGCTTCGCATTCACCTTCGATTC-3’	Cloning
For_SalI_DHAR3	5’-ACGCGTCGACGTATGATAAGCCTTAGGTTTCAACCAAGC-3’	Cloning
Rev_DHAR3_NotI	5’-ATTTGCGGCCGCTTACCCATAACCTTTGGTCTCC-3’	Cloning
For_pENTR2B	5’-CCAGGCATCAAACTAAGCAG-3’	Cloning
Rev_pENTR2B	5’-CTTGTGCAATGTAACATCAGAG-3’	Cloning