

1 Supplemental Data

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Supplemental Table S1. *BR-associated genes differentially expressed after P. graminicola infection.* See corresponding Excel file.

Supplemental Table S2. *GA metabolism genes significantly induced or repressed following inoculation of rice roots with P. graminicola.* Numerical values for the green-to-red gradient represent log₂-fold changes relative to the non-inoculated controls. Significant expression changes (threshold of 1.5-fold change and false discovery rate [FDR] *P*<0.05) are listed in bold. Dpi = days post inoculation.

Biological process	Locus	1dpi	2dpi	4dpi	Description
Diterpenoid biosynthesis	LOC_Os04g10060	3.79	3.04	3.54	1-deoxy-D-xylulose-5-phosphate reductoisomerase
	LOC_Os04g10010	2.88	2.43	2.81	acetyl-CoA C-acetyltransferase
	LOC_Os12g30824	5.53	3.57	2.81	farnesyl diphosphate synthase
	LOC_Os07g09190	3.27	2.92	2.69	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
	LOC_Os04g09900	2.78	2.27	2.37	diphosphomevalonate decarboxylase
	LOC_Os02g39160	2.74	2.02	2.34	ent-copalyl diphosphate synthase
	LOC_Os07g39270	3.05	1.99	2.25	ent-cassa-12,15-diene synthase
	LOC_Os01g01710	2.60	1.89	2.18	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase
	LOC_Os02g36140	3.06	2.68	2.14	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
	LOC_Os03g52170	2.48	1.93	1.97	hydroxymethylglutaryl-CoA synthase
	LOC_Os11g28530	2.04	1.93	1.97	4-hydroxy-3-methylbut-2-enyl diphosphate reductase
	LOC_Os02g45660	2.10	1.79	1.84	syn-copalyl-diphosphate synthase
	LOC_Os01g58790	1.92	1.33	1.47	momilactone-A synthase
	LOC_Os05g34180	0.96	0.76	1.02	syn-pimara-7,15-diene synthase
	LOC_Os01g02020	0.61	0.02	0.38	1-deoxy-D-xylulose-5-phosphate synthase
	LOC_Os03g02710	-0.01	-0.91	-0.40	isopentenyl-diphosphate delta-isomerase
	LOC_Os09g34960	-0.50	-0.61	-0.49	1-deoxy-D-xylulose-5-phosphate synthase
	LOC_Os02g17780	-0.95	-2.04	-0.59	geranylgeranyl diphosphate synthase, type II
	LOC_Os08g40180	-0.26	-0.77	-0.72	hydroxymethylglutaryl-CoA reductase (NADPH)
	LOC_Os02g01760	-0.91	-0.71	-0.75	hydroxymethylglutaryl-CoA synthase
LOC_Os05g33840	0.40	-1.42	-1.30	stemar-13-ene synthase	
LOC_Os01g50760	-1.13	-1.39	-2.04	ent-sandaracopimaradiene synthase	
GA ₁₂ biosynthesis	LOC_Os06g37224	2.03	2.30	1.96	ent-kaurene oxidase
	LOC_Os06g37300	3.90	3.13	3.24	D35, ent-kaurene oxidase
GA biosynthesis	LOC_Os05g34854	-1.03	0.34	0.69	gibberellin 20-oxidase
	LOC_Os07g01340	-0.54	-1.03	0.52	gibberellin 20-oxidase
GA inactivation	LOC_Os01g55240	2.16	1.78	2.00	gibberellin 2-beta-dioxygenase (GA2ox3)
	LOC_Os05g43880	2.02	1.79	1.25	gibberellin 2-beta-dioxygenase

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Supplemental Table S3. *Primer sequences used in quantitative RT-PCR.*

Gene	Locus	Forward	Reverse
<i>OsACTIN1</i>	LOC_Os03g50885	GCGTGGACAAAAGTTTTCAACCG	TCTGGTACCCTCATCAGGCATC
<i>OsBLE2</i>	LOC_Os07g45570	ACCAGCTGATCATAAGGCGGTGC	GGTGAACATCCTCGTGGCTTCTAG
<i>OsXTH1</i>	LOC_Os04g51460	GGTGGAGGTCCAAGAACACGTACC	TCCGACATGAAGTAGCAGGTGGTG
<i>OsCPD1</i>	LOC_Os11g04710	TTCCTTCTCCATCCCCTTTCCTCTCGCCA	CACCCTCCGCCTCAAGAAGCTCCTCAA
<i>OsDWARF2</i>	LOC_Os01g10040	ATTGTCGGCCTCATGTCCCTCC	TCGCCATCTTCTTCTGGCCTGG
<i>OsRAVLI</i>	LOC_Os04g49230	TCCTCACCAACTCCACATTACGGT	CAGATCGAGATCCAACGAGGA
<i>OsMADS55</i>	LOC_Os06g11330	TGGAAGAGCTGCAGCAGATG	TCATCACAGATTCAGATGATTG
<i>OsNPR1</i>	LOC_Os01g09800	CACGCCTAAGCCTCGGATTA	TCAGTGAGCAGCATCCTGACT
<i>OsWRKY45</i>	LOC_Os05g25770	GGACGCAGCAATCGTCCGGG	CGGAAGTAGGCCTTTGGGTGC
<i>GA2ox3</i>	LOC_Os01g55240	TTCGGGTACGGCAGCAAGCG	TCAGAGCGGCCCGGAAGACC
<i>GA20ox3</i>	LOC_Os07g07420	CTCGAGTTCACGCAGAGGCACTAC	TGTCGAGGCTTTCATAGCCATTCC
<i>SLRI</i>	LOC_Os06g03710	GCGTTCGGGCGAGTGACGTG	CGCTGCGGGTGCTCATCTG
<i>SPINDLY</i>	LOC_Os08g44510	TGCGGAGGCATGCAACAACC	AGCAGCATCCATCTTCCCTGGAC
<i>ELI</i>	LOC_Os03g57940	TTCAGTGGGACAGGCGATGTCTG	GACCTAAGTGGGCATGGACGCTAG

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9 Supplemental Figures

10 **Supplemental Figure S1.** Effect of BL pretreatment on resistance to *P. graminicola* in the
11 BR-deficient mutant *d2-2*.

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13 **Supplemental Figure S2.** Morphology and dynamics of *P. graminicola* colonization of rice
14 roots.

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16 **Supplemental Figure S3.** Expression of BR-responsive (*OsBLE2*, *OsXTH1*) and BR
17 biosynthetic (*OsCPD1*, *OsDWARF2*) genes in wild-type T65 and signal-defective *d61-1*
18 seedlings inoculated with *P. graminicola*.

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20 **Supplemental Figure S4.** Effect of BL pretreatment on transcript accumulation of the SA
21 marker genes *OsNPR1* and *OsWRKY45* in roots of cv Nipponbare inoculated with *P.*
22 *graminicola*.

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24 **Supplemental Figure S5.** Repression of GA biosynthesis is an integral part of BR-mediated
25 susceptibility to *P. graminicola*.

26

27 **Figure S6.** Uniconazole treatment mimics BL-induced susceptibility but attenuates BRZ-
28 triggered resistance.

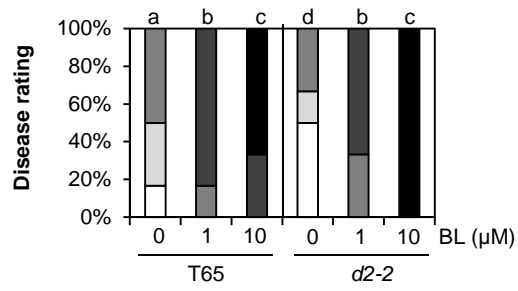
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30 **Supplemental Figure S7.** Physiological read-outs of GA-BL interactions in rice leaf and root
31 tissue.

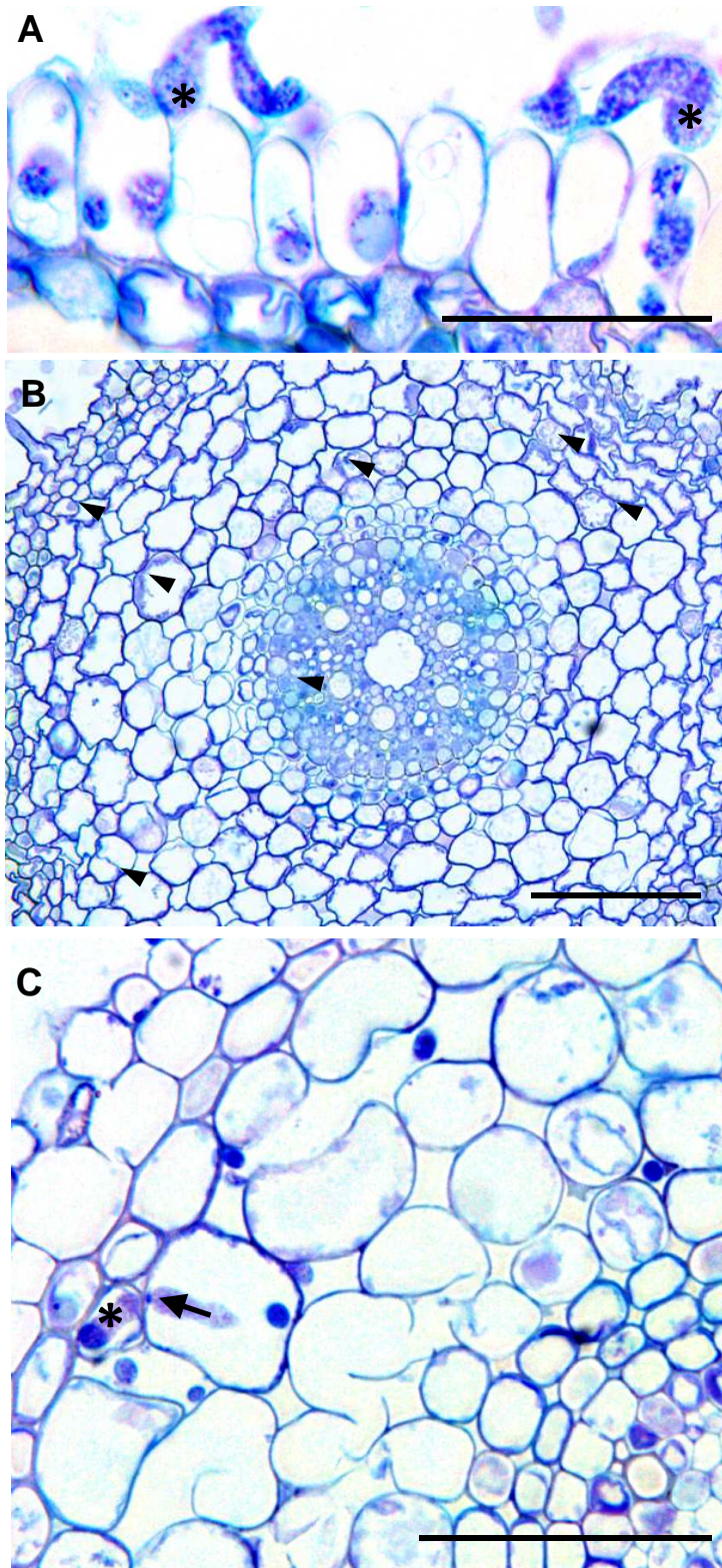
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33 **Supplemental Figure S8.** Effect of BL pretreatment on transcript accumulation of the
34 DELLA gene *SLR1* in roots of cv Nipponbare inoculated with *P. graminicola*.

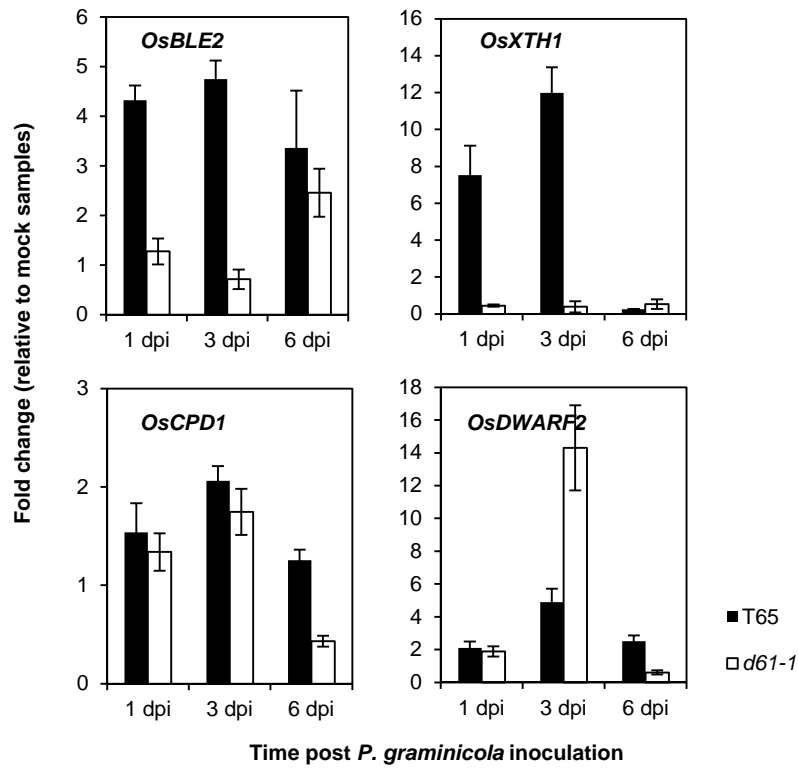
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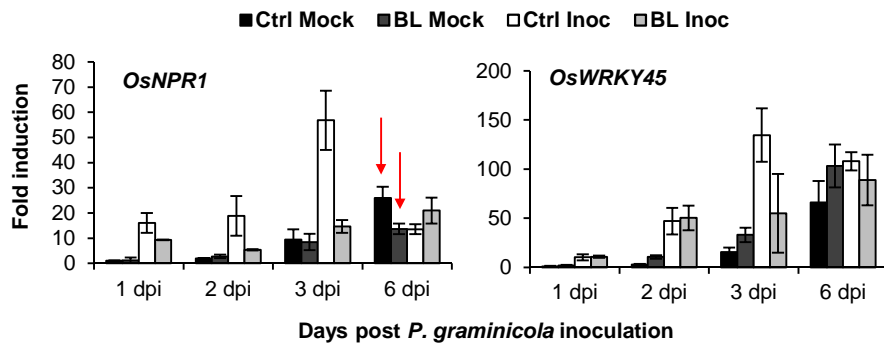
Supplemental Figure S1. Effect of BL pretreatment on resistance to *P. graminicola* in the BR-deficient mutant *d2-2*. Seeds (cv Nipponbare) were germinated on Gamborg B5 medium containing different concentrations of BL and, 3 days post imbibition, inoculated with 0.6-cm mycelial plugs of virulent *P. graminicola* PB912 132. Bars with different letters are significantly different (Mann-Whitney; $n \geq 12$; $\alpha = 0.05$). Chemical treatments, infection with *P. graminicola* 132, and disease evaluation were performed exactly as described in Fig. 1.



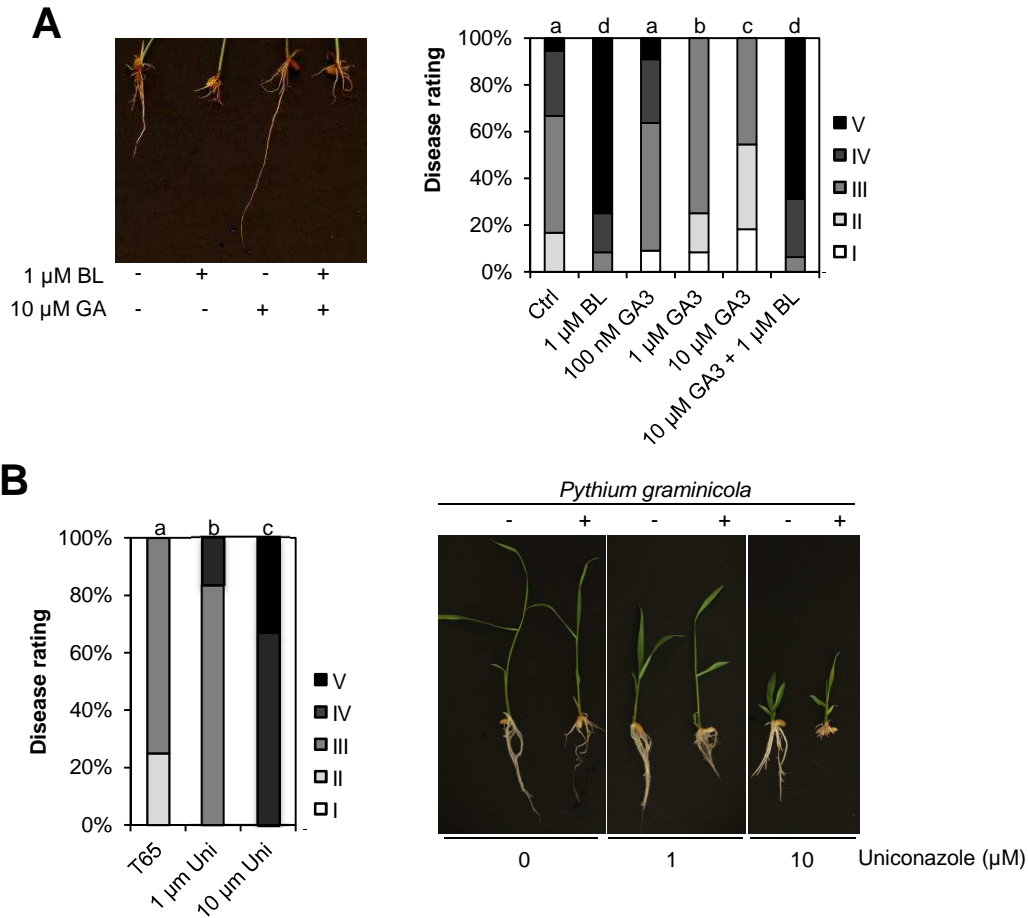
Supplemental Figure S2. Morphology and dynamics of *P. graminicola* colonization of rice roots. **A**, Penetration of root epidermal cells by appressoria-like structures (asterisks). **B**, Vigorous invasion of epidermis, cortex, endodermis and vascular tissue by intracellular hyphae (arrowheads) in roots of cultivar Nipponbare at 2 days post inoculation. Bar = 100 μ M. **C**, Bulbiform invading hyphae (asterisks) show a dramatic constriction (black arrow) prior to spreading to neighbouring cells. Bars = 50 μ M. Pathogen mycelium was stained with Trypan Blue and visualized using bright field microscopy.



Supplemental Figure S3. Expression of BR-responsive (*OsBLE2*, *OsXTH1*) and BR biosynthetic (*OsCPD1*, *OsDWARF2*) genes in wild-type T65 and signal-defective *d61-1* seedlings inoculated with *P. graminicola*. Transcript levels were normalized using actin as an internal reference and for each time point expressed relative to the normalized expression levels in the respective mock-inoculated control. dpi = days post inoculation.



Supplemental Figure S4. Effect of BL pretreatment on transcript accumulation of the SA marker genes *OsNPR1* and *OsWRKY45* in roots of cv Nipponbare inoculated with *P. graminicola*. RNA was extracted at the indicated times after inoculation, converted to cDNA and subjected to quantitative PCR analyses. Data are the same as those shown in Figure 3C, but expressed relative to the normalized expression levels in mock-treated control plants at 1 dpi.



Supplemental Figure S5. Repression of GA biosynthesis is an integral part of BR-mediated susceptibility to *P. graminicola*. **A**, Exogenous BL application suppresses GA₃-induced resistance. Different letters indicate statistically significant differences (Mann-Whitney; $n = 12$; $\alpha = 0.05$). **B**, Effect of Uniconazole, a GA biosynthesis inhibitor, on basal resistance to *P. graminicola*. Bars with different letters are significantly different (Mann-Whitney; $n \geq 12$; $\alpha = 0.05$). Chemical treatments, infection with *P. graminicola* 132, and disease evaluation were performed exactly as described in Fig. 1. Pictures were taken either 7 (panel B) or 10 (panel A) days post inoculation. Data represent one of three independent experiments with similar results

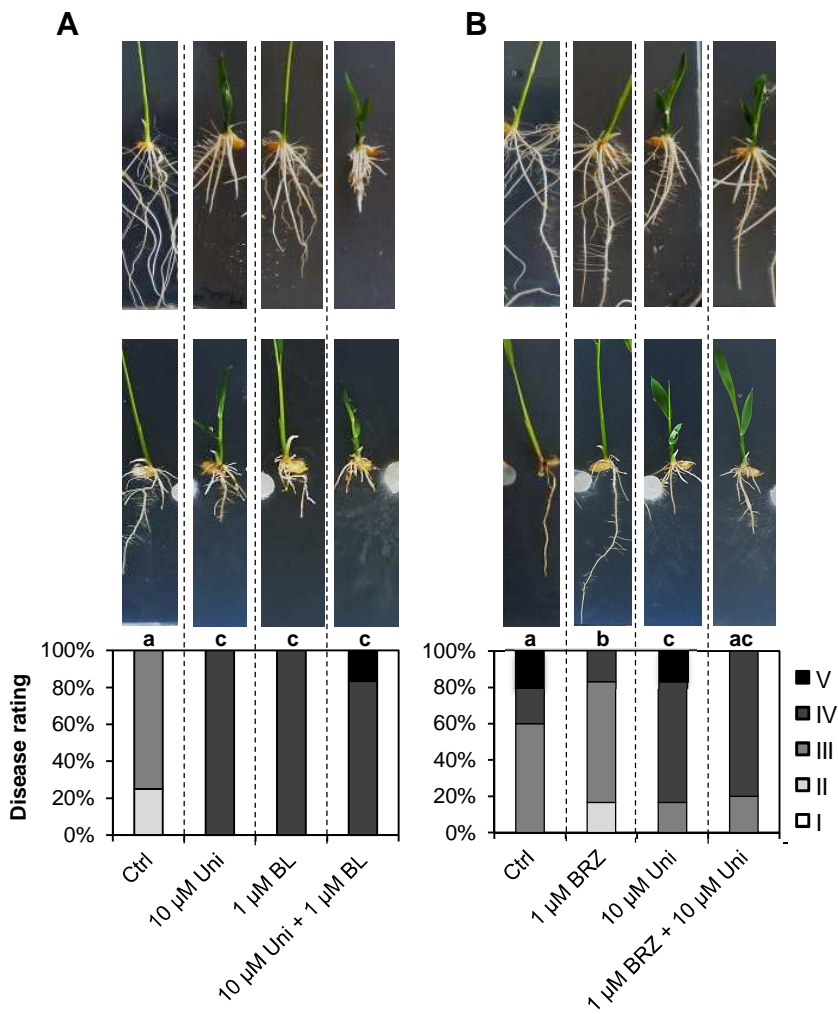
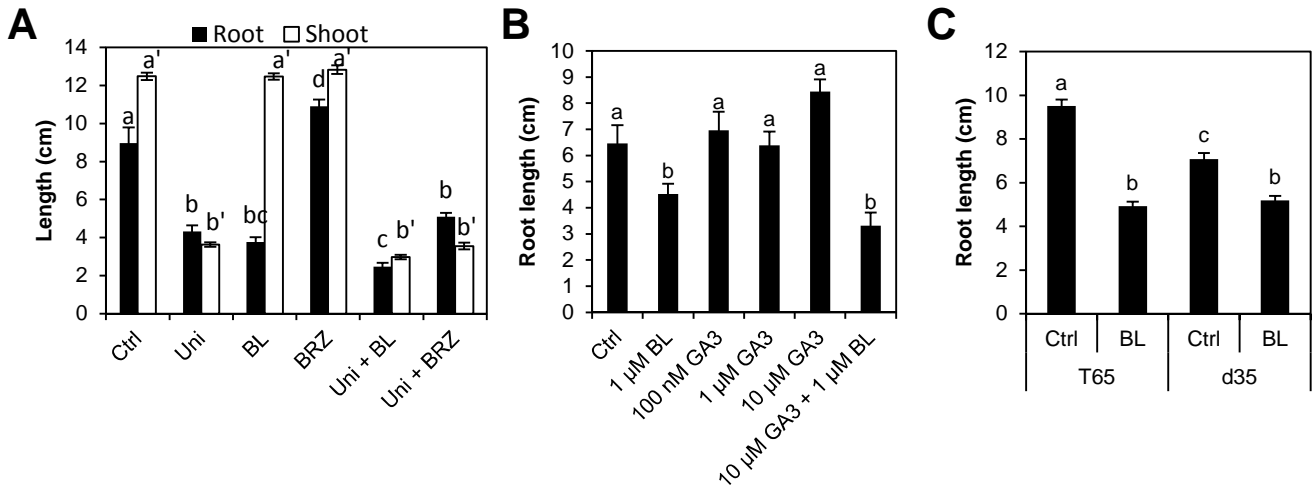
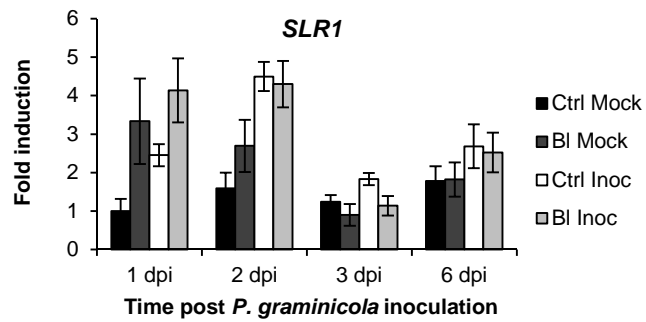


Figure S6. Uniconazole treatment mimics BL-induced susceptibility but attenuates BRZ-triggered resistance. Different letters indicate statistically significant differences (Mann-Whitney; $n \geq 21$; $\alpha = 0.05$). Chemical treatments, infection with *P. graminicola* 132, and disease evaluation were performed exactly as described in Fig. 1. Pictures were taken 7 days post inoculation; upper panels show non-inoculated controls, lower panels depict representative disease symptoms. Experiments were repeated at least twice with nearly identical results.



Supplemental Figure S7. Physiological read-outs of GA-BL interactions in rice leaf and root tissue. **A**, Root and shoot length of 10-day-old seedlings grown on GB5 medium with or without 10 μ M uniconazole, 1 μ M BL and/or 1 μ M BRZ. Each data point represents the mean \pm SE of at least 10 seedlings. Different letters indicate statistically significant differences (Bonferroni; $\alpha = 0.05$). **B**, Measurement of root lengths of 10-day-old seedlings grown in the presence or absence of different concentrations of BL and/or GA₃. The results are presented as mean values \pm SE from six to 12 plants. Bars with different letters are significantly different (Mann-Whitney; $\alpha = 0.05$). **C**, Root elongation of 10-day-old wild-type T65 and GA-deficient *d35* seedlings grown in the presence of 1 μ M BL. Values are mean \pm SE of at least 27 seedlings. Different letters indicate statistically significant differences (Bonferroni; $\alpha = 0.05$).



Supplemental Figure S8. Effect of BL pretreatment on transcript accumulation of the DELLA gene *SLR1* in roots of cv Nipponbare inoculated with *P. graminicola*. RNA was extracted at the indicated times after inoculation, converted to cDNA and subjected to quantitative PCR analyses. Transcript levels were normalized using actin as an internal reference and expressed relative to the normalized expression levels in mock-treated control plants at 1 dpi. Data are means \pm SD of two technical and two biological replicates from a representative experiment, each replicate representing a pooled sample of six individual roots. dpi = days post inoculation.