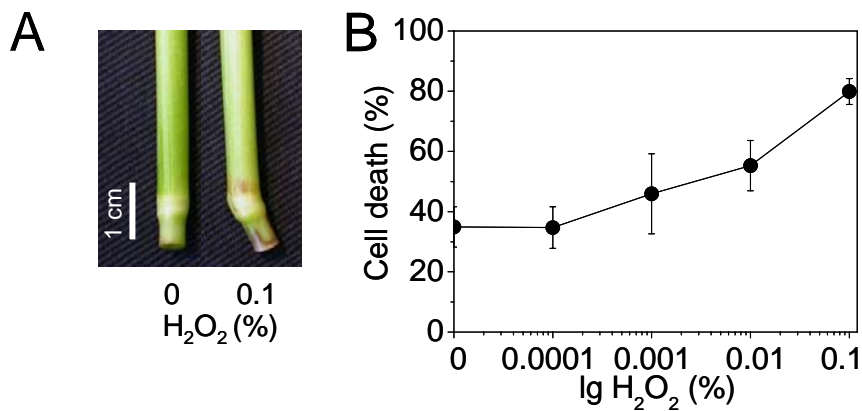


Supplemental Figure 1. Principal components analysis of RMA expression values.

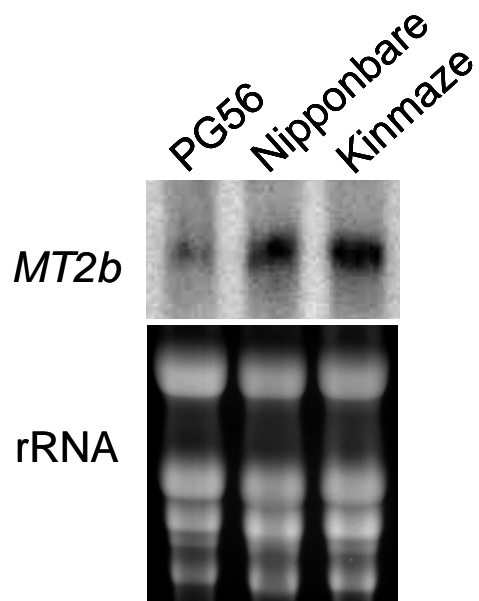
Components analysis shows that the main difference between the expression values of the different microarray hybridizations is attributable to differential gene expression between the two tissues and the three different treatments. This can be seen from the separation of arrays with epidermal cells above roots (Hyb-IDs 4884, 4963, 4969 for untreated controls, 4880, 4959, 4965 for ethephon-treated cells and 4882, 4961, 4967 for H₂O₂-treated cells) from control epidermal cell arrays (Hyb-IDs 4885, 4964, 4970 for untreated controls, 4881, 4960, 4966 for ethephon-treated cells, and 4883, 4962, 4968 for H₂O₂-treated cells).



Supplemental Figure 2. H₂O₂ Induces Death of Epidermal Cells Above Adventitious Roots in cv Kinmaze.

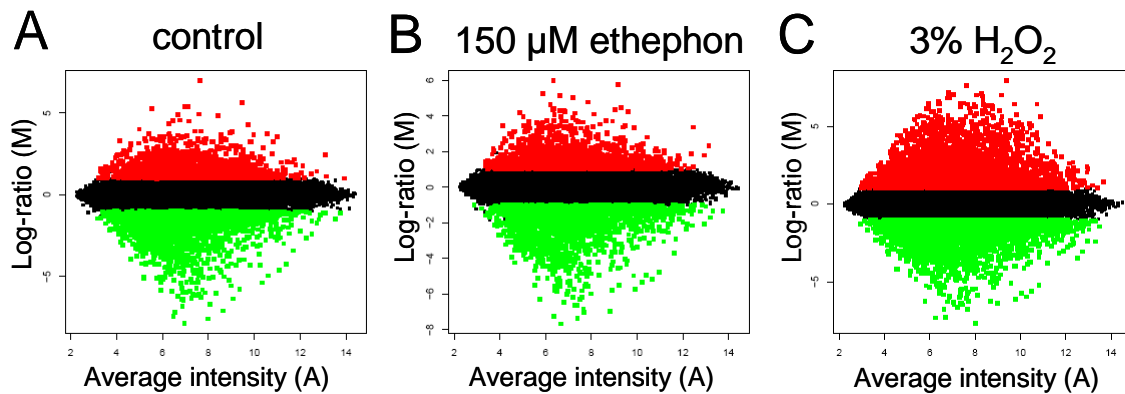
(A) Rice cv Kinmaze stem sections were treated with or without 0.1% (v/v) H₂O₂ for 26 h.

(B) Epidermal cell death in rice cv Kinmaze is induced by H₂O₂ in a dose-dependent manner. Stem sections were treated with 0.0001% (v/v) to 0.1% (v/v) H₂O₂ or without effector for 26 h. Dead cells were visualized using Evans Blue. Results are averages (\pm SE) from 6 to 19 stem sections analyzed per treatment. The cell death rate induced with 0.1% (v/v) H₂O₂ was significantly different from the control at $P < 0.001$ (Tukey-test).



Supplemental Figure 3. *MT2b* Transcript Levels in Rice Cultivars PG56, Nipponbare and Kinmaze.

Northern analysis of *MT2b* expression was performed on total RNA isolated from the second youngest leaf of 11-week-old plants from rice cultivars Pin Gaew 56 (PG56), Nipponbare and Kinmaze. As a control for RNA loading, ribosomal RNA was stained with ethidium bromide.



Supplemental Figure 4. MA plots of genes with altered expression in epidermal cells above roots as compared to control epidermal cells.

Genes that are expressed differentially in epidermal cells above roots as compared to control epidermal cells in (A) untreated stem sections, (B) in stem sections treated with 150 μM ethephon for 4 h or (C) in stem sections treated with 3% (v/v) H_2O_2 for 4 h. Regulated genes have large M values in the MA plot. The M values on the vertical axis represent differential expression. Red dots represent up-regulated and green dots represent down-regulated genes. The P value is $P < 0.05$ and \log_2 -ratio is > 1 for up- and < -1 for down-regulated genes. The A values on the horizontal axis represent average expression over all of the microarrays. (A) In untreated plants 1365 genes are up- and 2143 genes are down-regulated in epidermal cells above adventitious roots as compared to other epidermal cells. (B) In ethephon-treated plants 1565 genes are up- and 2122 genes are down-regulated. (C) In H_2O_2 -treated plants 2841 genes are up- and 3601 genes are down-regulated.

Supplemental Table 1. Genes regulated by ethylene and H₂O₂.

Differentially expressed genes with a minimum fold change (FCh) of 2 at $P < 0.001$ are shown.

Gene Name	FCh E	FCh H₂O₂	Putative Functions
Stress-Related			
Os01g0528800	↑ 2.0	6.4	CAD, cinnamyl alcohol dehydrogenase
Os01g0847700	↑ 2.3	2.5	aldose reductase
Os04g0346800	↑ 2.8	2.2	MazG RS21-C6 family protein, NTP-pyrophosphorylase
Os06g0103200	↑ 2.8	6.5	transferase
Os01g0124400	↑ 3.5	2.0	BBI3-3, Bowman-Birk type Ser protease inhibitor
Os10g0567000	↑ 2.3	6.7	crcB-like protein
Os01g0941800	↓ 0.3	0.3	PAP, purple acid phosphatase 16-like
Os05g0111300	↓ 0.4	0.2	MT2b, metallothionein
Os10g0547200	↓ 0.4	0.4	harpin-induced protein-related
Ethylene Synthesis			
Os03g0860600	↑ 2.3	2.3	<i>ACO1</i>
Os11g0585900	↓ 0.5	0.4	<i>EOL1</i> (ETO1-like)
Signaling and Transcription Factors			
Os08g0201700	↑ 2.2	5.4	LRR kinase, leucine-rich repeat kinase
Os02g0614300	↑ 2.3	2.5	ANT-like AP2/ERF family transcription factor
Os01g0693400	↓ 0.4	0.5	RAV-like AP2/ERF family transcription factor
Os01g0192300	↓ 0.4	0.3	myb family transcription factor
Os01g0227200	↓ 0.5	0.4	PERK1, putative proline-rich, extensin-like receptor kinase 1
Os01g0670800	↓ 0.5	0.3	ARF2 transcription factor
Os01g0753500	↓ 0.3	0.4	ARF3 transcription factor
Os10g0480200	↓ 0.4	0.4	Hox9 homeodomain leucine zipper

			transcription factor
Os01g0855900	↓ 0.4	0.4	CDC6, contains FAR1 DNA-binding domain
Os01g0107400	↓ 0.5	0.2	HT1-like Ser/Thr kinase, high leaf temperature protein 1
Os04g0683600	↓ 0.5	0.2	protein kinase

Protein Metabolism

Os03g0353400	↓ 0.4	0.5	ERD15-like, poly(A)-binding protein C-terminal interacting protein
Os04g0530500	↓ 0.5	0.3	specialized type of Zn-finger RING domain containing protein, putative E3 ubiquitin ligase
Os10g0126000	↓ 0.5	0.4	F-box family protein

Transport

Os05g0567700	↑ 2.3	2.3	MFS, major facilitator superfamily, sugar transporter
Os02g0695800	↑ 2.3	2.3	OPT4-like, oligopeptide transporter (OPT family)
Os02g0633300	↓ 0.5	0.4	YS (yellow stripe)-like, oligopeptide transporter (OPT family)
Os10g0554200	↓ 0.4	0.1	NRT1.1-like, nitrate or peptide transporter (PTR family)
Os02g0184200	↓ 0.5	0.4	AVP1, vacuolar H ⁺ -PPase
Os10g0561300	↓ 0.5	0.4	HEX6, hexose carrier protein

Metabolism

Os05g0408300	↓ 0.5	0.4	lipase
Os05g0580000	↓ 0.3	0.3	ADP-glucose synthase, large subunit
Os08g0162800	↓ 0.4	0.5	ACBP, acyl-CoA-binding protein

Others

Os01g0928100	↑ 2.1	4.3	hypothetical protein
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Os04g0616800	↑	2.2	2.6	hypothetical protein
Os05g0165500	↑	2.2	2.1	hypothetical protein
Os09g0515300	↑	2.2	2.0	hypothetical protein
Os11g0502700	↑	2.6	2.9	hypothetical protein
Os04g0101400	↑	2.0	4.0	cytochrome P450 93A2, putative
Os07g0682000	↑	2.1	2.3	protein of unknown function, no conserved domain
Os12g0145400	↓	0.5	0.4	DUF231 domain protein of unknown function
Os04g0203100	↓	0.4	0.4	DUF239 domain protein of unknown function
Os01g0565800	↓	0.4	0.5	DUF538 family protein of unknown function
Os01g0913100	↓	0.4	0.4	DUF538 family protein of unknown function
Os03g0858600	↓	0.4	0.5	DUF668 family protein of unknown function
Os02g0614600	↓	0.4	0.5	DUF869 family protein of unknown function
Os02g0107600	↓	0.4	0.5	DUF1668 family protein of unknown function
Os03g0157300	↓	0.4	0.3	DUF614 Cys-rich domain containing protein of unknown function
Os01g0584100	↓	0.5	0.1	hypothetical protein
Os01g0914000	↓	0.5	0.4	hypothetical protein
Os02g0441000	↓	0.4	0.3	hypothetical protein
Os04g0600500	↓	0.5	0.5	hypothetical protein
OSJNBa0015J03.15	↓	0.4	0.5	hypothetical protein
Os07g0100900	↓	0.5	0.2	unknown protein, no conserved domains
Os01g0719400	↓	0.5	0.5	Barentsz domain containing protein of unknown function
Os04g0579700	↓	0.4	0.4	prolactin-interacting factor-related protein
Os05g0550000	↓	0.5	0.4	Zn-finger, RING domain protein
Os07g0159900	↓	0.4	0.5	glutaredoxin domain-containing protein
Os07g0499800	↓	0.3	0.3	Zn-finger, RING domain protein
Os12g0572500	↓	0.5	0.4	XH domain containing protein, unknown function

Supplemental Table 2. Time-course of ethephon-induced epidermal cell death in cv Kinmaze.

Stem sections of rice cv Kinmaze were treated with or without 150 μ M ethephon for up to 48 h. Dead epidermal cells were visualized with Evans Blue. Results are averages (\pm SE) from a minimum of 5 stem sections analyzed per treatment. Cell death rates were significantly elevated after treatment with 150 μ M ethephon for 26 h and 48 h ($P < 0.05$; Tukey-test).

Time [h]	Cell death rate (%) of control treatment	Cell death rate (%) of ethephon treatment
0	20.7 (\pm 7.2)	-
6	14.9 (\pm 1.9)	35.1 (\pm 13.8)
18	27.7 (\pm 7.0)	44.7 (\pm 5.9)
26	22.0 (\pm 4.3)	47.7 (\pm 5.7)
48	46.1 (\pm 11.7)	88.8 (\pm 5.4)