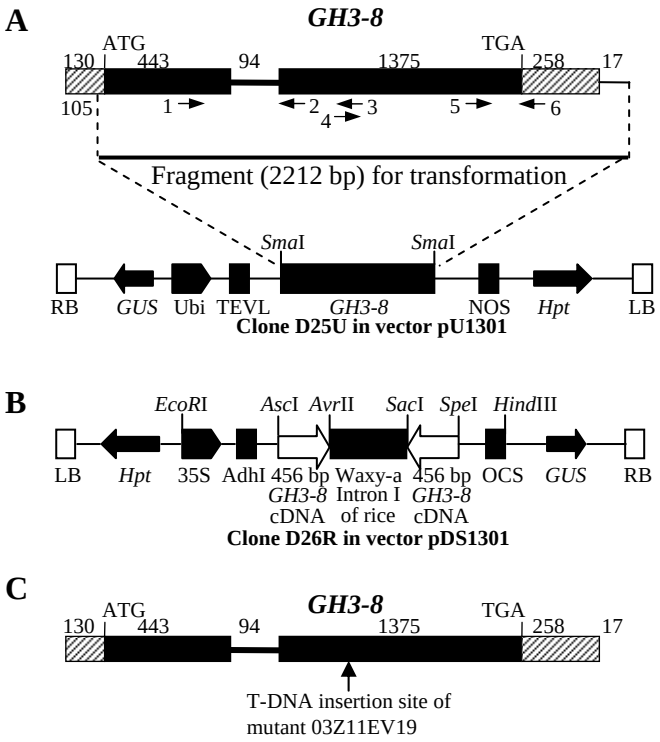
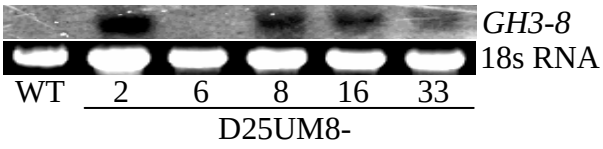
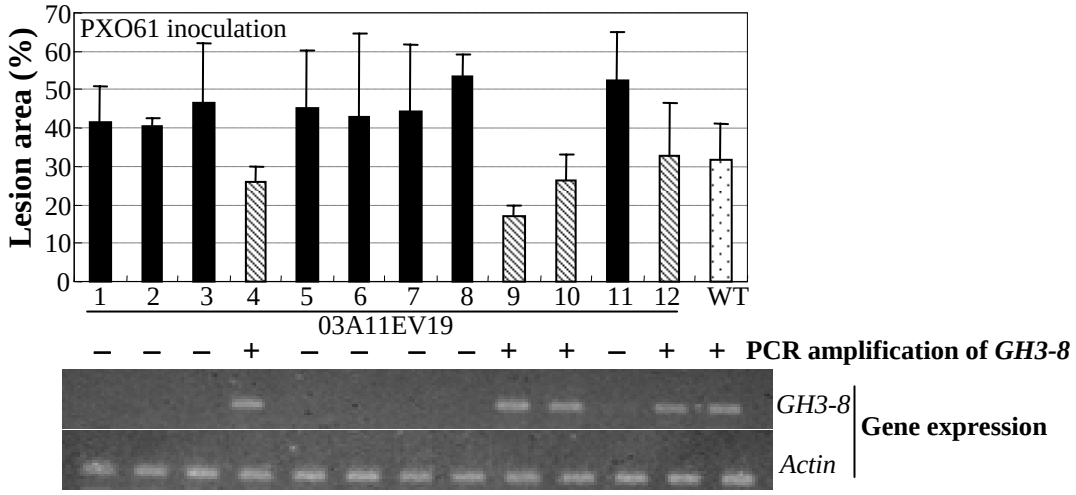


Supplemental Figure 1. Schematic diagrams of *GH3-8* gene, the transformation constructs of *GH3-8*, and the T-DNA insertion mutant of *GH3-8*.
RB and LB, right and left T-DNA border; *GUS*, β-glucuronidase gene; *Hpt*, hygromycin phosphotransferase gene; Ubi, maize ubiquitin gene promoter; 35S, cauliflower mosaic virus 35S promoter; TEVL, 5'-nontranslated region of the tobacco etch virus; NOS, napoline synthase polyadenylation signal; OCS, octopine synthase polyadenylation signal. **(A)** *GH3-8* gene (upper part) and overexpression construct of *GH3-8*, D25U (lower part). The coding region (black boxes) of *GH3-8* is interrupted by one intron (thick line). The positions of 5'- and 3'-untranslated regions (hatched boxes), translation start codon (ATG), translation stop codon (TGA), and downstream genomic regions of *GH3-8* (thin line) are also indicated. The numbers indicate the base pairs of each substructure. Arrows 1, 2, 3, 4, 5 and 6 represent primers 5P11F2, 5P11GSP2, 5P11GSP1, 5P113'GSP, 5P113'GSP2 and 5P11R1 for RACE and RT-PCR analyses (Supplemental Table 3). **(B)** RNA interference construct of *GH3-8*. To obtain the 456-bp cDNA fragment of *GH3-8*, primers dsF (5'-TAACTAGT GGCGCCTGCAGGTACCGGTCCG-3') and dsR (5'-TAGAGCTC GCCTAGGTGCACGCGTACGTACGTAAGC-3') were used to amplify the cDNA clone EI5P11, which cDNA insertion was truncated by use of restriction enzymes *Not*I and *Bam*HI followed by self-ligation in pSPORT1 vector. The dsF contained *Spe*I and *Asc*I restriction enzyme sites (underlined) at the 5'-end and dsR contained *Sac*I and *Avr*II restriction enzyme sites (underlined) at the 5'-end. The sequences following the restriction enzyme sites of dsF and dsR were complementary to the sequences flanking the multi-cloning sites of pSPORT1 vector. **(C)** T-DNA insertion site of *GH3-8*-knockout mutant 03Z11EV19.

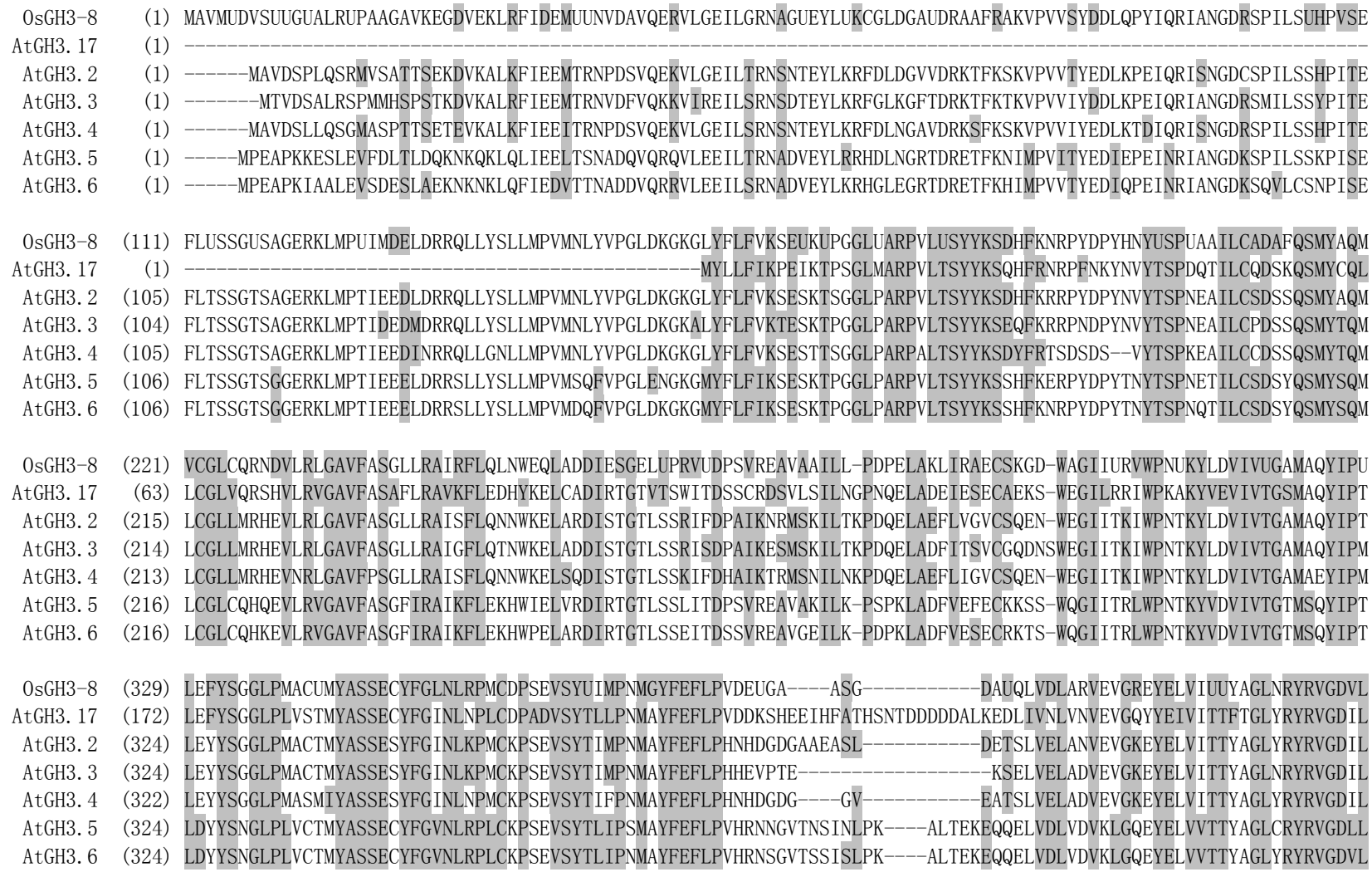


Supplemental Figure 2. *GH3-8* expression in T_0 *GH3-8*-overexpressing plants (D25UM8) and wild type (Mudanjiang 8).

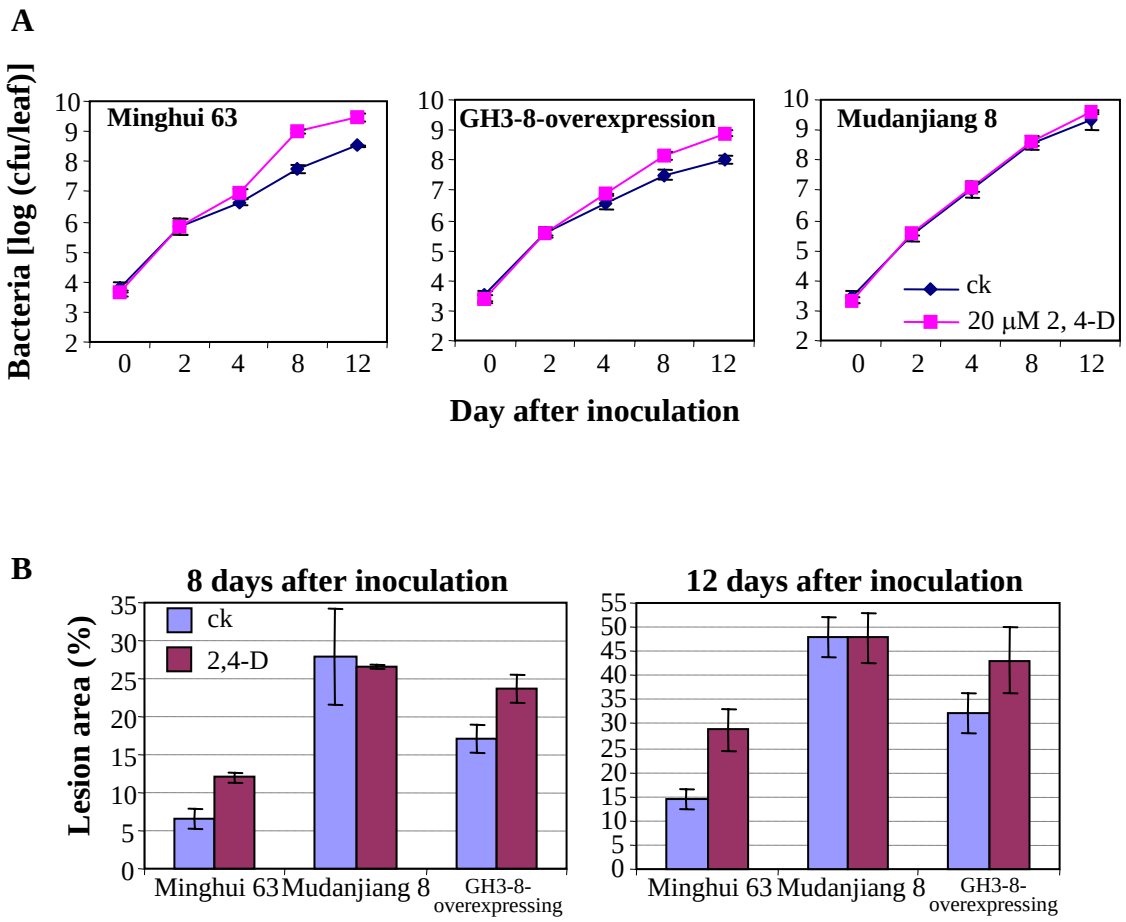


Supplemental Figure 3. Knockout of *GH3-8* (line 03A11EV19) increases rice susceptibility to *Xoo* strain PXO61.

The lesion area was measured at 14 d after PXO61 inoculation. Zhonghua 11 is the wild type (WT). PCR primers used for identification of the homozygote T-DNA insertion mutant 03Z11EV19 were GH3-8F1 (5'-CATTCCTTGGGCTTTTTTTCT-3') and GH3-8R1 (5'-TGGCACCTTGTACTGGTTGAT-3') designed according to *GH3-8* sequences flanking the T-DNA insertion. RT-PCR primers used for detection of the expression of *GH3-8* in 03Z11EV19 were OSDR2f2 (5'-GAACACGGTGTACAGGCAGA-3') and 5P11R1 (5'-TGGGGATTTGACCGACTATT-3'). The expression level of actin was used to standardize the RNA sample for each RT-PCR using primers actinF (5'-TGCTATGTACGTCGCCATCCAG-3') and actinR (5'-AATGAGTAACCACGCTCCGTCA-3'). –, homozygote T-DNA insertion mutant 03Z11EV19; +, negative plants segregated from 03Z11EV19.

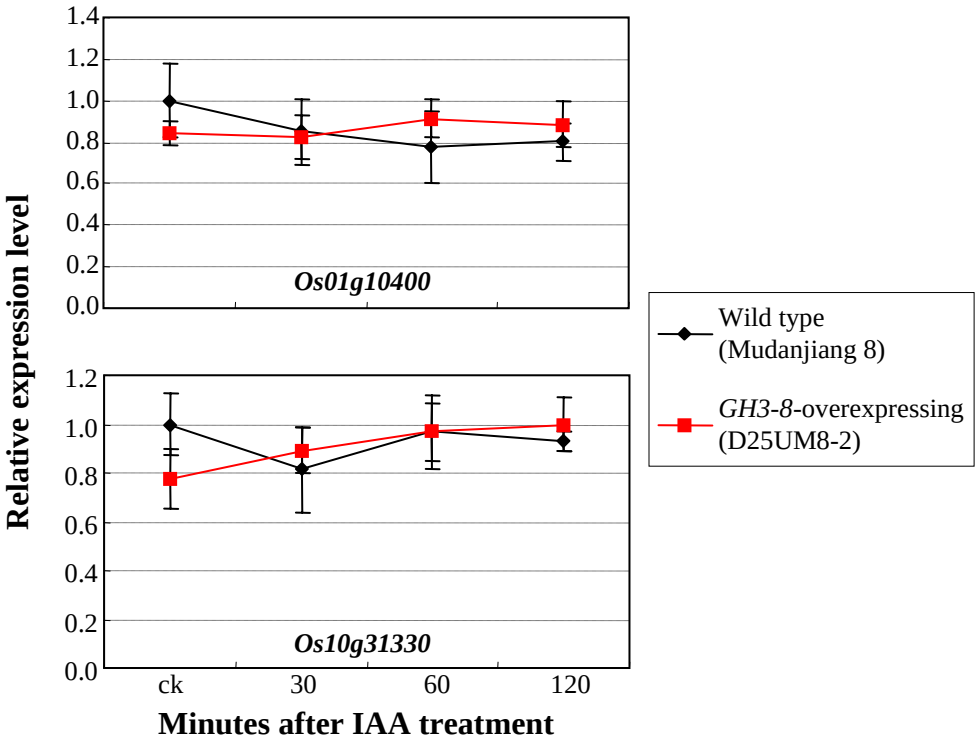


Supplemental Fiugre 4. Sequence comparison of rice GH3-8 protein and *Arabidopsis* GH3 proteins.



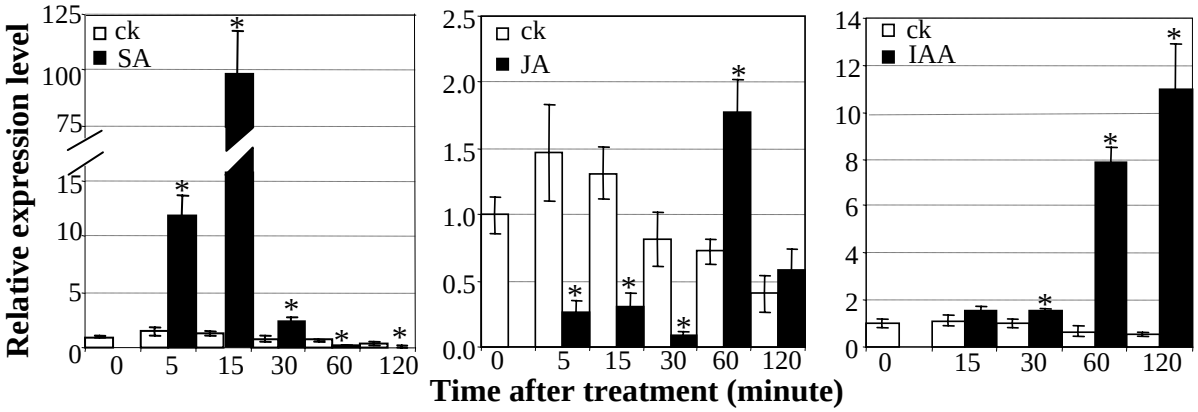
Supplemental Figure 5. Effect of auxin on the growth rate of *Xoo* and the development of disease.

The resistance lines Minghui 63 and *GH3-8*-overexpression plants (D25UM8-2) and the susceptible line Mudanjiang 8 were treated with 20 μM 2,4-D (one type of auxin). The plants were inoculated with *Xoo* strain PXO61. **(A)** Growth of PXO61 in leaves. The bacterial population was determined from three leaves at each time point by counting colony-forming units (cfu). 0 day, 2 h after bacterial inoculation. Each point represents mean ± standard deviation. **(B)** Development of lesion area in leaves. Bars represent mean (three replicates) ± standard deviation.



Supplemental Figure 6. Expression of two tissue-specific expressed genes after IAA treatment.

The two genes, *Os01g10400* and *Os10g31330*, are known to have tissue-specific expression (M. Cai and S. Wang, unpublished data). The PCR primers were O-10-1-2-REAL-F (5'-TCTTCGACCATGTCGGACAA-3') and O-10-1-2-REAL-R (5'-TCTTCACGCACTGGCTCTTG-3') for *Os01g10400* gene, and O-6-1-REAL-F (5'-TTTACAAAGAGCTTGTCGGATTGT-3') and O-6-1-REAL-R (5'-GCTTTGCCAACTTTATGTGATGAA-3') for *Os10g31330* gene. The expression level of actin was used to standardize the RNA sample for each RT-PCR using primers actinF (5'- TGCTATGTACGTCGCCATCCAG-3') and actinR (5'-AATGAGTAACCACGCTCCGTCA-3'). Each point represents mean (three replicates) ± standard deviation.



Supplemental Figure 7. The effects of different signal molecules on the expression of *GH3-8* analyzed by quantitative reverse transcription-PCR. Samples were collected at 5, 15, 30, 60 and 120 min after treatment or without treatment (0). Asterisks indicate that significant difference ($P < 0.05$) was detected between corresponding hormone treatment and wounding (also as control, ck) treatment. Bars represent mean (three replicates) ± standard deviation.

Supplemental Table 1. Performance of *GH3-8*-overexpressing plants (D25UM8) after pathogen (*Xoo* strain PXO61) inoculation.

Material	Lesion area (%)[a]	*P*[b]	Morphology	Expression[c]
Mudanjiang 8 (wild type)	77.9 ± 6.7			–
IRBB4 (resistance gene *Xa4*)	15.2 ± 1.9			
D25UM8-1	82.6 ± 18.7	0.325	normal	–
D25UM8-2	42.5 ± 14.6	0.002	dwarf	+
D25UM8-3	47.1 ± 14.3	0.003	dwarf	+
D25UM8-4	75.5 ± 8.3	0.386	normal	NA
D25UM8-5	89.0 ± 10.4	0.058	normal	NA
D25UM8-6	78.3 ± 6.5	0.473	normal	–
D25UM8-7	24.4 ± 14.8	0.002	dwarf	NA
D25UM8-8	34.9 ± 19.7	0.008	dwarf	+
D25UM8-9	33.8		dwarf	NA
D25UM8-10	54.1 ± 11.5	0.006	dwarf	NA
D25UM8-11	83.2 ± 20.7	0.309	normal	–
D25UM8-12	72.6 ± 9.3	0.195	normal	–
D25UM8-13	45.9 ± 15.9	0.011	dwarf	+
D25UM8-14	52.4 ± 16.9	0.012	dwarf	NA
D25UM8-15	81.5 ± 17.0	0.342	normal	–
D25UM8-16	37.2 ± 26.5	0.013	dwarf	+
D25UM8-17	59.0 ± 10.3	0.016	normal	NA
D25UM8-18	83.6 ± 5.2	0.148	normal	NA
D25UM8-19	49.9 ± 10.5	0.003	dwarf	+

D25UM8-20	65.5 ± 14.3	0.088	normal	NA
D25UM8-21	92.9 ± 3.9	0.019	normal	–
D25UM8-22	76.6 ± 14.7	0.433	normal	NA
D25UM8-23	88.8 ± 13.3	0.088	normal	NA
D25UM8-27	40.9 ±7.5	0.000	dwarf	+
D25UM8-28	48.0 ±4.1	0.000	dwarf	+
D25UM8-33	44.8 ±2.6	0.000	dwarf	+
D25UM8-36	81.4 ±2.4	0.384	normal	–
D25UM8-39	44.0 ±14.6	0.002	dwarf	+
D25UM8-40	44.1 ±7.8	0.000	dwarf	+
D25UM8-41	38.9 ±8.8	0.000	dwarf	+
D25UM8-42	82.8 ±3.0	0.240	normal	NA
D25UM8-43	75.8 ±14.5	0.78	normal	–
D25UM8-44	NA	NA	normal	NA
D25UM8-47	NA	NA	normal	NA

[a] Four to five uppermost fully expanded leaves of each plant were inoculated for most of the plants; transgenic plant D25UM8-9 was inoculated with only one leaf. Each data represents mean ± standard deviation.

[b] Each *P* value was calculated by *t*-test in comparison with susceptible control Mudanjiang 8.

[c] The "+" indicates that overexpression of *GH3-8* was detected by RNA gel blot analysis, and "-" indicates that the expression of *GH3-8* was not detected by RNA gel blot analysis.

NA, not analyzed.

Supplemental Table 2. Performance of *GH3-8*-suppressing plants (D26RMH) after pathogen (*Xoo* strain PXO61) inoculation.

Material	Lesion area (%)[a]	*P*[b]
Minghui 63 (wild type)	42.0 ± 11.0	
D26RMH1	55.1 ± 20.2	0.279
D26RMH2	62.6 ± 10.6	0.060
D26RMH3	48.9 ± 25.6	0.619
D26RMH4	40.0 ± 14.1	0.880
D26RMH5	51.6 ± 18.5	0.434
D26RMH6	43.1 ± 8.6	0.888
D26RMH7	45.5 ± 4.7	0.653
D26RMH8	47.9 ± 18.8	0.594
D26RMH9	58.6± 14.7	0.148
D26RMH0	39.1 ± 9.3	0.726
D26RMH11	39.8 ± 19.4	0.872

[a] Four to five uppermost fully expanded leaves of each plant were inoculated for most of the plants. Each data represents mean ± standard deviation.

[b] Each *P* value was calculated by *t*-test in comparison with susceptible control Minghui 63.

Supplemental Table 3. PCR primers used for gene structure and expression analyses and vector construction.

Gene	GenBank accession No.	Primer name	Forward primer (5'-3')	Reverse primer (5'-3')	Purpose
GH3-8	EF103572	5P11F1/5P11R2	TTTTCTTGTTCGGGGTTGAG	CGGTTTTGGAGGACAGGTTA	Gene isolation
		5P11F2/5P11GSP2	GTTCATCGACGAGATGACCA	GTCGTACGGCCGGTTCTTGA	Structure analysis
		5P113'GSP/5P11R1	CCCGTACCACAACTACACGA	TGGGGATTTGACCGACTATT	Structure analysis
		5P113'GSP2	GCTCATGGACTACGCCATCT		3'-untranslated region
		5P11GSP1		CTCGTGTAGTTGTGGTA	5'-untranslated region
		OSDR2F2/ OsDR2R1	ATGAATTCATGGCGGTGATGACTGATGT[a]	ATAAGCTTTGGGGATTTGACCGACTATT[c]	Amplifying coding region
		5P11F2	GTTCATCGACGAATGACC		RNA gel blot analysis

		OSDR2PROF1/ R1	ATGCTGCAGGCCGCACGGTCAGAAACAGG[b]	ATGAAGCTTGGAAGGCGAGGGACAAGGAA[c]	*GH3-8* promoter -*GUS* analysis
EXPA1	AK069548	EXPA1OVF/R	ATGGGTACCCATTAGCAGCACATTCACCG[d]	ATGGGTACCTCGATTGGCAAGCACCTC[d]	Amplifying coding region
EXPA5	AK073572	EXPA5OVF/R	ATGGGTACCGCGTGCGACGACTCCA[d]	ATGGGTACCCTAAATACTTTCCCAAGAACCAA[d]	Amplifying coding region
EXPA10	AK066414	EXPA10OVF/R	ATGGGTACCCTGAGGCATACCGACGAA[d]	TGGAGGCTCTGCACTAAAC	Amplifying coding region

[a]*Eco*RI digestion site (underlined sites).

[b]*Pst*I digestion site (underlined sites).

[c]*Hin*dIII digestion site (underlined sites)

[d]*Kpn*I digestion site (underlined sites).

Supplemental Table 4. Gene-specific primers for quantitative real-time PCR.

Genes	GenBank accession No.	Primer name	Forward primer (5'-3')	Reverse primer (5'-3')	Purpose
GH3-8	EF103572	OsDR2F3/R3	TTGGACCGTGTCCAAGAATCT	TCTTGCCACTAACTGACAGAGTTGA	Expression in wild-type and transgenic plants
AAO1	AK072847	208907-J023142J16.txt-668F/ 733R	TGTGTCGATGCACCGGTTA	GGTCAACATCCGATTCAAAACTT	Expression in wild-type plants
AAO2	AK103597	214450-J033133E15.txt-421F/ 486R	CGAACACCATCAGGAGGAAGA	CGCTGTCCCCGAAGAACA	Expression in wild-type plants
AAO3	AK065990	201387-J013044D18.txt-1591F/1646R	TGGAATGAACGGCGGAAT	CAATGGCGACTGGCAACA	Expression in wild-type plants
NIT1	AK104033	100932F2/R2	ACTGTTGTCTGCCCTGGAGGTA	CAAGACTTCTCCGGATGGTGAA	Expression in wild-type plants
NIT2	AK058965	100902F1/R1	ACGTCGTGGGACACTATGCA	GGCAGCTTTGATTCGGTTTTC	Expression in wild-type plants
NIT3	AK069786	205528-J023030L13.txt-896F/948R	AAAAGTTGAGGCTGTGCGAACT	CAAACTTCCGGTGCTCAGAGA	Expression in wild-type plants
IAA1	AK109373	OsIAA1F/R	GCCGCTCAATGAGGCATT	GCTTCCACTTTCTTTCAATCCAA	Expression in wild-type and transgenic plants
IAA4	AK103865	OsIAA4F/R	GCTCTTGCTGGATGGGTATGA	AGGTGATGGGCGTCTTGAAC	Expression in wild-type and transgenic plants
IAA9	AK073365	OsIAA9F/R	AAGAAAATGGCCAATGATGATCA	AAGAAAATGGCCAATGATGATCA	Expression in wild-type and transgenic plants
IAA14	AK059619	OsIAA14F/R	CCGTCGCCTATGAGGACAAG	CGCATTATCCGCAGCTTCTT	Expression in wild-type and transgenic plants

IAA20	AK102541	OsIAA20F/R	TTGTACGTGAACGGGATTATTTTG	CATGCTTATGAAATTGCTGAAACA	Expression in wild-type and transgenic plants
IAA24	AK103483	OsIAA24F/R	GGCTTGTGCTCTTCGTTGCT	CCTCTTGGATTCAGAAACACTGAA	Expression in wild-type and transgenic plants
ARF1	AK071997	OSARF1-2654F/2705R	CAATATGTTCCCCAGCTCATGG	TCCAAGGCGAGTATTTGGAGG	Expression in wild-type and transgenic plants
ARF6a	AK070569	OSARF6a-3239F/3290R	GTCGGCAGCTTGTATTTGTTGA	TCGCCAACTAGAAGAACGTCG	Expression in wild-type and transgenic plants
ARF6b	AK121703	OSARF6b-2339F/2389R	TCAGCAAGGCCATTGTCAGA	TGACCTTGAAGGAACCCAGAGT	Expression in wild-type and transgenic plants
ARF8	AK071455	OSARF8-2762F/2812R	GCAAGGAAATGATCCACGGTAT	TGGCACCATGTTCTCTCACTTC	Expression in wild-type and transgenic plants
EXPA1	AK069548	OsEXPA1F/R	CCTGCTTTTTTCAATGCGAAT	AAAGCATGCCGATCATCGA	Expression in wild-type and *GH3-8*-overexpressing plants
		OsEXPA1-979F/1042R	AGTGTTTGGTGTGGCGAGCTAT	GCATTGAAAAAAGCAGGTGTCC	Expression in wild-type and *EXPA1*-overexpressing plants
EXPA5	AK073572	OsEXPA5F/R	AAGGCTGTGGCTTGATTGACA	TTAGGCCCAATTTTGCTATTTTG	Expression in wild-type and *GH3-8*-overexpressing plants
		OsEXPA5-609F/708R	TCTTCAAGGCCGGCATTGT	AGGTTGAAGTAGGAGTGCCCGT	Expression in wild-type and *EXPA5*-overexpressing plants
EXPA10	AK066414	OsEXPA10F/R	CCAGTACCGCCGGTACGT	TGCAAAGTAGACTAAAGATAGCAGCAA	Expression in wild-type and *GH3-8*-overexpressing

					plants
		OsEXPA10-822F/877R	TGACCAACTACAACGTGGTCCC	GCCAGTGTATGTTTTGCCGAAG	Expression in wild-type and *EXPA10*-overexpressing plants
EXPB3	AF261271	OsEXPB3-AF261271.txt-70F/125R	CTTTGAGTGGTTGGAGTGGTGG	GCAGCCTTCTTGGAGATGGAA	Expression in wild-type and transgenic plants
EXPB4	AF261272	OsEXPB4-AF261272.txt-1058F/1130R	GTCGGTCTGTGTTGCGATTTG	CCTCCATTTCCCACACAGCTT	Expression in wild-type and transgenic plants
EXPB7	AF261275	OsEXPB7-AF261275.txt-537F/589R	ACGGTGATCATCACGGACAT	TCGAAGTGGTACAGCGACACT	Expression in wild-type and transgenic plants
PR1a	AJ278436	PR1aF/R	CGTCTTCATCACCTGCAACTACTC	CATGCATAAACACGTAGCATAGCA	Expression in wild-type and transgenic plants
PR1b/PR-1	U89895	PR1bF/R	GGCAACTTCGTCGGACAGA	CCGTGGACCTGTTTACATTTTCA	Expression in wild-type and transgenic plants
PAD4	CX118864	PAD4F/R	GCCAGCTCCCCTACGACTTC	CGTGTGCGGTGTAGGTTGTT	Expression in wild-type and transgenic plants
PR10/PBZ1	D38170	PR10F/R	CCCTGCCGAATACGCCTAA	CTCAAACGCCACGAGAATTTG	Expression in wild-type and transgenic plants
LOX	D14000	LOXF/R	GCATCCCCAACAGCACATC	AATAAAGATTTGGGAGTGACATATTGG	Expression in wild-type and transgenic plants
AOS2	AY062258	AOS2F/R	CAATACGTGTACTGGTCGAATGG	AAGGTGTCGTACCGGAGGAA	Expression in wild-type and transgenic plants
Actin	X15865	Actin120F/R	TGTATGCCAGTGGTCGTACCA	AGTCTGGAGTGTGTGGCTCAAG	Standardizing RNA sample

SUPPLEMENTAL METHODS

Gene Isolation and Structure Analysis

EI5P11, the partial cDNA sequence of a *GH3-8* allele from rice cultivar Minghui 63, was used as a query to search GenBank to identify homologous sequence using the BLAST program (Altschul et al., 1997). The rice genomic sequence identified was analyzed using the GenScan program (http://genes.mit.edu/GENSCAN.html) to predict the size and structure of the gene that was allelic to *GH3-8*. The sequences flanking the allele of *GH3-8* were then used to design primers, 5P11F1 (5'-TTTTCTTGTTCGGGGTTGAG-3') and 5P11R2 (5'-CGGTTTTGGAGGACAGGTTA-3'), for PCR isolation of *GH3-8* gene from resistant rice line C101LAC. The PCR product was cloned into pUC19 vector and the plasmid was named T5P11.

The structure of *GH3-8* was determined by sequencing the transcript of the gene. Part of the cDNA sequence of *GH3-8* was analyzed by sequencing the products of RT-PCR obtained using two pairs of primers, 5P11F2 (5'-GTTCATCGACGAGATGACCA-3')/5P11GSP2 (5'-GTCGTACGGCCGGTTCTTGA-3') and 5P113'GSP (5'-CCCGTACCACAACTACACGA-3')/5P11R1 (5'-TGGGGATTTGACCGACTATT-3') (Supplemental Figure 1A). The remaining cDNA sequence of *GH3-8* was determined by analyzing 3'- and 5'-untranslated regions with 3'- and 5'-rapid amplification of cDNA end (RACE) assays using the 3'-Full RACE Core Set (TaKaRa Biotechnology Co. Ltd, Dalian, China) and 5' RACE System for Rapid Amplification of cDNA Ends Version 2.0 (Invitrogen Life Technologies, Carlsbad, CA, USA) according to the manufactures' protocols. For 3'-RACE, the *GH3-8*-specific primer 5P113'GSP2 (5'-GCTCATGGACTACGCCATCT-3') was used for PCR amplification. The reverse transcirption primer was 5P11GSP1 (5'-CTCGTGTAGTTGTGGTA-3') and the PCR primer was 5P11GSP2 for 5'-RACE.

Quantification of IAA, IAA-Asp, IAA-Ala and JA

To prepare the samples for the quantification of IAA,IAA-amino acid conjugates, 1 g of leaves from plants at the booting stage was ground in liquid nitrogen and mixed with 3.5 ml of ice cold methanol containing 0.2 mM 2,6-di-tert-butyl-4-methylphenol, 12.5 μl trimethyl phosphate, and 500 ng D_2-IAA (as internal standard for IAA and IAA-amino acid quantification, Sigma-Aldrich, St. Louis, MO, USA), 50 ng DHJA (as internal standard for JA quantification, Olchemim, Olomouc, Czech Republic). The mixture was transferred into a 10-ml tube, rotated on a rotary shaker for 2 h at 4 °C, mixed with 1.5 ml of ice cold water, kept on ice for 5 min, and centrifuged for 15 min at 4 °C at 3500 ×*g*. The supernatant was transferred to a 50-ml tube and mixed with 90 μl

of 1 M ammonium hydroxide (pH 8–9). The sample was purified using a C18-SepPak cartridge (Waters Corporation, Milford, MA, USA) by the following steps: (1) conditioning the column with 6 ml 100% methanol, then with 6 ml 70% methanol; (2) passing the sample through the column and eluting it with 6 ml of 75% methanol; (3) adding 120 μl of 10% formic acid (pH 3–4) to the elute, further diluting the elute with water to 50 ml (final methanol should be less than 20%), and keeping the diluted elute on ice; (4) washing and conditioning the used column in the following order: 6 ml methanol supplemented with 40 μl formic acid, 5 ml methanol, 6 ml diethyl ether, 5 ml methanol, and 6 ml deionized water twice; (5) repassing the sample through the column and washing the column with 6 ml of 15% methanol and then with 6 ml of water; (6) eluting the sample from the column into a 10-ml tube and washing twice using about 8 ml diethyl ether; (7) removing the residual water in the elute with a pipette and then with anhydrous $MgSO_4$ by centrifugation for 5 min at 15 °C at 720 ×*g*; (8) transferring the supernatant to a new tube; (9) washing the residual ($MgSO_4$) with 2 ml diethyl ether by centrifugation for 5 min at 15 °C at 720 ×*g* and collecting the supernatant; and (10) combining the two elutes and drying the sample by evaporation with nitrogen gas at 40°C. The average recovery rate this procedure was approximately 80%.

To quantify free IAA IAA-Asp, IAA-Ala and JA, sample was diluted with 300 μl methanol and a 20-μl aliquot of the sample was injected into the HPLC/ESI-MS/MS system. An Agilent 1100 HPLC (Agilent Technologies, Palo Alto, CA, USA) was used with an Agilent C18 column (150 × 2.1 mm, 5 μm) using a gradient of increasing methanol content at a flow of 0.25 ml min^{-1}. The flow rate was 0.25 ml/min, and the sample was eluted with a mixture of methanol:0.1% acetic acid (gradient from 10:90 to 90:10 in 13 min), then was eluted with a mixture of methanol:0.1% acetic acid (gradient from 90:10 to 10:90 in 2min) and holding at this composition for an additional 15 min. An API3000 mass spectrometer (Applied Biosystems) was equipped with an electrospray interface, and the eluting ions were observed by multiple reaction monitoring. The former 14 min is monitored in positive ion mode, and the latter 14 min is monitored in negative ion mode. The levels of IAA in the samples were quantified in relation to the external standard using calibration curves that had been generated for each compound. The standard IAA IAA-Asp, IAA-Ala and JA were bought from Sigma-Aldrich (St. Louis, MO, USA). The quantitative data of IAA was obtained using the peaks of the precursor ion 176.3 and the product ion 130. The quantitative data of IAA-Ala was obtained using the peaks of the precursor ion 247.2 and the product ion 130. The quantitative data of IAA-Asp was obtained using the peaks of the precursor ion 291.2 and the product ion 130. The quantitative data of D_2-IAA was obtained using the peaks of the precursor ion 178.3 and the product ion 132. The quantitative data of JA was obtained using the peaks of the precursor ion 209.1 and the product ion 109. The quantitative data of DHJA was obtained using the peaks of the precursor ion 211.2 and the product ion 59.

GH3-8 Promoter-GUS Analysis

The promoter region of GH3-8 from rice variety Zhonghua 15 (~ 1.8 kb) was obtained by PCR amplification using primers OSDR2PROF1 (5'-ATGCTGCAGGCCGCACGGTCAGAAACAGG-3') harboring a *Pst*I digestion site and OSDR2PROR1 (5'- ATGAAGCTTGGAAGGCGAGGGACAAGGAA-3') harboring a *Hin*dIII digestion site (underlined sites). The promoter was fused with *GUS* and cloned into pCAMBIA1381 vector. The vector was introduced to rice variety Zhonghua 15 with *Agrobacterium*-mediated transformation. GUS histochemical staining of the leaves from transgenic plants was assayed as described previously (Wu et al., 2003). The stained leaves were then sectioned using a razor blade.

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