

Supporting Information

Ramel et al. 10.1073/pnas.1115982109

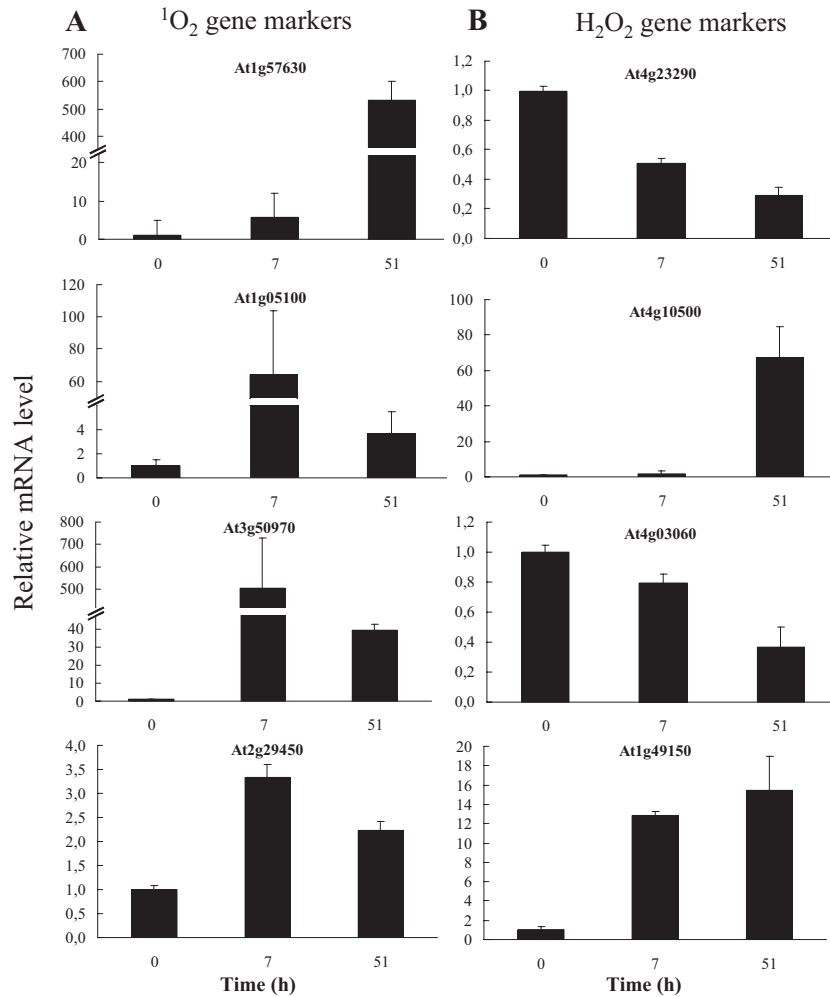


Fig. S1. Effects of high light stress on the changes of transcript levels of $^1\text{O}_2$ and H_2O_2 gene markers in *Arabidopsis* leaves. Transcript levels, measured by qRT-PCR of $^1\text{O}_2$ gene markers [Disease Resistance Protein (At1g57630), Mitogen activated protein kinase kinase kinase 18 (*MAPKKK18*, At1g05100), Toll-Interleukin-Resistance domain-containing protein (At3g50970), and GST 103-1A (*GSTU5*, At2g29450)] (A) and H_2O_2 gene markers [Cysteine-rich receptor-like protein kinase 21 (*CRK21*, At4g23290), Oxidoreductase (At4g10500), 2-oxoglutarate-dependent dioxygenase (*OAP2*, At4g03060), and Hypothetical protein (At1g49150)] (B) in *Arabidopsis* leaves. Data are expressed in relative values normalized to the value at time 0. Data are mean values of four to five independent measurements + SD.

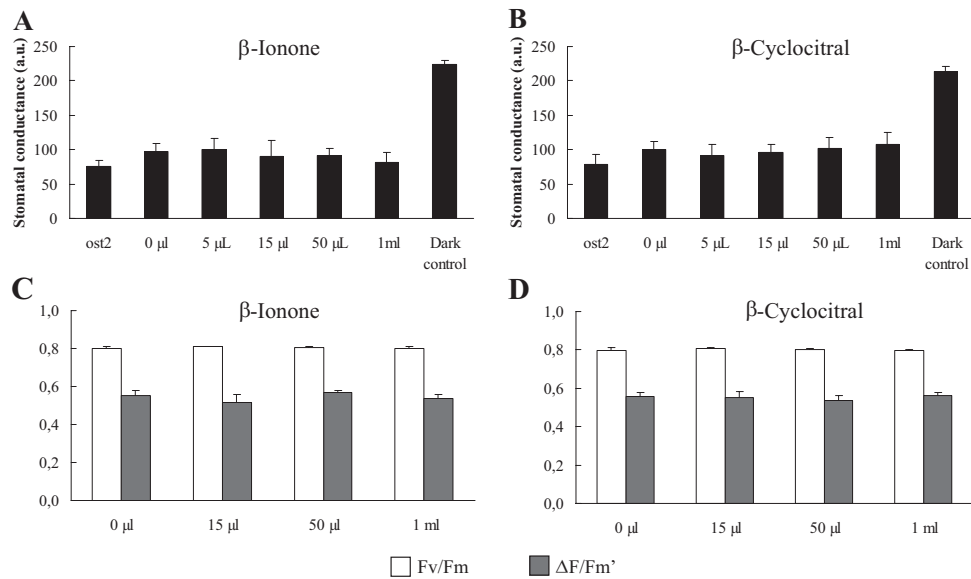


Fig. S2. Effects of β -ionone and β -cyclocitral treatments on stomatal conductance and photosynthetic electron transport. (A and B) Relative stomatal aperture in leaves of *Arabidopsis* plants exposed to β -ionone (A) and β -cyclocitral (B). The *Arabidopsis* mutant *ost2* (with stomata always open) and dark-adapted WT *Arabidopsis* plants (with closed stomata) are taken as references (maximal and minimal stomatal conductance, respectively). (C and D) Maximal efficiency of PSII photochemistry measured in the dark by the Fv/Fm chlorophyll fluorescence parameter (white bars) and efficiency of photosynthetic electron transport measured in the light ($200 \mu\text{mol m}^{-2} \text{s}^{-1}$) by the $\Delta F/Fm'$ chlorophyll fluorescence parameter (gray bars), following exposure to β -ionone (C) and β -cyclocitral (D). Data are mean values of at least 10 measurements + SD.

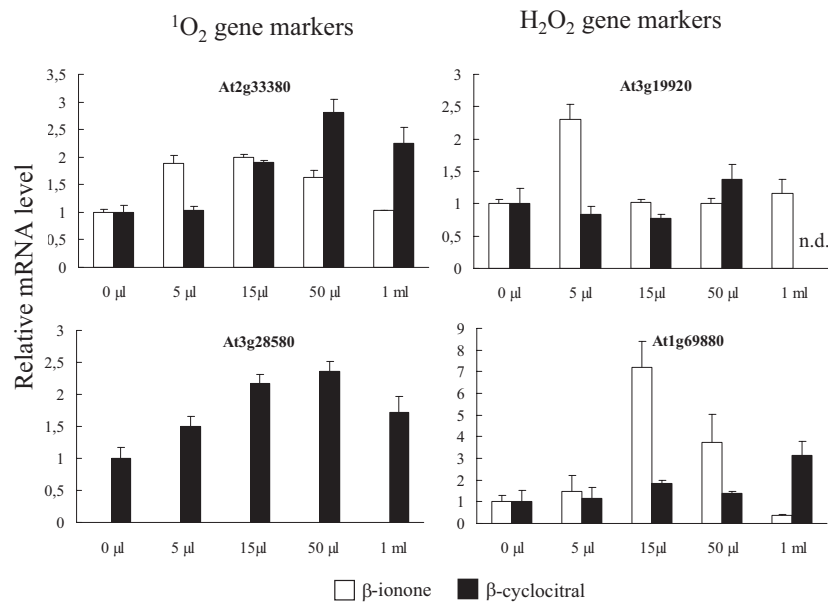


Fig. S3. Changes in the transcript levels of $^1\text{O}_2$ and H_2O_2 gene markers in *Arabidopsis* leaves exposed for 4 h to different amounts (0, 5, 15, 50 μL , and 1 mL) of β -ionone (open bars) or β -cyclocitral (filled bars) in an airtight box under a photon flux density of $60 \mu\text{mol photons m}^{-2} \text{s}^{-1}$. Transcript levels of two $^1\text{O}_2$ gene markers [Calcium binding protein (*RD20*, At2g33380) and AAA-type ATPase family protein (At3g28580)] and two H_2O_2 gene markers [hypothetical protein (At3g19920), thioredoxin H8 (*TH8*, At1g69880)] were measured. The effect of β -ionone was not tested on At3g28580. Data are expressed in relative values normalized to the value at time 0. Data are mean values of four to five independent measurements + SD. n.d., not determined.

Table S1. Functional classification of the genes induced by β -cyclocitral

Functional category	Category no.	Subcategory	Cyclo matches, %	Genome matches, %	P values	
Metabolism	1		26.6	17.3	4.85e-05	
	01.05.02	Sugar, glucosides, polyols and carboxylate metabolism	6.22	3	3.02e-03	
	01.05.02.01	Nucleotide-sugar metabolism	4.15	0.65	4.77e-07	
	1.2	Secondary metabolism	7.26	1.49	3.39e-09	
	01.20.05	Metabolism of acetic acid derivatives	1.73	0.08	3.05e-06	
	01.20.23	Metabolism of secondary products derived from L-methionine	1.03	0.09	2.54e-03	
	01.20.38	Metabolism of toxins/drugs	2.42	0.16	5.40e-07	
Protein with binding function or cofactor requirement	16		28	24.7	1.09e-01	
	16.17	Metal binding	9.34	4.56	3.64e-04	
	16.25	Oxygen binding	3.80	0.82	3.18e-05	
Cellular transport, transport facilities and transport routes	20		17.9	8.51	1.99e-07	
	20.01	Transported compounds	15.9	6.65	3.38e-08	
	20.01.01	Ion transport	4.15	1.61	2.74e-03	
	20.01.01.01	Cation transport	3.46	1.24	3.65e-03	
	20.01.01.07.01	Nitrate transport	0.69	0.03	4.40e-03	
	20.01.15	Electron transport	7.26	2.52	1.65e-05	
	20.01.27	Drug/toxin transport	1.38	0.22	4.13e-03	
	20.01.28	Hormone transport	1.03	0.04	3.49e-04	
	20.03	Transport facilities	4.84	2.11	3.59e-03	
	20.03.02	Carrier-driven transport	3.80	0.58	1.16e-06	
	20.03.02.02	Symporter	1.38	0.13	6.51e-04	
	20.03.02.03	Antiporter	2.42	0.45	3.47e-04	
	Cell rescue, defense and virulence	32		15.2	5.01	5.02e-11
		32.01	Stress response	8.99	2.92	4.77e-07
32.01.01		Oxidative stress response	3.46	0.70	4.18e-05	
32.07		Detoxication	4.15	0.93	2.01e-05	
32.07.07		Oxygen and radical detoxication	4.15	0.91	1.67e-05	
32.07.07.03		Glutathione conjugation reaction	3.11	0.20	6.04e-09	
Interaction with the environment	34		14.8	5.81	1.45e-08	
	34.11	Cellular sensing and response to external stimulus	14.5	5.24	2.20e-09	
	34.11.03	Chemoperception and response	11.7	2.95	9.04e-12	
	34.11.03.12	Water response	2.76	0.41	3.07e-05	
Systemic Interaction with the environment	36		10	2.66	1.16e-09	
	36.20	Plant fungal specific systemic sensing and response	8.30	2.43	2.11e-07	
	36.20.18	Plant hormonal regulation	7.61	2.07	1.97e-07	
	36.20.18.05	Abscissic acid response	3.11	0.56	4.26e-05	
	36.20.18.99	Other plant signaling molecules response	4.15	0.69	9.31e-07	
	36.25	Animal specific systemic sensing and response	2.42	0.37	1.15e-04	
	36.25.16	Immune response	2.42	0.35	7.48e-05	
	36.25.16.08	Response to wounding	2.07	0.28	1.68e-04	

Functional categories were defined by using MIPS Functional Catalogue (mips.helmholtz-muenchen.de/proj/funcat/DB). Only the data with a P value ≥ 0.005 are shown.

Table S2. Functional classification of the genes repressed by β -cyclocitral

Functional category	Category no.	Subcategory	Cyclo matches, %	Genome matches, %	P values
Cell rescue, defense and virulence	32		13.6	5.01	1.46e-03
	32.01	Stress response	11.3	2.92	2.52e-04
	32.01.06	Cold shock response	4.54	0.58	1.75e-03
Interaction with the environment	34		19.3	5.81	1.08e-05
	34.11	Cellular sensing and response to external stimulus	18.1	5.24	1.21e-05
	34.11.03	Chemoperception and response	10.2	2.95	1.18e-03
	34.11.09	Temperature perception and response	5.58	0.92	1.37e-03
Cell fate	40		6.81	1.58	2.77e-03
Development	40.01.03	Directional cell growth	4.54	0.57	1.71e-03
	41		5.68	3.68	2.24e-01
Biogenesis of cellular components	41.03.08	Fruit development and ripening	4.54	0.63	2.45e-03
	42		10.2	5.46	5.11e-02
Subcellular localization	42.01	Cell wall	9.09	0.92	1.64e-06
	70		40.9	37	2.60e-01
	70.01	Cell wall	11.3	1.51	9.14e-07

Functional categories were defined by using MIPS Functional Catalogue (mips.helmholtz-muenchen.de/proj/funcat/DB). Only the data with a P value ≥ 0.005 are shown.

Table S3. Transcript levels of $^1\text{O}_2$ specific genes identified by Gadjev et al. (1) induced by β -cyclocitral

Probe set	Locus identifier	Fold change		Description
		β -Cyclocitral	<i>flu</i>	
265194_at	At1g05010	2.21	5.248	EFE (ethylene forming enzyme)
262803_at	At1g21000	2.21	5.807	Unknown protein
255967_at	At1g22280	1.56	5.064	Protein phosphatase 2C, putative/PP2C, putative
245768_at	At1g33590	2.07	6.818	Disease resistance protein-related/LRR protein-related
259548_at	At1g35260	1.51	5.091	Bet v I allergen family protein
256297_at	At1g69500	3.41	9.382	Oxygen binding
266259_at	At2g27830	1.89	6.620	Unknown protein
266299_at	At2g29450	3.78	7.468	ATGSTU5 (<i>Arabidopsis thaliana</i> GST (class tau) 5); glutathione transferase
263904_at	At2g36380	3.10	7.589	ATPDR6/PDR6 (PLEIOTROPIC DRUG RESISTANCE 6); ATPase, coupled to transmembrane movement of substances
256999_at	At3g14200	2.17	8.607	DNAJ heat shock N-terminal domain-containing protein
252474_at	At3g46620	2.70	7.820	Zinc finger (C3HC4-type RING finger) family protein
252102_at	At3g50970	4.00	17.689	LT130/XERO2 (LOW TEMPERATURE-INDUCED 30)
246289_at	At3g56880	2.07	5.831	VQ motif-containing protein
253859_at	At4g27657	3.46	5.102	Unknown protein
246270_at	At4g36500	1.62	21.796	Unknown protein
245885_at	At5g09440	2.98	5.522	Phosphate-responsive protein, putative
250449_at	At5g10830	3.00	17.019	Embryo-abundant protein-related
246463_at	At5g16970	6.97	11.142	AT-AER (ALKENAL REDUCTASE); 2-alkenal reductase
246870_at	At5g26030	1.51	8.635	Ferrochelatase
249208_at	At5g42650	1.72	11.540	AOS (ALLENE OXIDE SYNTHASE); hydro-lyase/ oxygen binding
248232_at	At5g53760	1.63	6.557	MLO11 (MILDEW RESISTANCE LOCUS O 11); calmodulin binding
247193_at	At5g65380	2.56	5.295	Ripening-responsive protein, putative

1. Gadjev I, et al. (2006) Transcriptomic footprints disclose specificity of reactive oxygen species signaling in *Arabidopsis*. *Plant Physiol* 141:436–445.

