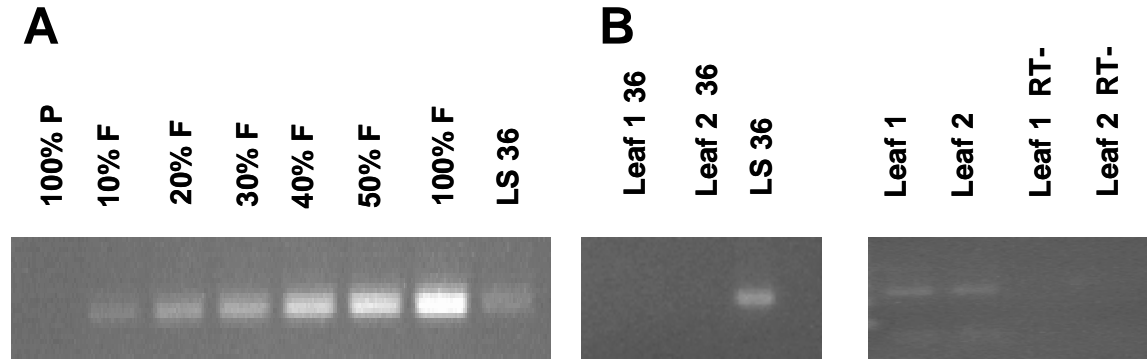


Supplemental Data: Mosquera et al. (2009). Interaction transcriptome analysis identifies *Magnaporthe oryzae* BAS1-4 as biotrophy-associated secreted proteins in rice blast disease.



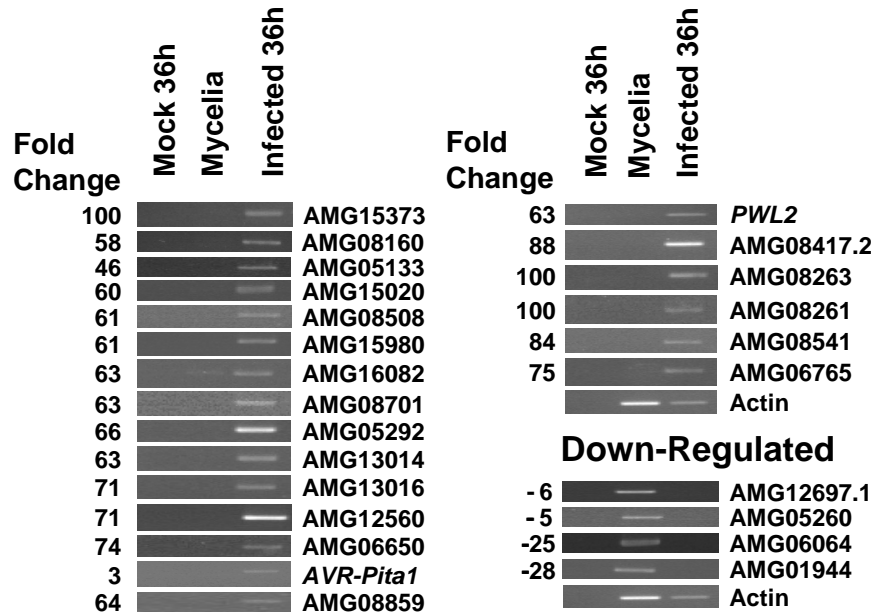
Supplemental Figure 1. RT-PCR experiments to assess fungal RNA content in infected tissue samples and to confirm invasion-specific expression of fungal and rice genes.

(A) Relative RT-PCR amplification of fungal actin in 36 hpi infected sheath tissue and control mixtures. RNA mixtures were obtained by combining defined amounts of RNA from fungal mycelium and mock-inoculated sheath. Percentage values (%F) correspond to the fungal RNA content. 100%P is pure plant RNA, and LS36 = RNA from infected leaf sheaths at 36 hpi. For each, 22 cycles of amplification were used.

(B) RT-PCR amplification of fungal actin in infected sheaths and leaves at 36 hpi. A prominent fungal actin band was seen from infected sheath RNAs after 28 cycles, but not from the infected leaf samples. After 35 cycles, faint bands were seen in the infected leaf samples, but not in controls that lacked reverse transcriptase (RT-). For infected leaf tissue, whole plants were inoculated. Samples were collected separately for the most susceptible leaf 1 (the half-extended youngest leaf at the time of inoculation), and the lesser susceptible leaf 2 (the next youngest leaf, fully extended at the time of inoculation). LS36 = Leaf sheath; Leaf 1= youngest leaf; Leaf 2 = older leaf.

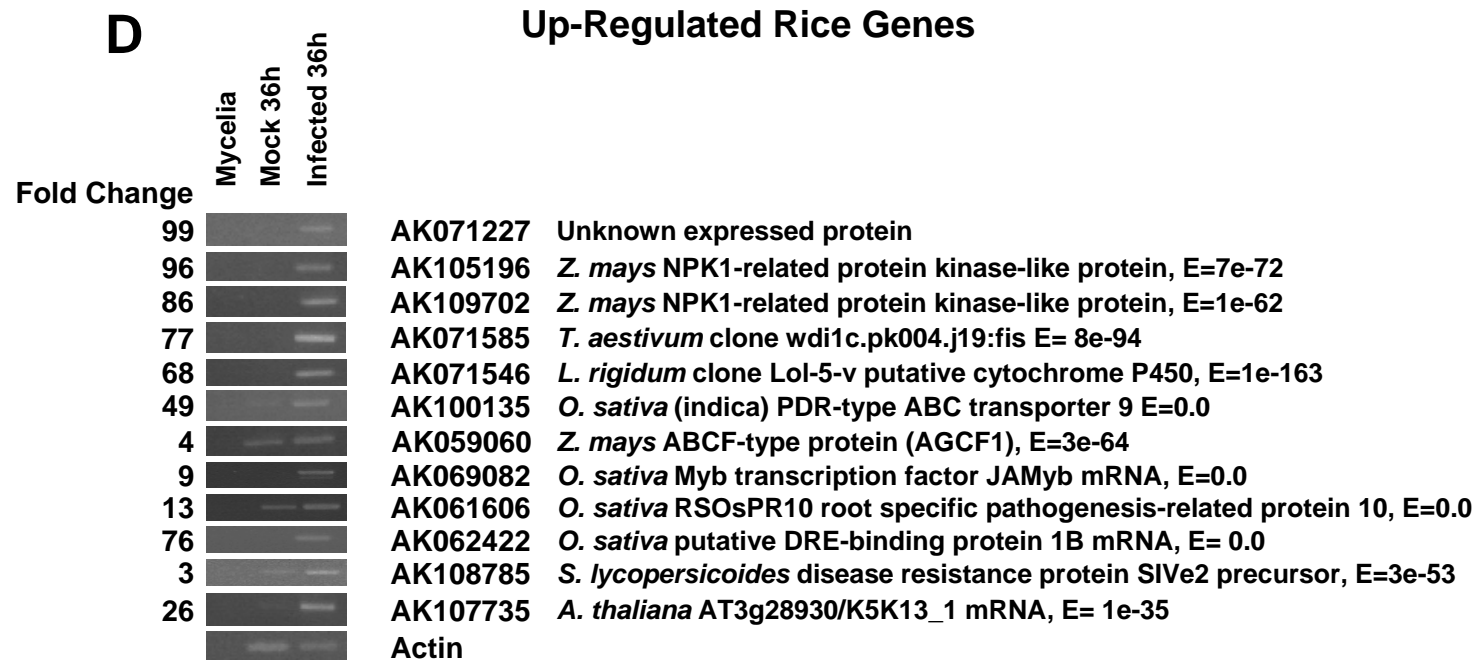
C

Up-Regulated Fungal Genes



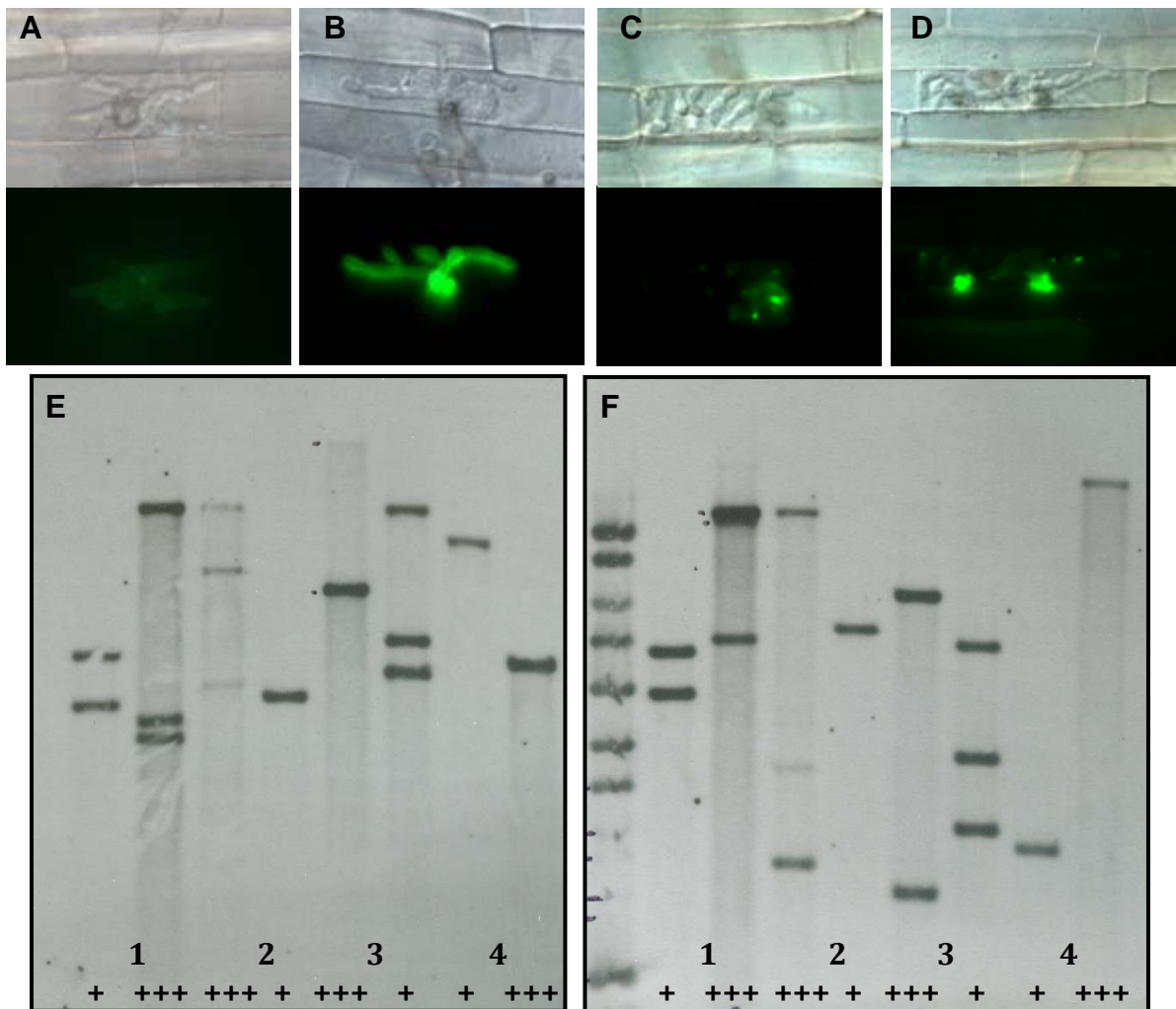
Supplemental Figure 1, continued.

(C) Confirmation of invasion-specific expression of fungal genes by RT-PCR. Twenty IH-enriched genes, including *PWL2*, *BAS1* (AMG08261), *BAS2* (AMG08541), *BAS3* (AMG12560), and *BAS4* (AMG15980) with expression levels >50-fold higher in IH were amplified from infected rice, but not from the mock-inoculated rice or mycelial samples. Four genes with higher expression levels in mycelium, a clock-controlled gene-9 homolog from *Neurospora crassa* (AMG12697.1), the G-protein coupled receptor *PTH11* (AMG05260), and the melanin biosynthesis genes scytalone reductase (AMG06064) and tetrahydroxynaphthalene reductase (AMG01944), were amplified only from mycelial RNAs. For this analysis, the RNAs (left to right) were from mock-inoculated sheath at 36 hpi (Mock 36h), from mycelium (Mycelia), and from infected sheath at 36 hpi (Infected 36h). A standard 27 rounds of PCR amplification were used for each primer pair. No amplification was seen from the Mock 36 hpi negative control. Amplification of the fungal actin gene control reflects the lower amount of fungal RNA in the infected tissue (20%) compared to mycelial RNA, resulting in increased significance for differential amplification of up-regulated genes. One predicted gene had two possible transcripts, AMG08417.1 and AMG08417.2, and primers designed to differentiate these transcripts showed AMG08417.2 was correct.



Supplemental Figure 1, continued

(D) Confirmation of invasion-specific expression of rice genes by RT-PCR. Using the same RNA samples as in (C), gene-specific fragments for rice genes expressed ≥ 26 -fold higher during infection were amplified from infected but not mock-inoculated rice. Genes with differential expression ratios from 3 and 13 sometimes amplified from both. For rice gene analysis, RNAs (left to right) were from mycelium (Mycelia), mock-inoculated sheath at 36 hpi (Mock 36h), and from infected sheath at 36 hpi (Infected 36h). For each, 27 rounds of PCR amplification were used. No amplification was seen from the negative control mycelial RNA. Primers for the rice actin gene were used as controls. Gene-specific fragments for eight rice genes expressed ≥ 26 -fold higher during infection were amplified from infected but not mock-inoculated rice. Although a gene with 10-fold higher expression was only amplified from infected tissue, genes with 4-, 13-, and 3-fold up-regulation were amplified from both infected and mock-inoculated tissues.



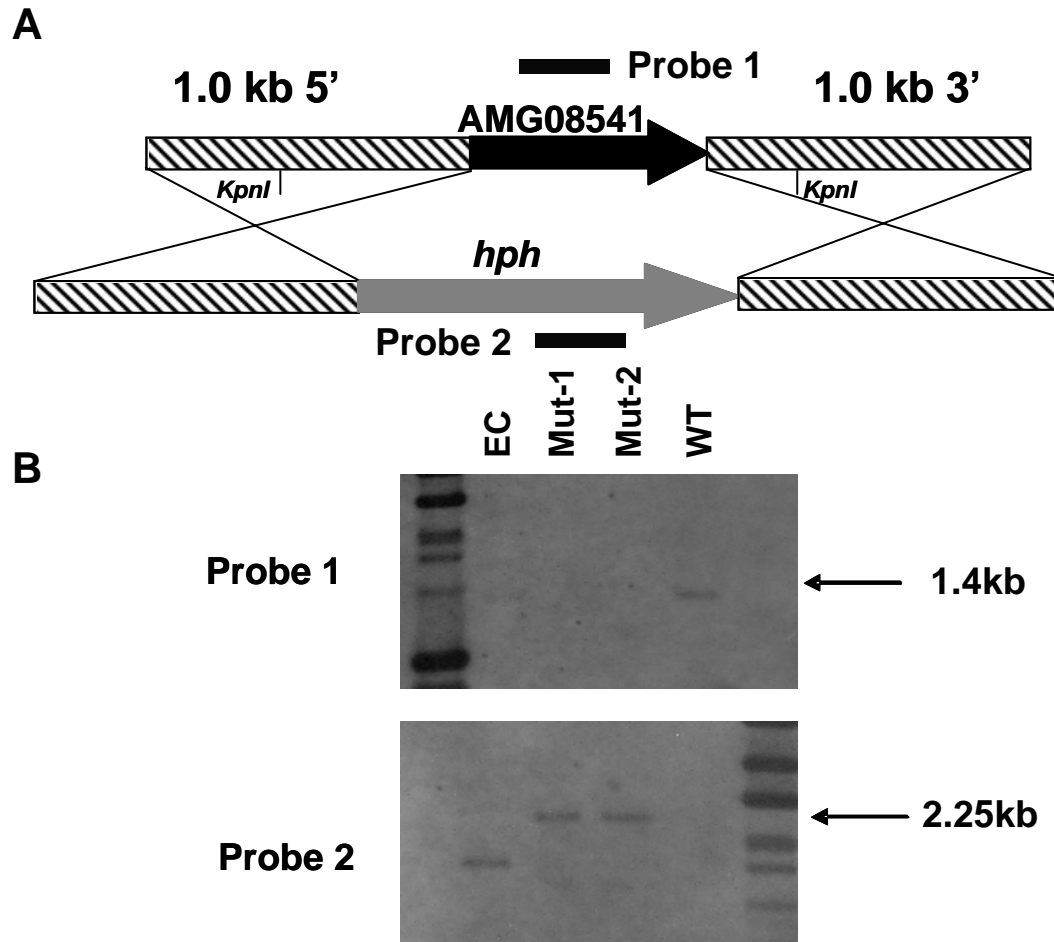
Supplemental Figure 2. Fluorescence expression patterns are conserved for independent fungal transformants expressing putative BAS:YFP proteins, although fluorescence intensities vary due to position effects.

For each gene, the 1-kb promoter and coding sequence was cloned with a C-terminal fusion of YFP. For each, 10 independent transformants were observed during invasion of sheath epidermal cells. Images: DIC (top) and YFP (bottom). For comparison, excitation exposure time was standardized at 2 seconds.

(A) and **(B)** Variation between two independent fungal transformants with **BAS4:YFP**, showing the lowest (+) and the strongest (+++).

(C) and **(D)** Variation between two independent fungal transformants of **BAS3:YFP**, showing the lowest (+) and the strongest (+++).

(E) and **(F)** Southern hybridization analysis was performed with the least (+) and the strongest (+++) fluorescent transformants of **(1) BAS1, (2) BAS2, (3) BAS3** and **(4) BAS4**. The analysis used restriction enzymes EcoRI (E) and BamHI (F), and YFP as a probe. This analysis suggested that the intensity did not depend on copy number, but on position effect instead. Since fluorescence patterns were consistent for each gene, we worked with transformants with the strongest fluorescence.



Supplemental Figure 3. Gene Replacement Analysis of *BAS2*.

The same methods were used for gene knock-out analyses of the other genes.

(A) Schematic diagram of the MGG_09693.6 (black arrow) genomic locus. The gene replacement construct contained the *hph* gene (gray arrow) flanked by ~1000-bp of sequences up-stream and down-stream from the coding sequence.

(B) Southern hybridization analysis was performed using genomic DNAs from an ectopic transformant (EC, KV56), two independent knock-out mutants, Mut-1 (KV54) and Mut-2 (KV55), and the wild-type strain KV1 (WT). *Kpn*I-digested genomic DNAs were separated by electrophoresis in an 0.8% agarose gel. Probe 1 (wild-type coding sequence) hybridized to the expected 1.4-kb fragment in the wild type strain and ectopic transformant, but not in the mutants. Probe 2 (*hph* coding sequence) hybridized with DNAs from the ectopic transformant and the mutants, but not from wild-type.

Supplemental Table 1A. Properties of the 50-most down-regulated genes in IH; most have been previously identified as expressed by fungal cell types *in vitro*.

Probe	Fold change	Putative identity ^a	Signal Peptide	EST / SAGE ^c
AMG06063.1	-83 (0)	Hypothetical protein ^b		cs, cw, my
AMG13759.1	-77 (0)	Hypothetical protein		cm, MG_SGa
AMG06063.2	-60 (2.14E-40)	Hypothetical protein ^b		cs, cw, my
AMG11634.1	-55 (0)	Hypothetical protein ^b		cs, mk, mt, MG_SGa
AMG09784.1	-54 (2.91E-41)	Hypothetical protein		ap, cs, mt, ns
AMG00941.1	-46 (0)	Copper radical oxidase [Q0ZKA5_PHACH, E = 0.0]		mt, ns, su, MG_SGa, OSJNGg
AMG14000.1	-43 (0)	UVI-1, Near-UV induced [Q9P338_9PLEO, 2e-65]	SP	ap cs mk mt ns su
AMG15966	-39 (0)	Short chain dehydrogenase [Q4W9L2_ASPFU, 1e-36]		cm, mt, MG_SGa
AMG09317	-39 (0)	Hypothetical protein, no Broad hit in version 5		cm, cs, cw
AMG01344.2	-38 (0)	Hypothetical protein ^b		cw, MG_SGa, OSJNGg
AMG12371.1	-38 (5.76E-22)	Hypothetical protein ^b		-
AMG09954	-38 (0)	amdA-like protein [A2QBB3_ASPNG, 3e-62]		cs, cw, MG_SGa
AMG08367	-37 (0)	Aminotransferase (A1DHN5_NEOFI, 1e-91)		mk, mt, MG_SGa, OSJNGg
AMG04896.2	-37 (0)	LysM Domain Protein (A1DKY1_NEOFI, 9e-32)	SP	my, ns
AMG01490	-37 (0)	Hypothetical protein, No Broad hit in version 5		cm, ns
AMG01344.1	-36 (0)	F-box domain protein (A1DH69_NEOFI, 6e-39)		cw, su, my, MG_SGa
AMG10496	-36 (0)	Metalloprotease 1 precursor [Q71H76_COCP0, 4e-32]	SP	cm
AMG05375	-35 (0)	Hypothetical protein		cm
AMG07022	-34 (0)	Hypothetical protein		-

AMG05270	-34 (0)	Hypothetical protein (Interpro: Major intrinsic protein)		cm, cs, cw, mt, my, ns, su, MG_SGa
AMG04953	-34 (2.09E-34)	dicarboxylic amino acid permease [Q0C9B3_ASPTN, 1e-120]		cm, cw, mt, MG_SGa
AMG10872	-33 (0)	AAA-family ATPase [A1DD11_NEOFI, 3e-147]		cs, ns, MG_SGa, OSJNGg
AMG14477	-33 (0)	Hypothetical protein	SP	ns, MG_SGa
AMG13759.2	-33 (0)	Hypothetical protein		cw
AMG07762	-32 (0)	Hypothetical protein		cm, cs, cw, MG_SGa
AMG11366	-31 (3.54E-16)	ThiJ/Pfpl family protein [Q4WW31_ASPFU, 2e-34]		cm, MG_SGa, OSJNGg
AMG12878.2	-31 (0)	Hypothetical protein		cm, su, ns, MG_SGa
AMG01944	-28 (0)	Tetrahydroxynaphthalene Reductase [<i>M. oryzae</i> ; E-value = 0]		mk, cm, MG_SGa, OSJNGg
AMG04981	-28 (0)	cytochrome P450 monooxygenase [A4RAE7_MAGGR, E=0.0]		cm, ns, su
AMG05178	-28 (4.13E-07)	DnaJ domain protein [Q4WY25_ASPFU, 1e-20]		cm
AMG05092.2	-27 (0)	Hypothetical protein		cm
AMG13068.2	-27 (0)	Hypothetical protein		ns
AMG06334	-27 (1.74E-31)	IgE-binding protein [O74263_ASPFU, 1e-22]	SP	cm, cw
AMG06993.1	-26 (0)	Hypothetical protein		MG_SGa
AMG06707	-26 (0)	Dipeptidyl-peptidase [A1DGJ8_NEOFI, E = 0]	SP	ns, su
AMG01829.1	-25 (8.91E-34)	Hypothetical protein		cm, cw, my, ns, MG_SGa
AMG02948	-25 (1.19E-21)	BUF1, trihydroxynaphthalene reductase		ap, cm, cs, cw, mk, mt, ns, su, MG_SGa
AMG08668.3	-25 (0)	Hypothetical protein		-
AMG06064	-25 (1.39E-37)	RSY1, scytalone dehydratase (EC 4.2.1.94) - <i>M. oryzae</i>		ap, cm, mt, ns, su

AMG00656	-24 (5.82E-41)	Hypothetical protein		cm, cw, mk, mt, su, MG_SGa, OSJNGg
AMG02248	-24 (0)	Hypothetical protein		-
AMG07563	-24 (1.64E-10)	NF-X1 finger transcription factor [A1DCD3_NEOFI, E= 2e-46]		MG_SGa
AMG14788	-24 (0)	AAA family of ATPase [A2QW59_ASPNG, 9e-127]		ns, MG_SGa
AMG06740	-24 (5.06E-42)	Hypothetical protein		mt
AMG06595	-24 (0)	Hypothetical protein		cm, cw, mt, my
AMG11066	-24 (0)	Fungal-specific transcription factor [O14130_SCHPO, 1e-25]		-
AMG07092	-24 (0)	Hypothetical protein		-
AMG06010	-23 (0)	Hypothetical protein (Interpro: Amidase signature enzyme)		-
AMG01617	-23 (0)	Beta-1, 3 exoglucanase [Q9HE44_NEUCR, E= 0.0]	SP	-
AMG04610.2	-22 (0)	Hypothetical protein		cm, cw, MG_SGa

^aUnless stated otherwise, putative functions are indicated by the UniprotKB/TrEMBL ID (<http://us.expasy.org/>), with corresponding e-value, for the best Uniprot blast match (<http://www.mgosdb.org>)

^bThis predicted gene was deleted from *M. oryzae* genome version 5.

^cLibrary abbreviations: ap = appressoria, cm = mycelium from complete medium, cs = conidiospores, cw = mycelium grown on rice cell walls, mk = *pmk1*⁻ mutant, mt = mating culture, my = mycelium from minimal medium, ns = nitrogen-starved mycelium, and su = subtracted library (Ebbole et al., 2004). SAGE library abbreviations: MG_SGa = mycelium from minimal medium, OSJNGg = compatible interaction at 96 hpi (Gowda et al, 2006).

Supplemental Table 1B. Putative secreted proteins with 10-fold and higher differential expression levels in IH compared to mycelium.

Probe (MGOS name^a)	Fold change (P-value)	Putative identity^b and chromosome location	EST / SAGE^c
AMG08263	100 (0)	Hypothetical protein, Chr. IV	-
AMG08261	100 (0)	BAS1, Hypothetical protein, Chr. IV	-
AMG08417.2	88 (0)	Hypothetical protein, Chr. IV	-
AMG08541	84 (0)	BAS2, Hypothetical protein, Chr. V	-
AMG06765	75 (0)	Hypothetical protein, Chr. III	-
AMG06650	74 (0)	Hypothetical protein, Chr. III	-
AMG12560	71 (0)	BAS3, Hypothetical protein, Chr. IV	-
AMG07384	71 (0)	Hypothetical protein, Chr. IV	-
AMG08859	64 (0)	Hypothetical protein, Chr. V	-
AMG13014	63 (0)	Hypothetical protein, Chr. VI	-
AMG11184	63 (0)	PWL2 protein [NCBI AAA91019 <i>M. oryzae</i> , E = 0.0], Chr. IV and III	-
AMG15980	61 (0)	BAS4, Hypothetical protein, Chr. VI	-
AMG08160	58 (0)	Endochitinase [Q9C199_ANAMU, E = 2e-75], Chr. IV	MG_SGa, OSJNGg
AMG08787	57 (0)	Hypothetical protein (eliminated from Genome assembly 6)	-
AMG08432	51 (0)	Hypothetical protein, Chr. IV	-
AMG14799	49 (0)	Cytosine methyltransferase [Q8NJV9_NEUIN;E = 9e-89]	MG_SGa
AMG16216	48 (0)	Hypothetical protein	-
AMG05133	46 (0)	Multicopper oxidase [Q2UV32_ASPOR, E = 0.0]	-
AMG03019	43 (0)	Hypothetical protein	-
AMG02875	38 (0)	Aspartic proteinase precursor (Q00895_COLGL, e=3e-66)	-
AMG13593.2	36	Hypothetical protein	cw

	(0)		
AMG13918	36 (2.7E-24)	Hypothetical protein	-
AMG02533	36 (1.29E-29)	Hypothetical protein	-
AMG05132	35 (0)	Hypothetical protein	-
AMG15524	33 (0)	Hypothetical protein	-
AMG07601.1	30 (0)	Hypothetical protein	cm
AMG12804	29 (0)	Hypothetical protein	
AMG02457	28 (0)	Acetylcholinesterase [Q2TZ03 ASPOR, 3e-93]	-
AMG13251	28 (0)	Hypothetical protein	-
AMG01557	28 (0)	Hypothetical protein	-
AMG02692	27 (0)	Hypothetical protein	-
AMG03089	27 (0)	Hypothetical protein	my, mt, MG SGa
AMG07577	25 (0)	Hypothetical protein	-
AMG06843	22 (0)	Hypothetical protein	-
AMG11086	22 (0)	Hypothetical protein	-
AMG08195	21 (1.01E-41)	Hypothetical protein	su
AMG09820	20 (0)	Hypothetical protein	-
AMG07137	20 (0)	Hypothetical protein	-
AMG12553	19 (0)	Subtilisin-like serine protease; [Q8X1Y7 METAN; 6e-74]	-
AMG15040	18 (0)	Hypothetical protein	-
AMG04878	17 (0)	Cellulase CelA [A1DF29 NEOFI, 1e-61]	-
AMG13227	17 (0)	Hypothetical protein	-
AMG02455	16 (2.45E-12)	Hypothetical protein	-
AMG13025	15	Hypothetical protein	-

	(5.7E-35)		
AMG07056	15 (0)	Hypothetical protein	-
AMG02439	15 (5.1E-23)	Hypothetical protein	-
AMG06036	14 (0)	Endonuclease/Exonuclease/Phosphatase [Q4WZ13_ASPFU, 3e-43]	-
AMG08482	14 (3.41E-28)	Hypothetical protein	-
AMG02914	13 (3.39E-30)	Hypothetical protein	-
AMG12924	13 (0)	Hypothetical protein	-
AMG02925	13 (0)	Hypothetical protein	-
AMG13855	13 (8.01E-41)	Hypothetical protein	-
AMG00035	13 (1.40E-45)	Hypothetical protein	-
AMG07561	13 (0)	Hypothetical protein	cm
AMG02702	12 (0)	Hypothetical protein	-
AMG04075	11 (3.71E-42)	Hypothetical protein	-
AMG08865	10 (0)	Hypothetical protein	-
AMG08416.1	10 (0)	Hypothetical protein	ns
AMG06620	10 (2.60E-29)	Hypothetical protein	-

^aMGOS gene names correspond to the probes used in version 2 of the Agilent *M. oryzae* microarray. They will not change with new releases of the genome sequence. MGOS names can be converted to Broad Database gene names at www.mgosdb.org.

^bUnless stated otherwise, putative functions are indicated by the UniprotKB/TrEMBL ID (<http://us.expasy.org/>), with corresponding e-value, for the best Uniprot blast match (<http://www.mgosdb.org>)

^c“-“ indicates no EST or SAGE hits. Hits are labeled according to the library in which they occurred. EST library abbreviations: ap = appressoria, cm = mycelium from

complete medium, cs = conidiospores, cw = mycelium grown on rice cell walls, mk = *pmkI*⁻ mutant, mt = mating culture, my = mycelium from minimal medium, ns = nitrogen-starved mycelium, and su = subtracted library (Ebbole et al., 2004). SAGE library abbreviations: MG_SGa = mycelium from minimal medium, OSJNGg = compatible interaction at 96 hpi (Gowda et al, 2006).

Supplemental Table 1C. Expression levels of characterized *M. oryzae* pathogenicity genes in IH relative to mycelium.

Probe	Fold Change (P-value)	Gene Identity	E-value, NCBI Accession #	Role ^b
AMG04255	3 (4.8E-04)	<i>ACII</i> , MAC1 (adenylate cyclase)-interacting protein 1	4e-45, AY166602	C, A
AMG05982	2^a (5.0E-09)	<i>MST12</i> , transcription factor downstream of <i>PMKI</i>	7e-37, AF432913	P, INF
AMG02428	2 (0.08)	<i>ACE1</i> , Appressorium-specific PK-NRPS enzyme	0.0, AJ704622	AVR
AMG03578.1	2 (0.004)	<i>CALM</i> , Calmodulin	7e-74, AF103729	A
AMG06876	2 (5.6E-04)	<i>NTH1 (PTH9)</i> , neutral trehalase	0.0, AAN46743	INF
AMG14183	2 (0.086)	<i>MgAPT2</i> , P-type ATPase	0.0, XM_366691	INF
AMG10289	1 (0.025)	<i>SPMI</i> , vacuolar subtilisin-like serine proteinase	0.0, AB070268	C, A, INF
AMG07015	1 (0.1)	<i>PMKI</i> , pathogenicity MAP kinase	0.0, U70134	A, INF
AMG12418.1	1 (0.47)	<i>MAGB</i> , G α subunit of a heterotrimeric G protein	1e-98, AF011341	A
AMG06279	1 (0.73)	<i>MGB1</i> , G β subunit of a heterotrimeric G protein	0.0, AB086901	C, A, P
AMG08776	1 (0.75)	<i>ABC1</i> , ATP-driven efflux pump protein	0.0, AF032443	INF
AMG08216	-1 (0.61)	<i>ABC3</i> , MDR efflux pump	0.0 DQ156556	P
AMG05260	-5^a (1.3E-08)	<i>PTH11</i> , integral membrane protein AF119670	0.0, AF119670	A
AMG06174	-21^a (0.0)	<i>AOX</i> , alternative oxidase	1e-66, AB005144	INF?
AMG14765	-22^a (3.1E-40)	<i>MPG1</i> , hydrophobin	6e-54, L20685	A
AMG06064	-25^a (1.4E-37)	<i>RSY1</i> , scytalone dehydratase	0.0, AB004741	P
AMG02948	-25^a (1.2E-21)	<i>BUF1</i> , trihydroxynaphthlene reductase	0.0, AY846878	P
AMG01944	-28^a (0.0)	<i>4HNR</i> , tetrahydroxy-naphthalene reductase	0.0, XM_365550	P

^aP-value still significant after Bonferroni correction.

^bPathogenicity trait affected: C=conidiation, A=appressorium formation, P=penetration, INF=infectious growth (usually defined as inability to infect wounded tissue), AVR=avirulence activity in rice with corresponding *R* gene

Supplemental Table 2: Rice gene categories with members that were up- or down-regulated >3-fold in rice tissue undergoing biotrophic invasion.

Gene Id	Fold change	Best Homology (E-value)	Comments
WRKY			
AK106282	19	<i>Oryza sativa</i> (indica cultivar-group) transcription factor WRKY09 (WRKY09) mRNA, complete cds (5.0E-80)	
AK102093	12	<i>O. sativa</i> (indica cultivar-group) WRKY DNA-binding protein (WRKY89) mRNA, complete cds (1.0E-121).	
AK066255	11	<i>O. sativa</i> (japonica cultivar-group) WRKY45 mRNA, complete cds (0.0).	
AK108860	10	<i>Solanum tuberosum</i> StWRKY mRNA for WRKY-type DNA binding protein, complete cds (5.0E-42).	
AK108555	8	<i>Arabidopsis thaliana</i> WRKY transcription factor 51 (WRKY51) mRNA, complete cds (8.0E-29)	
AK065265	5	<i>O. sativa</i> (indica cultivar-group) transcription factor WRKY31 mRNA, complete cds (1.0E-164).	
AK101653	4	<i>A. thaliana</i> putative WRKY-type DNA binding protein (At2g46400) mRNA, complete cds (5.0E-14).	
AK108389	3	<i>O. sativa</i> (indica cultivar-group) transcription factor WRKY08 mRNA, complete cds (2.0E-50).	
AK109568	3	<i>O. sativa</i> (japonica cultivar-group) WRKY17 mRNA, complete cds (0.0).	
AK107199	3	<i>O. sativa</i> (japonica cultivar-group) WRKY24 mRNA, complete cds (0.0).	
Defense / Resistance Related			
AK100135*	49 (0)	<i>O. sativa</i> PDR-type ABC transporter	Regulated by abiotic stress in rice roots (Moons et al 2003 FEBS Lett. 553:370)
AK063248	28	<i>Hordeum vulgare</i> HvPR-1a mRNA for a basic PR-1-type pathogenesis-related protein (2.0E-34).	
AK060005	14	<i>H. vulgare</i> HvPR-1a mRNA for a basic PR-1-type pathogenesis-related protein (1.0E-32)	

AK066825	14	<i>O. sativa</i> lipoxygenase (CM-LOX2) mRNA, partial cds (0.0).	
AK061606	13 (0)	<i>O. sativa</i> (japonica cultivar-group) RSOsPR10 mRNA for root specific pathogenesis-related protein 10 (0.0).	
AK105311	12	Pleiotropic drug resistance-like protein	Homology to NtPDR, an elicitor-responsive gene in tobacco (Sasabe et al. 2002 FEBS Lett. 518:164)
AK101439	8	<i>H. vulgare</i> mRNA for NBS-LRR disease resistance protein homologue (rga S-9202 gene) (1.0E-51).	
AK064985	6	<i>A. thaliana</i> RPT2 (RPT2) mRNA, complete cds (1.0E-100).	
AK060057	5	<i>O. sativa</i> (japonica cultivar-group) Prb1 mRNA, complete cds (0.0).	
AK111104	5 (0)	<i>Arabidopsis thaliana</i> putative thaumatin (At4g38660) mRNA, complete cds. PLN	Only 2 out of 6 thaumatin-like genes were differentially regulated at the ≥ 3 -fold
AK099946	4 (8.69E-09)	<i>O. sativa</i> mRNA for thaumatin-like protein. PLN	2 nd thaumatin-like gene
AK101496	3	<i>H. vulgare</i> partial mRNA for NBS-LRR disease resistance protein (rga S-9203 gene) (7E-90).	
AK073881	3	<i>Prunus persica</i> put. NBS-LRR type disease resistance protein (RPM1) mRNA, complete cds (2E-47).	
AK108785	3 (5.8E-4)	<i>Solanum lycopersicoides</i> disease resistance protein SIVe2 precursor, mRNA, complete cds (3.0E-53).	
AK111610	-3	resistance to <i>Pseudomonas syringae</i> protein 5 [imported] - <i>A. thaliana</i> (2.0E-86).	
Peroxidases			
AK102307	14	<i>O. sativa</i> cationic peroxidase (OsCPX1) mRNA, complete cds (0.0).	
AK104277	13	<i>H. vulgare</i> peroxidase BP 1 (Prx5) mRNA, complete cds (6.0E-99).	
AK072761	9	<i>Gossypium hirsutum</i> bacterial-induced peroxidase mRNA, complete cds (1.0E-62).	
AK064918	9	<i>A. thaliana</i> mRNA for peroxidase ATP22a (1.0E-84).	
AK109480	9	<i>H. vulgare</i> peroxidase BP 1 (Prx5) mRNA, complete cds (1.0E-101).	

AK069456	8	<i>Asparagus officinalis</i> mRNA for peroxidase (prx3 gene) (1.0E-125).	
AK065893	7	<i>A. thaliana</i> At4g32320 mRNA for putative L-ascorbate peroxidase, complete cds (1.0E-85).	
AK065090	7	<i>Z. mays</i> mRNA for anionic peroxidase (4.0E-71).	
AK070715	5	<i>Triticum monococcum</i> peroxidase 8 (POX8) mRNA, complete cds (1.0E-120).	
AK067667	5	<i>Z. mays</i> mRNA for anionic peroxidase (9.0E-73).	
AK067416	4	<i>Z. mays</i> partial mRNA for peroxidase (pox3 gene) (1.0E-123).	
AK058883	4	<i>Z. mays</i> mRNA for peroxidase (pox1 gene) (4.0E-84).	
AK104633	3	<i>Ipomoea batatas</i> mRNA for peroxidase (pod gene) (7.0E-94).	
AK106200	3	<i>Spinacia oleracea</i> peroxidase prx12 precursor, mRNA, complete cds (3.0E-72).	
AK103558	3	<i>Z. mays</i> mRNA for anionic peroxidase (1.0E-79).	
AK109551	3	<i>Nicotiana tabacum</i> mRNA for cationic peroxidase isozyme 40K, complete cds (2.0E-70).	
AK073202	3	<i>O. sativa</i> peroxidase (POX22.3) mRNA, complete cds (0.0).	
AK060007	3	<i>S. oleracea</i> mRNA for peroxidase, clone PC55 (3.0E-92).	
AK101508	-3	<i>Nicotiana tabacum</i> mRNA for cationic peroxidase isozyme 40K, complete cds (1.0E-72).	
AK069281	-3	<i>Triticum monococcum</i> peroxidase 7 (POX7) mRNA, complete cds (0.0).	
Kinases			
AK105196	96	<i>Z. mays</i> NPK1-related protein kinase-like protein (mapkkk1) mRNA, partial cds (7.0E-72).	
AK109702	86	<i>Z. mays</i> NPK1-related protein kinase-like protein (mapkkk1) mRNA, partial cds (1.0E-62).	

AK071585	77	NPK1-related protein kinase homolog T26B15.7 - <i>A. thaliana</i> (1.0E-58).	
AK107168	44	<i>Z. mays</i> NPK1-related protein kinase-like protein (mapkkk1) mRNA, partial cds (3.0E-93).	
AK111977	35	<i>Z. mays</i> Avr9/Cf-9 induced kinase 1 (ACIK1) mRNA, complete cds (1.0E-124).	
AK058518	29	NPK1-related protein kinase homolog F10M23.230 - <i>A. thaliana</i> (6.0E-64).	
AK105946	26	<i>Z. mays</i> NPK1-related protein kinase-like protein (mapkkk1) mRNA, partial cds (2.0E-70).	
AK107566	12	<i>O. sativa</i> (japonica-group) clone OsJalk8 putative leucine-rich repeat receptor-like kinase (0.0).	
AK099582	13	wall-associated serine/threonine kinase (EC 2.7.1.-) 2 [imported] - <i>A. thaliana</i> (6.0E-89).	
AK100906	10	probable diacylglycerol kinase [imported] - <i>A. thaliana</i> (0.0).	
AK102590	10	<i>Lycopersicon esculentum</i> diacylglycerol kinase (DGK1) mRNA, complete cds (0.0).	
AK072014	8	<i>A. thaliana</i> WNK3 mRNA for protein kinase, complete cds (1.0E-63).	
AK069094	8	<i>A. thaliana</i> protein kinase-like protein (At3g25840) mRNA, complete cds (5.0E-94).	
AK068330	6	<i>Nicotiana tabacum</i> Avr9/Cf-9 induced kinase 1 (ACIK1) mRNA, complete cds (1.0E-133).	
AK105337	6	<i>A. thaliana</i> At5g47070 mRNA for putative serine /threonine kinase, clone: RAFL17-20-O04 (2.0E-95).	
AK106447	6	receptor-protein kinase-like protein - <i>A. thaliana</i> (2.0E-98).	
AK069157	6	<i>O. sativa</i> subsp. indica pyruvate dehydrogenase kinase 1 mRNA, complete cds (0.0).	
AK110253	6	<i>Z. mays</i> mRNA for putative protein kinase (0.0).	
AK109607	6	<i>A. thaliana</i> putative protein kinase (At2g05940) mRNA, complete cds (1.0E-119).	
AK100357	6	<i>A. thaliana</i> putative casein kinase (At3g13670) mRNA, complete cds (0.0).	

AK100082	5	<i>A. thaliana</i> putative receptor protein kinase (At1g28440) mRNA, complete cds (0.0).	
AK068025	5	<i>O. sativa</i> (japonica cultivar-group) mRNA for orthophosphate dikinase, complete cds (0.0).	
AK102758	5	<i>Z. mays</i> KI domain interacting kinase 1 (KIK1) mRNA, complete cds (0.0).	
AK072243	5	<i>O. sativa</i> fructose-6-phosphate-2-kinase/fructose-2,6-bisphosphatase mRNA, complete cds (0.0).	
AK106421	4	<i>A. thaliana</i> Columbia protein kinase mRNA, complete cds (7.0E-97).	
AK100389	4	<i>O. sativa</i> (japonica cultivar-group) MAPK6 mRNA, complete cds (0.0).	
AK066978	4	<i>Lycopersicon esculentum</i> auxin-regulated dual specificity cytosolic kinase mRNA, complete cds (2.0E-50).	
AK061645	4	<i>O. sativa</i> (japonica cultivar-group) MAPK6 mRNA, complete cds (0.0).	
AK108455	4	<i>A. thaliana</i> putative protein kinase (At1g67580; F12B7.13) mRNA, complete cds (5.0E-40).	
AK110482	3	<i>A. thaliana</i> putative receptor serine/threonine kinase PR5K (PR5K) mRNA, complete cds (1.0E-93).	
AK071798	3	<i>Prunus armeniaca</i> pyrophosphate-dependent phosphofructo-1-kinase mRNA, partial cds (1.0E-109).	
AK111550	3	<i>A. thaliana</i> At4g23180 mRNA for putative receptor-like protein kinase 4 (RLK4), complete cds (1.0E-110).	
AK105151	3	<i>O. sativa</i> (indica cultivar-group) choline kinase (CK) mRNA, complete cds (0.0).	
AK071968	3	<i>O. sativa</i> (indica cultivar-group) choline kinase (CK) mRNA, complete cds (0.0).	
AK103306	3	<i>A. thaliana</i> calcium-dependent protein kinase (At3g51850) mRNA, complete cds (1.0E-162).	
AK067266	3	<i>A. thaliana</i> ATPK64 mRNA for protein kinase, complete cds (3.0E-47).	
AK109954	3	<i>Nicotiana tabacum</i> cytokinin-regulated kinase 1 (CRK1) mRNA, complete cds (4.0E-78).	

AK101080	3	<i>Z. mays</i> phosphoenolpyruvate carboxylase kinase 1 (PPCK1) mRNA, complete cds (1.0E-149).	
AK111842	3	leucine-rich repeat transmembrane protein kinase 1 - <i>Z. mays</i> (fragment) (1.0E-170).	
AK061220	3	serine/threonine protein kinase-like protein - <i>A. thaliana</i> (1.0E-138).	
AK065374	3	<i>A. thaliana</i> SOS2-like protein kinase PKS8 mRNA, complete cds (1.0E-121).	
AK064359	-3	<i>A. thaliana</i> putative receptor protein kinase (At5g53890) mRNA, complete cds (0.0).	
AK067238	-3	<i>A. thaliana</i> clone RAFL15-23-F05 (R20566) putative cell division-related protein (At1g53050) mRNA (1.0E-162).	
AK067723	-3	<i>A. thaliana</i> putative receptor protein kinase (At1g28440) mRNA, complete cds (0.0).	
AK103166	-4	<i>A. thaliana</i> putative receptor protein kinase (At5g53890) mRNA, complete cds (0.0).	
AK073574	-5	<i>Saccharum</i> hybrid cultivar SP70-1143 SHR5-receptor-like kinase mRNA, partial cds (1.0E-142).	
Chitinases			
AK059767	20	<i>Tulipa bakeri</i> tbc1 mRNA for bulb chitinase-1, complete cds (1.0E-74).	
AK071453	11	<i>O. sativa</i> (japonica cultivar-group) class III chitinase RCB4 (Rcb4) mRNA, complete cds (1.0E-150).	
AK100973	9	<i>O. sativa</i> (japonica cultivar-group) mRNA for acidic class III chitinase OsChib3a, complete cds (0.0).	
AK102505	7	<i>O. sativa</i> (japonica cultivar-group) mRNA for chitinase, complete cds (8.0E-69).	
AK108949	5	<i>O. sativa</i> mRNA for endochitinase (0.0).	
AK073843	4	<i>O. sativa</i> (japonica cultivar-group) mRNA for chitinase, complete cds (2.0E-87).	
AK064180	3	<i>O. sativa</i> (japonica cultivar-group) mRNA for chitinase, complete cds (2.0E-58).	

AK061042	3	<i>O. sativa</i> mRNA for endochitinase (0.0).	
Membrane Proteins			
AK06487	59 (5.4E-19)	<i>A. thaliana</i> At2g46890 mRNA for unknown protein, clone: RAFL17-06-H20 (1E-100).	
AK107700	26 (0)	<i>Z. mays</i> plasma membrane integral protein ZmPIP2-6 mRNA, complete cds (1.0E-127).	
AK072632	6	<i>Z. mays</i> plasma membrane integral protein ZmPIP2-6 mRNA, complete cds (0.0).	
AK061898	5	<i>O. sativa</i> (japonica cultivar-group) mRNA for membrane related protein (mrp1 gene) (0.0).	
AK065035	5	<i>O. sativa</i> (japonica cultivar-group) mRNA for membrane related protein (mrp1 gene) (0.0).	
AK061782	5	<i>Triticum aestivum</i> plasma membrane intrinsic protein 2 (PIP2) mRNA, complete cds (0.0).	
AK102174	4	<i>Z. mays</i> plasma membrane integral protein ZmPIP1-5 mRNA, complete cds (0.0).	
AK058648	4	<i>Saccharum</i> hybrid cultivar H65-7052 membrane protein mRNA, complete cds (2.0E-80).	
AK102748	3	<i>Gossypium hirsutum</i> membrane-anchored endo-1,4-beta-glucanase (CEL) mRNA, complete cds (0.0).	
AK066134	3	(O49621) MLO-like protein 1 (AtMlo1) (MLO protein homolog 1) (AtMLO-H1) (1.0E-101).	
AK107345	-43 (8.8E-10)	<i>A. thaliana</i> integral membrane protein, putative (At3g21690) mRNA, complete cds (1.0E-126).	
Heat Shock proteins			
AK100412	5	<i>O. sativa</i> (japonica cultivar-group) Spl7 mRNA for heat stress transcription factor Spl7, complete cds (0.0).	
AK064271	5	<i>A. thaliana</i> At2g26150 mRNA for putative heat shock transcription factor, complete cds (5.0E-54).	
AK101934	4	<i>Lycopersicon peruvianum</i> heat stress transcription factor A3 (HSFA3) mRNA, complete cds (1.0E-68).	

AK101824	4	<i>O. sativa</i> (japonica cultivar-group) heat shock factor RHSF5 mRNA, complete cds (0.0).	
AK066844	3	<i>O. sativa</i> (japonica cultivar-group) heat shock factor RHSF7 mRNA, complete cds (1.0E-149).	
AK062091	3	<i>Fragaria x ananassa</i> LMW heat shock protein mRNA, complete cds (2.0E-24).	
Glucanases			
AK063953	32 (0)	<i>O. sativa</i> endo-1,3-beta-glucanase mRNA, complete cds (0.0).	
AK058891	4	Sorghum bicolor beta-1,3-glucanase mRNA, partial cds (5.0E-89).	
AK069096	3 (3.9E-29)	<i>O. sativa</i> endo-1,3-beta-glucanase mRNA, complete cds (0.0).	
AK104139	-4 (0)	<i>O. sativa</i> endo-1,3-beta-glucanase mRNA, complete cds (0.0).	
AK103072	-4 (3.9E-33)	<i>A. thaliana</i> putative beta-1,3-glucanase (At2g27500) mRNA, complete cds (1.0E-122).	
Pectin-Degrading Enzymes			
AK073853	4	<i>A. thaliana</i> putative polygalacturonase (At1g60590/F8A5_12) mRNA, complete cds (1.0E-139).	
AK100257	-3	<i>Z. mays</i> mRNA for pectin methylesterase-like protein (1.0E-126).	
AK105858	-4	<i>Lycopersicon esculentum</i> polygalacturonase (XOPG1) mRNA, complete cds (1.0E-112).	
AK106049	-4	<i>Lycopersicon esculentum</i> polygalacturonase (XOPG1) mRNA, complete cds (1.0E-108).	
AK101962	-5	<i>A. thaliana</i> clone U11512 putative pectin methylesterase (At5g09760) mRNA, complete cds (1.0E-135).	

Phenylalanine Ammonia Lyases			<i>Note that the 4 additional PAL genes were not differentially regulated in this category.</i>
AK068993	5	<i>Bambusa oldhamii</i> phenylalanine ammonia-lyase (PAL1) mRNA, complete cds (0.0).	
AK067801	5	<i>Bambusa oldhamii</i> phenylalanine ammonia-lyase (PAL1) mRNA, complete cds (0.0).	
Expansins			
AK060313	3	<i>O. sativa</i> expansin Os-EXP3 (Os-EXP3) mRNA, complete cds (0.0).	
AK064012	3	<i>O. sativa</i> beta-expansin (EXPB4) mRNA, complete cds. PLN	
AK062225	-3	<i>O. sativa</i> alpha-expansin OsEXP10 mRNA, complete cds (0.0).	
AK061068	-5	<i>O. sativa</i> beta-expansin (EXPB2) mRNA, complete cds (1.0E-155).	
AK100959	-9	<i>O. sativa</i> beta-expansin (EXPB3) mRNA, complete cds (0.0).	

SUPPLEMENTAL TABLE 3. Comparison of rice gene expression in our study with expression during wounding in the study of Katou et al. (2007).

Gene	Putative Function	Expression during biotrophic invasion	Expression 24 hr after wounding ^a
AK060800	<i>O. sativa</i> chlorophyll a/b-binding protein precursor	-29.	6
AK063251	Unknown expressed protein	-3	3
AK064485	<i>A. thaliana</i> At5g41080, unknown protein	21	1
AK065358	<i>Gossypium hirsutum</i> dehydration-induced protein RD22-like protein (RDL)	-3	1
AK069119	Unknown expressed protein	6	0
AK069313	<i>A. thaliana</i> clone 40186 mRNA	3	2
AK070656	<i>O. sativa</i> (indica cultivar-group) osnas3, nicotianamine synthase 3	-2	0
AK070684	<i>A. thaliana</i> putative purple acid phosphatase (At1g14700)	-3	1
AK099574	<i>O. sativa</i> (japonica cultivar-group) small subunit of ribulose-1,5-bisphosphate carboxylase	4	0
AK100959	<i>O. sativa</i> beta-expansin (EXPB3) mRNA	-9	2
AK105666	<i>Nicotiana tabacum</i> , CND41, chloroplast nucleoid DNA binding protein	-6	2
AK106493	Unknown expressed protein	4	3
AK107926	<i>Triticum aestivum</i> pathogenesis-related protein 1	-2	7

^aData from Katou et al. (2007), also using the Agilent rice array. They analyzed cut leaf tissue. Additionally, a mitogen-activated protein kinase phosphatase OsMKP1 (AK105748) that was highly induced by wounding showed no change in expression levels in our infected tissue.

Supplemental Table 4. Primers used in this study

Primer Name	Sequence 5'-3'	Description
Fungal primers for gene knock-out cassette		
AMG08541-5'F	CGGAATTCTAGATCATGGGCGGTTGTC	1-kb 5'-flanking region of MGG_09693.6
AMG08541-5'R	TTGACCTCCACTAGCTCCAGCCAAGCCGT TAGTGGAACGTCACCATC	
AMG08541-3'F	GAATAGAGTAGATGCCGACCGCGGGTTGA CTAGTTCTAGGTCTGGTG	1-kb 3'-flanking region of MGG_09693.6
AMG08541-3'R	GCTCTAGAGTGGTTGTACACAATGGCG	
AMG12560-5'F	GGCAAGCTTCGATTTGGCGACTGGTGTA	1-kb 5'-flanking region of MGG_11610.6
AMG12560-5'R	TTGACCTCCACTAGCTCCAGCCAAGCCAC TGCATCTTGATGGTTGGG	
AMG12560-3'F	GAATAGAGTAGATGCCGACCGCGGGTTCA TCGCTAGTGTGGCTCTC	1-kb 3'-flanking region of MGG_11610.6
AMG12560-3'R	GGCCCCGGGGCTGTATTGATCGAGCCGAG	
AMG08261-5'F	CGGAATTCTGCGACAATACCATAACGCC	1-kb 5'-flanking region of MGG_04795.6
AMG08261-5'R	TTGACCTCCACTAGCTCCAGCCAAGCCTG TGTTAGAACCTTGGTCGG	
AMG08261-3'F	GAATAGAGTAGATGCCGACCGCGGGTTAT CGGCTTGGTCGATTACGG	1-kb 3'-flanking region of MGG_04795.6
AMG08261-3'R	GCTCTAGAGTCGCGTCAGTGAACCTAACC	
HYG-1F	GGCTTGGCTGGAGCTAGTGGAGG	1.4-kb hygromycin gene
HYG-2R	AACCCGCGGTCGGCATCTACTCTA	
Fungal primers for fluorescent protein fusion		
AMG08261-SP2-F	CCGGAATTCACAGAATAAGACACGGCAAG ATTTA	1.3-kb MGG_04795.6 promoter plus entire coding sequence
AMG08261-SP2-R	CGCGGATCCCGGTAATAATTCTCCACCC GTCTA	
AMG08261-SP2-R2	GGATCCTTTAGGAATAATTGGTAAAGAT	1.0-kb MGG_04795.6 promoter sequence; used with the primer AMG08261-SP2-F
AMG08541-SP3-F	CCGGAATTCGAAAGCTCGACTCCCGAGG AGCTG	1.4-kb MGG_09693.6 promoter plus entire coding sequence
AMG08541-SP3-R	CGCGGATCCGAAACCCTGCTTCTTGACCT GCTCC	
AMG12560-SP4-F	CCGGAATTCGCAGAGTGTCATCCGATAAT CACAT	1.5-kb MGG_11610.6 promoter plus entire coding sequence
AMG12560-SP4-R	CGCGGATCCGTGGGCACTGTTGGCAGCGC CGTTC	
AMG12560-SP4-R2	GGATCCCTTGATGGTTGGGTTTTGG	1.0-kb MGG_11610.6

		promoter
AMG15980-SP5-F	CCGGAATTCGGTAGCTTCTACGGATGCGT CCGAT	1.5-kb MGG_10914.6 promoter plus entire coding sequence
AMG15980-SP5-R	CGCGGATCCAGCAGGGGGGATAGACGAGC CAGTA	
FBamYFP	CGCGGATCCGCGATGGTGAGCAAGGGCGA GGAGCTGT	1.0-kb EYFP and <i>Neurospora crassa</i> β - tubulin terminator
RHind3T	CCCAAGCTTGGGATCATCATGCAACATGC ATGTACTG	
CKP23_EcoRI- RP27	GAATTCGAATTGGGTACTCAAATTGG	0.5-kb <i>M. oryzae</i> ribosomal protein 27 promoter
CKP16_RP27- BamHI-atgg	CCATGGATCCTTTGAAGATTGGGTTCCTA C	
CKP17_EGFP-PstI	CTGCAGGTGTGAGCAAGGGCGAGGAG	1.0-kb EGFP and <i>Neurospora crassa</i> β - tubulin terminator
CKP18_RB-p2	GGGCCTCTTCGCTATTAC	
CKP35_mRFP-Bam	GGATCCGCCTCCTCCGAGGACGTC	mRFP reporter gene
CKP36_mRFP-Sph	GCATGCTTAGGCGCCGGTGGAGTG	
CKP110_SP5P-F	GAATTCGGTAGCTTCTACGGATGC	MGG_10914.6 (<i>BAS4</i>) promoter
CKP111_SP5P-R	GGATCCTGTGAAAAGATTCGTTGTG	
CKP104_SP5SP-F	GGATCCATGCAGCTCTCATTCTC	MGG_10914.6 (<i>BAS4</i>) sequence for signal peptide
CKP105_SP5SP-R	CTGCAGGGTGCAGATCGGCCGTAG	
AVR-Pita1-P1	CGGAATTCGCCGAGTCGTTCTGA	<i>AVR-Pita1</i> promoter plus the sequence for signal peptide
AVR-Pita1-S1	GGGATCCAATGTTGGTGAAGGCC	
Fungal primers for RT-PCR		
AMG15373-3-F	CGCCGTCTACGCCATCCTGG	
AMG15373-4-R	CCGCCTGGTGATGACGTCGG	
AMG08263-F	AAATCAATCAAACGCGGGACTGGC	
AMG08263-R	ACATGGCGTCCTCATCATCGGAAT	
AMG08261-F	TTTACGGTGCTTGCCACCTTTACC	
AMG08261-R	GCCTTCCATTGCTCGAATCTGCTT	
AMG08541-F	AAGAACGTCGGCACAGGTAACGG	
AMG08541-R	CTTAACGGTCTGGGCCTTGTTGG	
AMG06765-F	GAAGGCGACCGTGCTTGCAATTT	
AMG06765-R	TTGCATCCCCTCTCCTTCAGAGCAA	
AMG06650-F	GCAGCTCCACAACGTCTGTTCAAT	
AMG06650-R	AGTCACAGTAGCCGCACGAGTATT	
AMG12560-F	AGACTTCCCCGGTGCCAAAGC	
AMG12560-R	AGATGCAGGGGTTGTCCCCG	
AMG13016-F	TTTCGCTACTGTTGCCACCTTGG	
AMG13016-R	TTAGTTAAGCTGGGTACCCTCCGC	
AMG05292-F	AGCACCTCGACCAAAGTCAAGCTA	

AMG05292-R	TGGCAAGTGTAGCCGTTGATAAGC	
AMG13014-F	GGACAACTTTACGCCGCTCAACAA	
AMG13014-R	TATCATCCCTCAACCAGCCCAACA	
AMG08701-F	CCGTGGGCTACGGCTATGAAATTA	
AMG08701-R	ATGGAACCTGCATGTGACGCGTAT	
AMG15980-F	AGCTCTCATTCTCAGCAATCGCCA	
AMG15980-R	TCATTTCCGTCCAGAGACTTGGCA	
AMG08508-F	TGTTACCATGTTTCGCCGTTGGT	
AMG08508-R	CATAGTCCGAGAACTTTGCTTGGC	
AMG08160-2-F	ATGTCACTCGTTAACCTCTCCAGG	
AMG08160-3-R	AACGAGATGAAGTTGGCCGTGT	
AMG05133-F	TGGCATCCGACAGAACTACACCAA	
AMG05133-R	TCAAGCGAGAACTTCCAGTGCGTA	
AMG08859-F	GCGATGTTACCTGACCTGGG	
AMG08859-R	AGCCGTA CTGTAGCTGGTGCG	
AMG08417.2-F	AAAGATCCTGCACTCGCTCATCGT	
AMG08417.2-R	ACCTGGTCCCAATACTCAGTGCAA	
AMG16082-F	CGCAAGCAGTTCCATCGAAGCTTTAC	
AMG16082-R	ATTGCTCCACTTCTTCGAATCGGG	
AMG15020-F	TGACCAATGGCAACAAGCGCGA	
AMG15020-R	TCTTGGAGCCAGTCTTGGTGCTA	
PWL2-F	GTGGCGGGTGGACTAACAAACAAT	
PWL2-R	AAACTCGCCTGGCGGTCCATAATA	
AVR-PITA-F	GCACCTTTTCACACCCAGTT	
AVR-PITA-R	CTCGGACGCACGTATAAACA	
AMG12697.1-F	ATTTCCGACAATGCACAGCCGCTAC	
AMG12697.1-R	CATGTCGGCACCTTTGATGTTGCT	
AMG05260-F	AATCCGACTCTTTCAGTAGCGGCA	
AMG05260-R	CTCCATGCATTTGCCTTCGATGCT	
AMG06064-F	ATGACTTGCCTATGAGTGGGCA	
AMG06064-R	TATTTGTCGCCAAAGGTCTCCCGT	
AMG01994-F	CTTTGT CATGTCCAACAGCGGCAT	
AMG01944-R	CAAATGCACGGCAGAAACCCTCAA	
MgACTIN328-F	TCCCATGTCACCACTTTCAA	
MgACTIN328-R	TTCGAGATCCACATCTGCTG	
Rice primers for RT-PCR		
RICE PRIMERS		
OsACTIN-F	GAAGATCACTGCCTTGCTCC	
OsACTIN-R	CGATAACAGCTCCTCTTGGC	
MOS41902-F	ATCTTGGCCGAGTGTGACGAGAT	AK071227
MOS41902-R	TCAAAGTTGTTTGCTCGCCGAAGG	
MOS04462-F	TACTGGAGCACCCATTTCTCGCAT	AK105196
MOS04462-R	TCCGAAACTTCAGATGGGTGCTT	

MOS28016-F	ATTGGAATCAGACGATGGCTGGA	AK109702
MOS28016-R	TTGGCGGAGCTGTTTCATCCACAAA	
MOS04461-F	AAGGACTTCCTGGATGGCTGCTT	AK071585
MOS04461-R	TGGAGGATTCGATCGCTTCTGCTT	
MOS45375-F	ACATGCCGCTCTGGAGCTACTAAT	AK062422
MOS45375-R	AGCTCTTTGGAGAGGAGAAGTAAA	
MOS19247-F	AGCATCAGGGTGATTCCCTTGTCA	AK071546
MOS19247-R	TCAATCAGGCCCTCATGGTCTTGT	
MOS03724-F	CAGTGGAGCTTGTTGCAAACCCTT	AK100135
MOS03724-R	TCACCACCTCGCTTCATCAGGAAA	
MOS52342-F	GCTTGCCTTCGTCAAGTTCTTGGT	AK059060
MOS52342-R	TCTCACTTCCACCTCTTCGCGTTT	
MOS56011-F	ATGAAGCTCAACCCTGCTGTGGAT	AK061606
MOS56011-R	AGGAAGCAGCAATACGGAGATGGA	
MOS52906-F	CGACCATCGGCAATTTTCATTCGGT	AK069082
MOS52906-R	ACCGTTAAGCTGGTTGGTCCTGAA	
MOS00599-F	TGGAGCTCCTGGATGCTGGAAATA	AK108785
MOS00599-R	AGGAGCTGATGCACTTGGAGATGT	
AK107735-F	AGCAAGAAAGTTGCTGGCAAGGTC	
AK107735-R	TCAAATCTCAACCTGGGTCGTCGT	

Supplemental Table 5. Key Plasmids Used in This Study

Clone	Description
pBV14	ECFP expression vector derived from pSM324 (Bourett et al., 2002). <i>Used in transformant KV9.</i>
pBV138	3.4-kb <i>EcoRI-XbaI</i> fragment of knock-out cassette for gene MGG_04795.6 (<i>BAS1</i>) cloned in <i>EcoRI-XbaI</i> sites of binary vector pGKO2 (Khang et al., 2005). <i>Used in transformants KV34, KV35, KV36, and KV37.</i>
pBV139	3.4-kb <i>EcoRI-XbaI</i> fragment of knock-out cassette for gene MGG_09693.6 (<i>BAS2</i>) cloned in <i>EcoRI-XbaI</i> sites of pGKO2. <i>Used in transformants KV54, KV55, and KV56.</i>
pBV140	3.4-kb <i>HindIII-SmaI</i> fragment of knock-out cassette for gene MGG_11610.6 (<i>BAS3</i>) cloned in <i>EcoRI-XbaI</i> sites of pGKO2. <i>Used in transformants KV71, KV72, and KV73.</i>
pBV176	EGFP expression binary vector derived from pBHt2 (Mullins et al., 2001), containing unique <i>BamHI</i> and <i>PstI</i> sites located between <i>M. oryzae</i> ribosomal protein 27 promoter (P27) and EGFP. This clone consists of three modules, (1) P27 (<i>EcoRI-PstI</i> fragment), (2) EGFP (<i>PstI-SphI</i> fragment), and (3) <i>Neurospora crassa</i> β -tubulin terminator (<i>SphI-HindIII</i> fragment), which were cloned in <i>EcoRI-HindIII</i> sites of pBHt2. P27 was amplified by PCR from pBV11 (=pSM565; Bourett et al., 2002), and EGFP: <i>N. crassa</i> β -tubulin terminator from pSK1810 (Seogchan Kang, unpublished results).
pBV181	EYFP expression binary vector derived from pBHt2, containing unique <i>EcoRI</i> and <i>BamHI</i> sites located upstream of EYFP; 1.0-kb PCR product of EYFP and <i>N. crassa</i> β -tubulin terminator was amplified from pBV13 (Berruyer et al., 2006), digested with <i>BamHI</i> and <i>HindIII</i> , and subsequently cloned in <i>BamHI</i> and <i>HindIII</i> sites of pBHt2.
pBV192	0.7-kb PCR product of mRFP reporter gene (monomeric red fluorescence protein; Campbell et al., 2002) cloned in pGEM-T vector (Promega)
pBV197	1.0-kb <i>EcoRI-BamHI</i> fragment of MGG_04795.6 (<i>BAS1</i>) promoter cloned in <i>EcoRI-BamHI</i> sites of pBV176 (Transcriptional fusion of the <i>BAS1</i> promoter to the EGFP reporter gene). <i>Used in transformant KV93.</i>
pBV227	1-kb <i>EcoRI-BamHI</i> fragment of MGG_11610.6 (<i>BAS3</i>) promoter cloned in <i>EcoRI-BamHI</i> sites of pBV176 (Transcriptional fusion of the <i>BAS3</i> promoter to the EGFP reporter gene). <i>Used in transformant KV94.</i>

pBV231	1.3-kb PCR product of MGG_04795.6 (<i>BAS1</i>) promoter plus entire coding sequence was amplified by PCR, digested with <i>EcoRI</i> and <i>BamHI</i> , and subsequently cloned in <i>EcoRI-BamHI</i> sites of pBV181 (C-terminal translational fusion of <i>BAS1</i> entire coding sequence to the EYFP reporter gene). <i>Used in transformant KV89.</i>
pBV232	1.5-kb PCR product of MGG_11610.6 (<i>BAS3</i>) promoter plus entire coding sequence was amplified by PCR, digested with <i>EcoRI</i> and <i>BamHI</i> , and subsequently cloned in <i>EcoRI-BamHI</i> sites of pBV181 (C-terminal translational fusion of <i>BAS3</i> entire coding sequence to the EYFP reporter gene). <i>Used in transformant KV90.</i>
pBV233	1.3-kb PCR product of MGG_10914.6 (<i>BAS4</i>) promoter plus entire coding sequence was amplified by PCR, digested with <i>EcoRI</i> and <i>BamHI</i> , and subsequently cloned in <i>EcoRI-BamHI</i> sites of pBV181 (C-terminal translational fusion of <i>BAS4</i> entire coding sequence to the EYFP reporter gene). <i>Used in transformant KV91.</i>
pBV234	1.4-kb PCR product of MGG_09693.6 (<i>BAS2</i>) promoter plus entire coding sequence was amplified by PCR, digested with <i>EcoRI</i> and <i>BamHI</i> , and subsequently cloned in <i>EcoRI-BamHI</i> sites of pBV181 (C-terminal translational fusion of <i>BAS2</i> entire coding sequence to the EYFP reporter gene). <i>Used in transformant KV92.</i>
pBV324	1.0-kb <i>EcoRI-BamHI</i> fragment of MGG_10914.6 (<i>BAS4</i>) promoter and 72-bp <i>BamHI-PstI</i> fragment of MGG_10914.6 (<i>BAS4</i>) sequence for signal peptide cloned in <i>EcoRI-PstI</i> sites of pBV176 (C-terminal translational fusion of <i>BAS4</i> sequence for signal peptide to the EGFP reporter gene). <i>Used in transformant KV97.</i>
pBV367	mRFP expression binary vector derived from pBGt (Seogchan Kang, unpublished results), consisting of three modules of P27 (<i>EcoRI-BamHI</i> fragment), mRFP (<i>BamHI-SphI</i> fragment of pBV192), and <i>N. crassa</i> β -tubulin terminator (<i>SphI-HindIII</i> fragment) that were cloned in <i>EcoRI-HindIII</i> sites of pBGt
pBV377	1.4-kb <i>EcoRI-BamHI</i> fragment of <i>PWL2</i> promoter plus entire coding sequence of SK1885 (Seogchan Kang, unpublished results) cloned in <i>EcoRI-BamHI</i> sites of pBV367 (C-terminal translational fusion of <i>PWL2</i> entire coding sequence to the mRFP reporter gene). <i>Used in transformant KV98.</i>
pBV440	1.3-kb <i>EcoRI-BamHI</i> fragment from pBV231 cloned in <i>EcoRI-BamHI</i> sites of pBV367 (C-terminal translational fusion of <i>BAS1</i> entire coding sequence to the mRFP reporter gene). <i>Used in transformants KV95 and KV96.</i>

pSK1743	EGFP expression binary vector derived from pBHt2, consisting of three modules, (1) P27 (<i>EcoRI-BamHI</i> fragment), (2) EGFP (<i>BamHI-SphI</i> fragment), and (3) <i>N. crassa</i> β -tubulin terminator (<i>SphI-HindIII</i> fragment), which were cloned in <i>EcoRI-HindIII</i> sites of pBHt2 (Seogchan Kang, unpublished results)
pSK1877	0.5-kb PCR product of <i>AVR-Pita1</i> promoter plus the sequence for signal peptide in pGEM-T Easy vector (Promega)
pSK1880	0.5-kb <i>EcoRI-BamHI</i> fragment of pSK1877 cloned in <i>EcoRI-BamHI</i> sites of pSK1743 (C-terminal translational fusion of <i>AVR-Pita1</i> sequence for signal peptide to the EGFP reporter gene). <i>Used in transformant Ft080.</i>

Supplemental Table 6. Fungal Transformants Used in This Study

Name	Used in:	Description [background strain; plasmid used]
KV1	Figure 1	Transformant with constitutive, cytoplasmic expression of EYFP [O-137; pBV13] (Kankanala et al., 2007).
KV9		Transformant with constitutive, cytoplasmic expression of ECFP [Guy11; pBV14]
KV34		MGG_04795.6 (<i>BAS1</i>) knock-out transformant [KV1; pBV138]
KV35		MGG_04795.6 (<i>BAS1</i>) knock-out transformant [KV1; pBV138]
KV36		MGG_04795.6 (<i>BAS1</i>) ectopic transformant [KV1; pBV138]
KV37		MGG_04795.6 (<i>BAS1</i>) ectopic transformant [KV1; pBV138]
KV54	Sup.Fig.3 online	MGG_09693.6 (<i>BAS2</i>) knock-out transformant [KV1; pBV139]
KV55	Sup.Fig.3 online	MGG_09693.6 (<i>BAS2</i>) knock-out transformant [KV1; pBV139]
KV56	Sup.Fig.3 online	MGG_09693.6 (<i>BAS2</i>) ectopic transformant [KV1; pBV139]
KV71		MGG_11610.6 (<i>BAS3</i>) knock-out transformant [KV1; pBV140]
KV72		MGG_11610.6 (<i>BAS3</i>) knock-out transformant [KV1; pBV140]
KV73		MGG_11610.6 (<i>BAS3</i>) ectopic transformant [KV1; pBV140]
KV89	Figure 3B	Transformant containing a fusion of MGG_04795 (<i>BAS1</i>) promoter and entire coding sequence with EYFP reporter gene [CP987; pBV231]
KV90	Figure 3D	Transformant containing a fusion of MGG_11610.6 (<i>BAS3</i>) promoter and entire coding sequence with EYFP reporter gene [CP987; pBV232]
KV91	Figure 3E	Transformant containing a fusion of MGG_10914.6 (<i>BAS4</i>) promoter and entire coding sequence with EYFP reporter gene [O-137; pBV233]
KV92	Figure 3C	Transformant containing a fusion of MGG_09693.6 (<i>BAS2</i>) promoter and entire coding sequence with EYFP reporter gene [O-137; pBV234]

KV93	Figure 2B	Transformant containing a fusion of MGG_04795 (<i>BASI</i>) promoter with EGFP reporter gene [Guy11; pBV197]
KV94	Figure 2C	Transformant containing a fusion of MGG_11610.6 (<i>BAS3</i>) promoter with EGFP reporter gene [Guy11; pBV227]
Ft080		Transformant containing a fusion of <i>AVR-Pital</i> promoter and sequence for signal peptide with EGFP reporter gene [CP987; pSK1880]
KV95	Figure 4B	Transformant containing both a fusion of <i>AVR-Pital</i> promoter and sequence for signal peptide with EGFP reporter gene, and a fusion of MGG_04795 (<i>BASI</i>) promoter and entire coding sequence with mRFP reporter gene [Ft080; pBV440]
KV96	Figure 4A	Transformant containing a constitutive, cytoplasmic ECFP reporter gene, and a fusion of MGG_04795 (<i>BASI</i>) promoter and entire coding sequence with mRFP reporter gene [KV9; pBV440]
KV97		Transformant containing a fusion of MGG_10914.6 (<i>BAS4</i>) promoter and sequence for signal peptide with EGFP reporter gene [O-137; pBV324]
KV98	Figure 4C,D,E	Transformant containing both a fusion of MGG_10914.6 (<i>BAS4</i>) promoter and sequence for signal peptide with EGFP reporter gene, and a fusion of <i>PWL2</i> promoter and entire coding sequence with mRFP reporter gene [KV97; pBV377]