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Mutation of Arabidopsis HY1 causes UV-C hypersensitivity by impairing carotenoid and flavonoid biosynthesis and the down-regulation of antioxidant defence . Yanjie Xie, Daokun Xu, Weiti Cui, and Wenbiao Shen.

SUPPLEMENTARY DATA

Supplementary Table S1. The sequences of PCR primers for genotyping.

Primer name	Sequences (5'→3')
SALK_025840-LP	GGAAGAACAAGCAGGAGAA
SALK_025840-RP	TTAGCAACTGGTGGAATGA
SALK_034321-LP	GACTCAAAAGGTCAATCACA
SALK_034321-RP	TTTTACAGCAAGATAGCCAC
SALK_044934-LP	ATTGCAGTTTGCGTGTCTATT
SALK_044934-RP	GTTCTTTCTCCGATTTCTCCT
LBb1.3	ATTTTGCCGATTTCGGAAC

Supplementary Table S2. The sequences of PCR primers for real-time RT-PCR.

Primer name	Sequences (5'→3')
HY1-F	CGTCCTGTTGCTAAATG
HY1-R	TTCCAGCCCCGTGTTCT
HO-2-F	TTGCGGTTATGGTGGGTATC
HO-2-R	TCCCGACTCCAGTGCTCC
HO-3-F	CCACTTTCCAGCGAGCACA
HO-3-R	ATAGCCGCCGCAGTCAC
HO-4-F	TCTTGCCGCTTTCCTGC
HO-4-R	GCTGCTGCCACAACATTC
GPS-F	AGTATGGGAGGAATCTGGGTTT
GPS-R	ACTCTTCCATGGCAAAGAGGAT
PSY-F	GACACCCGAAAGGCGAAAGG
PSY-R	CAGCGAGAGCAGCATCAAGC
PDS1-F	AAGTAGAAGACGCAGAGTCA
PDS1-R	ATCAGAGCCAGATGTTGTAG
ZDS-F	AGATAGAGGTGGCAGAATCC
ZDS-R	GGTGTTAGAACGCACTGAAG
CHS-F	GGCTCAGAGAGCTGATGGAC
CHS-R	CGTTTCCGAATTGTCGACTT
CHI-F	TCAAACTGGGAACTACGTCTCTCGT
CHI-R	ATTTCCAACTGAAGAAGCGGCGG
F3H-F	GACAAAAACATCATACTCCACCTGT
F3H-R	CCAACAATGTATGTATGCCACTG
FLS-F	GGGATTCTCTCGGATGGATT
FLS-R	TGAGCCGGTACACCTAAAGC
HY5-F	CAGGCGACTGTCGGAGAAAGTCAAAGG
HY5-R	TCAACAACCTCTTCAGCCGCTTGTTCTC

HYH-F	GCCTCAAGAGATTATTGAGGA
HYH-R	CTCTTGATTCCAAATCACTCAC
MYB11-F	CCCAAAAATGCCGGGCTAAAGAGATG
MYB11-R	CTTCTTCGGGAGTTATGTTT
MYB12-F	CACTTTGGGAAACAGGTGGTCACT
MYB12-R	GTTGTGGAGTTTACGGCTGA
CSD1-F	TGATGGAACTGCCACCTTCACA
CSD1--R	ATGGCCTCCCTTTCCGAGGT
CAT1-F	CGCCATGCCGAAAAATACCC
CAT1-R	CTTGCCTGTCTGAATCCCAGGAC
CAT2-F	TCCGCCTGCTGTCTGTTCTG
CAT2-R	TGGGTCGGATAGGGCATCAA
FSD1-F	GCTCGGCTCTTTCCCATTGC
FSD1-R	CAGCTTCCCAAGACACAAGATTGG
cAPX1-F	ACTCTGGGACGATGCCACAAG
cAPX1-R	TCTCGACCAAAGGACGGAAAA
cAPX2-F	TGGTCGGATGGGACTCAAT
cAPX2-R	AAGAGCCTTGTCGGTTGGT
actin2/7-F	TCGTTTCGCTTTCCTTAG
actin2/7-R	CTTCACCATTCCAGTTCC

Figure S1.

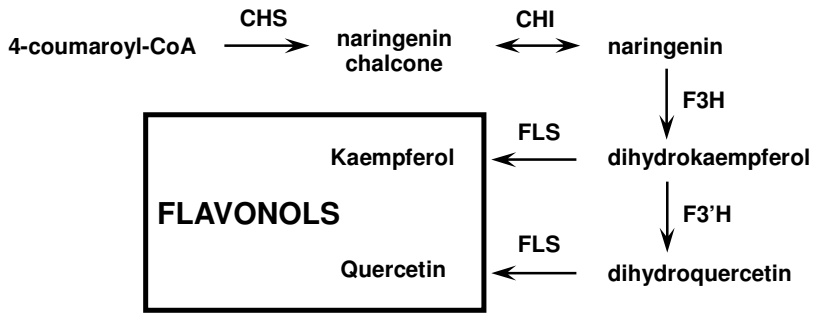

Figure S1. Scheme of the flavonoid biosynthetic pathway in *Arabidopsis* (Qin *et al*. 2007; Buer *et al*. 2010; Castells *et al*. 2010).

Figure S2.

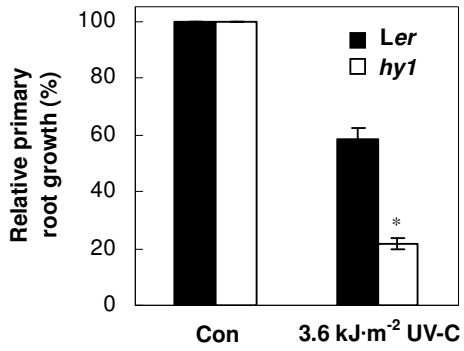

Figure S2. Primary root growth of wild-type (L*er*) and *hy1* mutant seedlings in response to 3.6 kJ·m^{-2} UV-C irradiation. After exposed to 3.6 kJ·m^{-2} UV-C and then transferred to normal growth condition for 5 days, primary root growth rate of each ecotype was measured, taking growth rate of each ecotype grown under MS medium (Con) as 100% (a). Data were means ± SE from three independent experiments. Bars with an asterisk were significantly different in comparison with the wild-type at $P<0.05$ according to the *t*-test.

Figure S3.

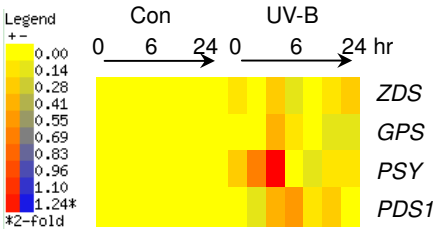

Figure S3. Representation of carotenoid biosynthetic genes in Arabidopsis seedling root tissues upon UV-B irradiation. The data were from microarray analyses from AtGenExpress-UV-B Stress. Left bar: induction scale. The experimental details can be accessed at the Botany Array Resource database (Toufighi *et al.*, 2005; http://www.bar.utoronto.ca/affydb/cgi-bin/affy_db_exprss_browser_in.cgi?pub=&dataset=atgenexp_stress).

Figure S4.

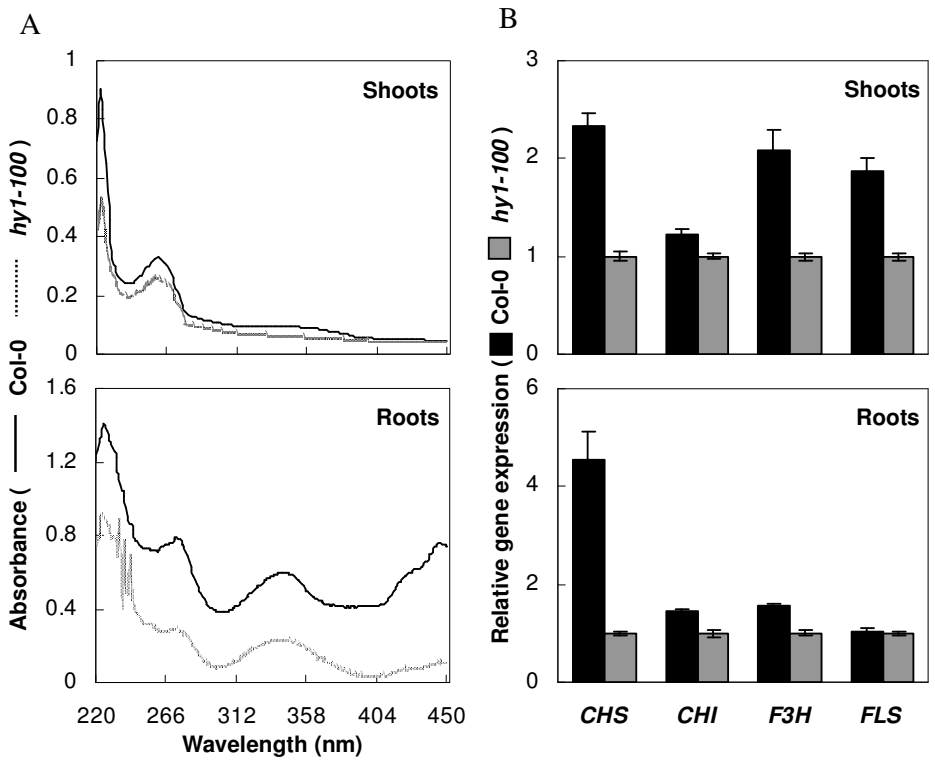

Figure S4. The *hy1-100* mutant under-produces UV-absorbing compounds. Profile of UV-absorbing compounds in shoot and root tissues of wild-type and the *hy1-100* mutant (A). Soluble pigments were methanol-extracted from equal amounts of fresh material and the absorbance was scanned from 220-450 nm. qRT-PCR analysis of genes, including *Chalcone Synthase* (*CHS*; At5g13930), *Chalcone Isomerase* (*CHI*; At3g55120), *Flavonol 3-Hydroxylase* (*F3H*; At3g51240), and *Flavonol Synthase* (*FLS*; At5g08640), encoding representative enzymes of the flavonoid biosynthetic pathway in wild-type and *hy1-100* mutant shoot and root tissues (B). Data were means ± SE from three independent experiments. For each gene, the transcript levels in the *hy1-100* mutant were arbitrarily set to 1.

Figure S5.

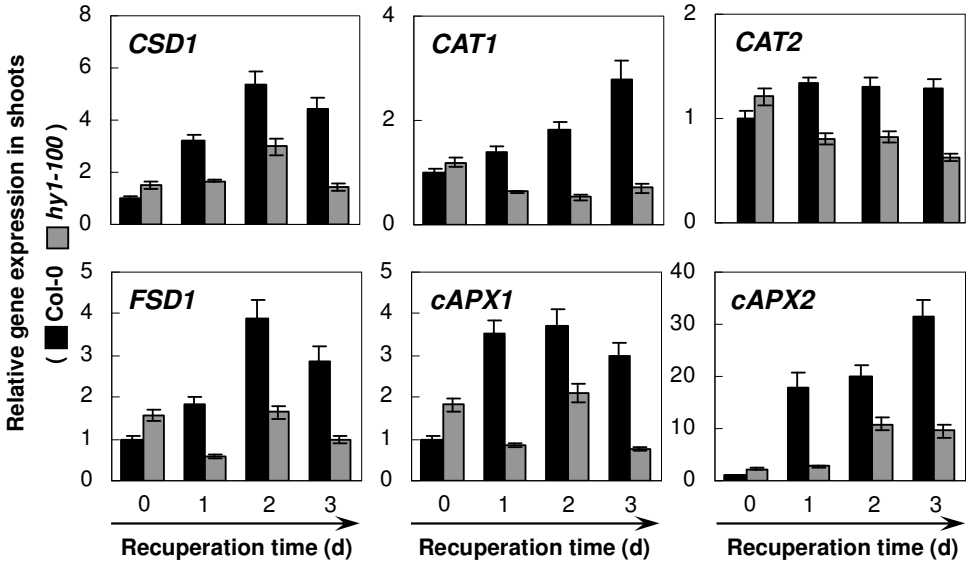

Figure S5. Effects of 3.6 kJ·m^{-2} UV-C on antioxidant defence genes expression. After UV-C irradiation, 5-d-old seedlings of wild-type and the *hy1-100* mutant were recuperated under normal growth condition, and transcript levels of *Copper/zinc Superoxide Dismutase* (*CSD1*; At1g08830), *Catalase1* (*CAT1*; At1g20630), C*catalase2* (*CAT2*; At4g35090); *Fe Superoxide Dismutase1* (*FSD1*; At4g25100), *cytosolic Ascorbate Peroxidase1* (*cAPX1*; At1g07890); and *cytosolic Ascorbate Peroxidase2* (*cAPX2*; At3g09640) of shoot tissues of each ecotype were analyzed by real-time PCR at the indicated times. Expression levels of each gene were presented relative to Col-0 samples at 0 d. Data were means ± SE from four independent experiments.