Supporting Information

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SI Materials and Methods

DNA Recombination Procedures. Template cDNA for all cloning procedures was created from RNA extracted using the RNeasy Plant kit (Qiagen) according to the manufacturer's instructions with the addition of 25 mg polyethylene glycol 8000/mL RLC buffer to the extraction solution from *Populus trichocarpa* roots undergoing colonization by *Laccaria bicolor* S238N. An on-column DNA digestion step with DNase I (Qiagen) was also included to avoid DNA contamination. RNA quality was verified by Experion HighSens capillary gels (Bio-Rad). Template cDNA for yeast II hybrid was prepared and amplified as described in ref. 1. Synthesis of cDNA for single gene cloning was synthesized from 100 ng of total RNA was performed using the iScript kit (Bio-Rad) according to the manufacturer's instructions. For cloning procedures all primers were ordered from Eurogentec and PCR amplification was performed using Accuprime Pfx Taq (Invitrogen) according to the manufacturer's instructions and optimized according to each primer pairing. All primers were designed using *L. bicolor* genome v2.0 (http://genome.jgi-psf.org) and *P. trichocarpa* genome v3.0 (www.phytozome.net). All vectors, with the exception of the bimolecular fluorescence complementation (BiFC) vectors, used in this study were GATEWAY compatible (Invitrogen) and BP and LR clonase recombination reactions were performed according to instructions provided by the manufacturer (Invitrogen). Genes used in BiFC cloning were inserted directly into the vectors (pSATN-cCFP and pSATN-nVenus) using BglII and BamHI site using the In-Fusion recombination enzyme as per the manufacturer's instructions (Clontech). *Escherichia coli* strain DH5α was used for all subcloning procedures.

Yeast One- and Yeast Two-Hybrid Analyses. Yeast one- and two-hybrid screens were carried out according to refs. 1 and 2. Yeast two mating were performed with MiSSP7 as bait protein against a cDNA library of *P. trichocarpa* roots colonized with *L. bicolor* at different stages of development. In each case, at least one-third of the mated cells (usually 1×10^6 to 3×10^6 zygotes) were plated on selective medium and analyzed for interacting proteins. For drop tests presented in Figs. 1, 2, and S1, yeast were pregrown overnight at 30°C with shaking. The following morning all cultures were adjusted to an OD600 of 1 after which they were serially diluted to 10^{-1}, 10^{-2}, 10^{-3}, and 10^{-4} and spotted on selective medium. Colonies were left to develop at 30°C for 3–5 d. To ascertain if coronatine would affect the level of the interaction between MiSSP7 (Mycorrhiza-induced Small Secreted Protein of 7 kDa) and PtJAZ6 or if MiSSP7 would interfere with the interaction between PtCOI1 and PtJAZ6, we grew *Saccharomyces cereviseae* Mav203 colonies expressing MiSSP7 and PtJAZ6 on minimal selective medium (SC-L-W) supplemented with a range of coronatine concentrations (0, 15, 30, 50 μM) or *S. cereviseae* Mav203 colonies expressing PtCOI1 and PtJAZ6 on medium supplemented with 15 μm coronatine and 0, 15, 30, or 50 μM MiSSP7 for 3 d in selective SD medium. MiSSP7 uptake into—and localization in—yeast cells was verified (Fig. S4*C*). After 3 d cells were supplemented with new media containing both chemicals to assure the presence of those chemicals. Yeasts were allowed to grow for another 24 h. Then OD600 was determined and cells were harvested (4,000 × *g* for 5 min), twice frozen in −80 °C, and defrosted at 37 °C. Thereafter, cells were resuspended in 150 μL Z-buffer (60 mM Na_2HPO_4, 40 mM NaH_2PO_4, 10 mM KCl, 1 mM $MgSO_4$, 50 mM β-mercaptoethanol) and 70 μL of 1% SDS were added. Hard vortexing for 30 s served to break the yeast cells. The assay was started by addition of 70 μL CPRG solution (10 mM in Z-buffer) and incubated at 37 °C. After reaction turned red, 60 μL of 1 M Na_2CO_3 was added to stop the galactosidase reaction. Time until color change was observed was recorded. After reaction was stopped, cells debris was sedimented (4,000 × *g*, 15 min, 4 °C) and the absorbance of 200 μL supernantant at 575 nm was determined in a Tecan Infinity M200 Pro plate reader. The calculation of galactosidase units followed Clontech Yeast Handbook.

DivIVa Interaction Tests. In the DivIVa interaction test, one protein is constitutively expressed with a GFP-tag and the other protein is inducibly expressed with a DivIVa-tag (a tag that causes localization of the tagged protein to the poles of the *E. coli* cell). Before induction of the DivIVa-tagged protein, or in the case of a negative interaction between the two proteins, the GFP signal remains localized within the general cytoplasm of the *E. coli*. In the case of a positive interaction between the proteins of interest, however, the DivIVa-tagged protein together with the GFP-tagged protein (and thus the GFP signal) will relocate to the poles of the cell. Full-length genes of interest were cloned into either pNDIV, pCDIV, pNGFP, or pCGFP for the in vivo DivIVa interaction tests (3). For the interaction tests, *E. coli* strain BL21(DE3) (Invitrogen) were freshly cotransformed with two plasmids (one p*DIV and one p*GFP) and grown in Luria-Bertani (LB) medium supplemented with 15 μg/mL chloramphenicol and 50 μg/mL ampicillin for each test, and were grown at 37 °C for all tests. Positive colonies containing the two vectors were subculutred into fresh 1/2 LB medium supplemented with chloramphenicol and ampicilin and grown for 2–3 h. At this point, the cells were observed to ensure that the GFP-tagged protein was being expressed and was located in the cytoplasm, after which the DivIVa-tagged protein was induced with L-arabinose to a final concentration of 0.2% in LB medium. Cultures were induced for a maximum of 30–45 min and observed within this time-frame for relocalization of the GFP marker. Images were captured with a Zeiss LSM710 scanning confocal microscope. A positive interaction was met if at least 50% of the cells exhibited GFP relocalization to the poles of the bacterium.

In Vitro Mycorrhiza Formation. An in vitro assay was used to determine the effects of different chemicals on the ability of *L. bicolor* S238N to colonize poplar roots. In this assay, *P. tremula* × *Populus alba* clone 717–1B4 was rooted in between two cellophane membranes on the surface of solid MS medium (4). At the same time, new *L. bicolor* fungal colonies were grown on a cellophane membrane on Pachlewski solid medium [2.7 mM di-ammonium tartrate, 7.3 mM KH_2PO_4, 2.0 mM $MgSO_4 \cdot 7\,H_2O$, 13 mM maltose, 110 mM glucose, 2.9 μM thiamine-HCl, and 1 mL of a trace-element stock solution Kanieltra medium solidified with 1.2% (wt/vol) agar]. Once the poplar roots had achieved a length of between 2 and 3 cm, they were transferred onto a cellophane membrane on mycorrhization media low-glucose Pachlewski solid medium (control) or medium supplemented with a final concentration of 10^{-8} M MeJA or jasmonic acid (JA), 100 μM aspirin or SHAM, and placed into direct contact with 10 d old *L. bicolor* or *L. bicolor Δmissp7* RNAi mutant colonies, as per Felten et al. (4). Concentrations of these compounds were chosen based on previous work which showed their biological activities at these dosages (5–8). To test if MiSSP7 could block the effect of MeJA, after 1 wk of direct contact between *L. bicolor* and *P. tremula* × *P. alba*

clone 717–1B4 on low-glucose Pachlewski medium supplemented to a final concentration of 10^{-8}–10^{-14} M MeJA (test) or the equivalent amount of water (control), newly emerged lateral roots in contact with *L. bicolor* were dosed with either sterile distilled water (control) or with 15 μM of MiSSP7 peptide in water (Southeastern BioLab). The synthesis of the MiSSP7 peptide followed strict quality control to avoid contamination with pirate peptides and was controlled using HPLC to ensure the production of a full-length product. Mycorrhizal root tips were allowed to develop for 2 wk, at which point at least three mycorrhizae were harvested from each root and fixed in 4% (wt/vol) paraformaldehyde solution and treated as described below to analyze the development of the Hartig net.

Microscopy. Because MiSSP7 expression during the mycorrhization process is essential for the formation of the Hartig net, we used a microscopic method to analyze the development of the Hartig net as described by Plett et al. (9). Briefly, mycorrhizal root samples were fixed in 4% (wt/vol) paraformaldehyde for 24 h at 4 °C and then embedded in 6% (wt/vol) agarose. Next, 25- to 30-μm-thick sections of the mycorrhizal roots were taken using a Leica 1200 series vibratome. Attention was paid to always take sections in the middle of the colonized root (~2 mm from the root apex) to ensure the ability to compare the development of the Hartig net between samples. The development of the Hartig net is defined here as the depth of penetration within the apoplastic space between the rhizodermal cells of the root (Fig. S6). The depth of penetration was determined using ImageJ analysis of our microscopic images. The data presented in this paper for the development of the Hartig net is the average of at least three biological replicates.

Stable Expression of PtJAZ6 in *Populus* Roots. To test if transgenically altering the transcription of *PtJAZ6* (either by overexpressing the gene under the control of a 35S:: promotor or by reducing the level of transcripts using RNAi knockdown) could complement the loss of MiSSP7 in *L. bicolor Δmissp7* RNAi mutants during mycorrhiza formation, we used *Agrobacterium rhizogenes* strain 15834 to generate transformed roots of *P. tremula* × *P. alba* 717–1B4 using a technique similar to that described in Chabaud et al. (10). The strain of *A. rhizogenes* was chosen based on its relatively high transformation rate (~50%) and the ability to produce roots with a normal architecture. Briefly, the coding sequence of *PtJAZ6* was cloned into the vector pH2GW7 for overexpression using the primer set: GGACAAGTTTGTACAAAAAAGCAGGCTCGATGGCGAATATGGCACAG (forward primer) and GGACCACTTTGTACAAGAAAGCTGGGTCCAATTTAAGCTCGAGC (reverse primer), and into the vector pH7GWIWG2(II) for RNAi knockdown using the primer set GGACAAGTTTGTACAAAAAAGCAGGCTCGATGAAGACAGGGTTACAGCAAGAGC(forward primer) and GGACCACTTTGTACAAGAAAGCTGGGTCTCTGGGAGGCCTAGGATGATCC (reverse primer). These vectors were transformed into *A. rhizogenes* strain 15834 and selected for on LB media supplemented with 75 μg/mL spectinomycin. To generate transgenic roots, 1-cm shoot cuttings of *P. tremula* × *P. alba* 717–1B4 were taken from 1.5-mo-old plants and a sterile syringe tip coated in transgenic *A. rhizogenes* was used to puncture the stem of the cutting several times. These cuttings were placed in MS agar media and left to root at 22 °C for 3 wk. In vitro mycorrhization experiments were carried out as above. Because the transformation process never yields 100% transformed roots, we also took samples of each root tested after the mycorrhization tests were completed and extracted the RNA (using the QIAgen RNeasy Plant extraction Kit) and DNA (using the QIAgen DNeasy Plant extracion kit) to ensure the integration of the T-DNA (Fig. S7 *A* and *C*) as well as the altered expression of *PtJAZ6* (Fig. S7 *B* and *D*), respectively. Within this paper, each transformed root is considered as an independent transformation event, and the development of the Hartig net between the three mycorrhizal root tips was used to calculate the SD within each independently transformed root.

Transient Expression of PtJAZ6 in *Nicotiana benthamiana*. *Nicotiana benthamiana* plants for leave infiltration studies were grown for 4–6 wk in a growth chamber with constant humidity (60%), 22 °C, and 16 h light. *Agrobacterium tumefaciens* strain GV3101 was transformed with a pMDC plasmid containing the full-length cDNA sequence for PtJAZ6 in phase with a GFP tag or a pTRBO vector containing cDNA of MiSSP7. The transformed Agrobacteria were grown overnight at 28 °C in 5 mL of YEB medium supplemented with Rifampicine (100 μg/mL), Gentamycine (10 μg/mL), and Kanamycine (50 μg/mL). After overnight growth, *Agrobacterium* cultures were pelleted by spinning at 4,000 rpm for 15 min and resuspended in an equal volume of infiltration buffer (10 mM $MgCl_2$, 10 mM Mes, pH5.6, 200 μM Acetosyringone). Bacteria were left in the infiltration buffer for at least 2 h at 28 °C with gentle shaking in the dark. Each *Agrobacterium* culture was used at an OD600 = 0.1–0.2. After incubation, *Agrobacterium* suspensions for protein coexpression were combined and 4- to 6-wk-old *N. benthamiana* leaves were infiltered. Between three and seven biological repetitions were performed. Agro-infiltered plants were incubated 24–48 h at room temperature until GFP signal was visible in nuclei of epidermal cells. At this stage the leaves were then sprayed with 10^{-8}M MeJA (supplemented with 0.5% Tween 20) and left for an additional 24 h. Small fragments (0.5–1 cm^2) of leaves were excised from the infiltrated area and mounted on slides with water or 60% (wt/vol) glycerol and analyzed with confocal microscope using the same exposure time and laser settings. For Western detection 5 cm^2 of transformed leaf tissue was cut and frozen in liquid nitrogen. The presence of MiSSP7 within the transformed leaves was determined by RNA isolation and subsequent PCR-amplification.

Transcriptional Analyses. Two separate techniques were used for transcriptional analyses of MeJA and MiSSP7 effect on JA marker genes in poplar. For the affect of MeJA on the root transcriptome, roots were grown for 2 wk on MS medium supplemented with 10–8 M MeJA for 2 wk and then harvested, frozen in liquid nitrogen, and their RNA extracted using the RNeasy Plant kit available from Qiagen. RNA-Seq of two independent biological replicates for both MeJA treated as well as untreated, control roots, were sequenced using Illumina technology. Library construction and 100-bp paired-end reads sequencing was performed by IGA Technology services. Raw reads were trimmed for quality and aligned to Ptrichocarpa_210_transcript_primaryTranscriptOnly taken from Phytozome v9.1 (www.phytozome.net/poplar.php) and corresponding to the *P. trichocarpa* genome v3 using CLC Genomics Workbench 6. For mapping, the minimum-length fraction was 0.9, the minimum similarity fraction 0.8, and the maximum number of hits for a read was set to 10. The unique and total mapped reads number for each transcript were determined, and then normalized to reads per kilobase of exon model per million mapped reads. A Baggerly test included in the CLC software was applied to the data. The samples are given different weights depending on their sizes (total counts). The weights are obtained by assuming a β-distribution on the proportions in a group, and estimating these, along with the proportion of a binomial distribution, by the method of moments. The result is a weighted *t*-type test statistic. The complete expression dataset is available as series (accession nos. GSE56865, GSE56863, GSE56864, and GSE53475) at the Gene Expression Omnibus at the National Center for Biotechnology Information (NCBI).

The analysis of the impact of colonization by *L. bicolor* and of MiSSP7 on these same marker genes was analyzed using data

obtained from microarray analyses. In all cases, RNA from three biological replicates was extracted as described above and cDNA was synthesized using the SMART PCR cDNA Synthesis Kit (Clontech) according to the manufacturer's instructions for microarray analysis. Microarray experiments were performed as described previously (11). A Student *t* test with false-discovery rate (Benjamini–Hochberg) multiple testing correction was applied to the data using Cyber-T software (http://cybert.ics.uci.edu). Based on the statistical analysis, a gene was considered significantly induced if it met the following two criteria: (*i*) *t* test P value < 0.05; (*ii*) fold-change > 2. Before transcripts were declared present, the signal-to-noise threshold (signal background) was calculated based on the mean intensity of random probes present on the microarray. Cut-off values for signal intensity were then subtracted from the normalized intensity values. The highest signal intensity values observed on these arrays were ~65,000 arbitrary units. The complete expression dataset is available as series (accession nos. GSE56865, GSE56863, GSE56864, and GSE53475) at the Gene Expression Omnibus at NCBI (www.ncbi.nlm.nih.gov/geo).

Microarray results, the effect of Asp and SHAM treatment of the roots and the repression of JA marker genes by *PtJAZ6* overexpression were verified using quantitative PCR. Briefly, cDNA was synthesized from 500 ng total RNA per sample using the iScript cDNA synthesis kit (Bio-Rad) following manufacturer's instructions iScript kit. Real-time PCR was performed using a Chromo4 Light Cycler and OpticonMonitor Software. Real-time PCR analyses were performed using three biological replicates, with a technical replicate for each reaction using the SYBRGreen Supermix following the manufacturer's instructions (Bio-Rad). Fold-changes in gene expression between treated and control roots were based on ΔΔCt calculations according to Pfaffl (12).

Statistical Analysis. At least three independent biological replicates were performed for each test outlined in this paper, unless otherwise noted, to ensure reproducibility and significance of data reported. A one-way ANOVA followed by a Tukey HSD (honestly significant difference) multiple comparison test ($P < 0.05$) was used unless otherwise noted.

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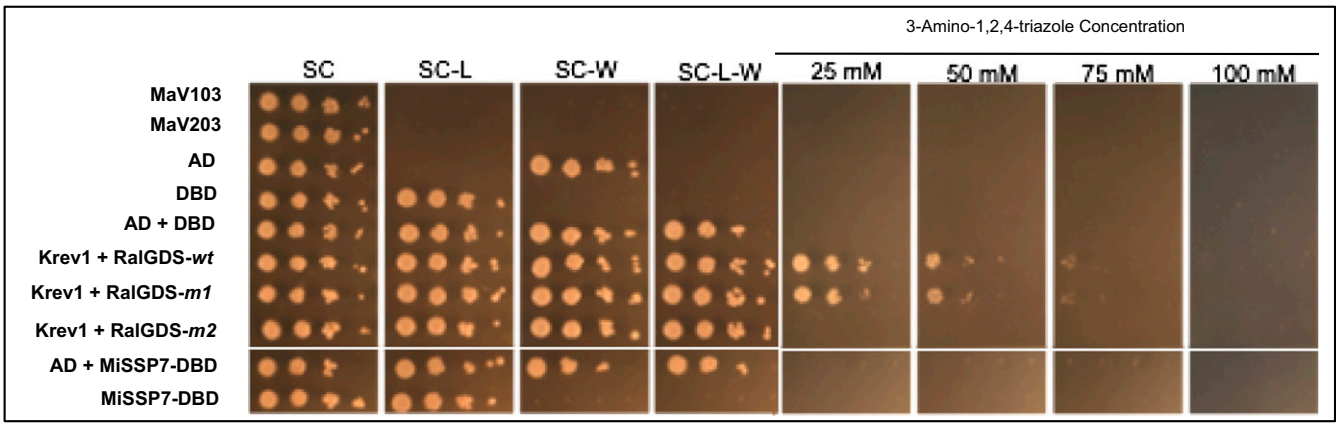

Fig. S1. MiSSP7 cannot induce gene expression in yeast reporter system. Yeast analysis demonstrates that MiSSP7 (AD + MiSSP7-DBD or MiSSP7-DBD) is not able to activate transcription of the histidine biosynthesis reporter gene compared with a strong interaction positive control (Krev1 + RalGDS-*wt*), a weak interaction control (Krev1 + RalGDS-*m1*), and all negative controls [Krev1 + RalGDS-*m2*; MaV103; MaV203; Activation Domain (AD); DNA Binding Domain (DBD); AD + DBD]. SC, synthetic complete medium; SC-L, synthetic complete medium without leucine; SC-W, synthetic complete medium without tryptophan; SC-L-W, synthetic complete medium without both leucine and tryptophan.

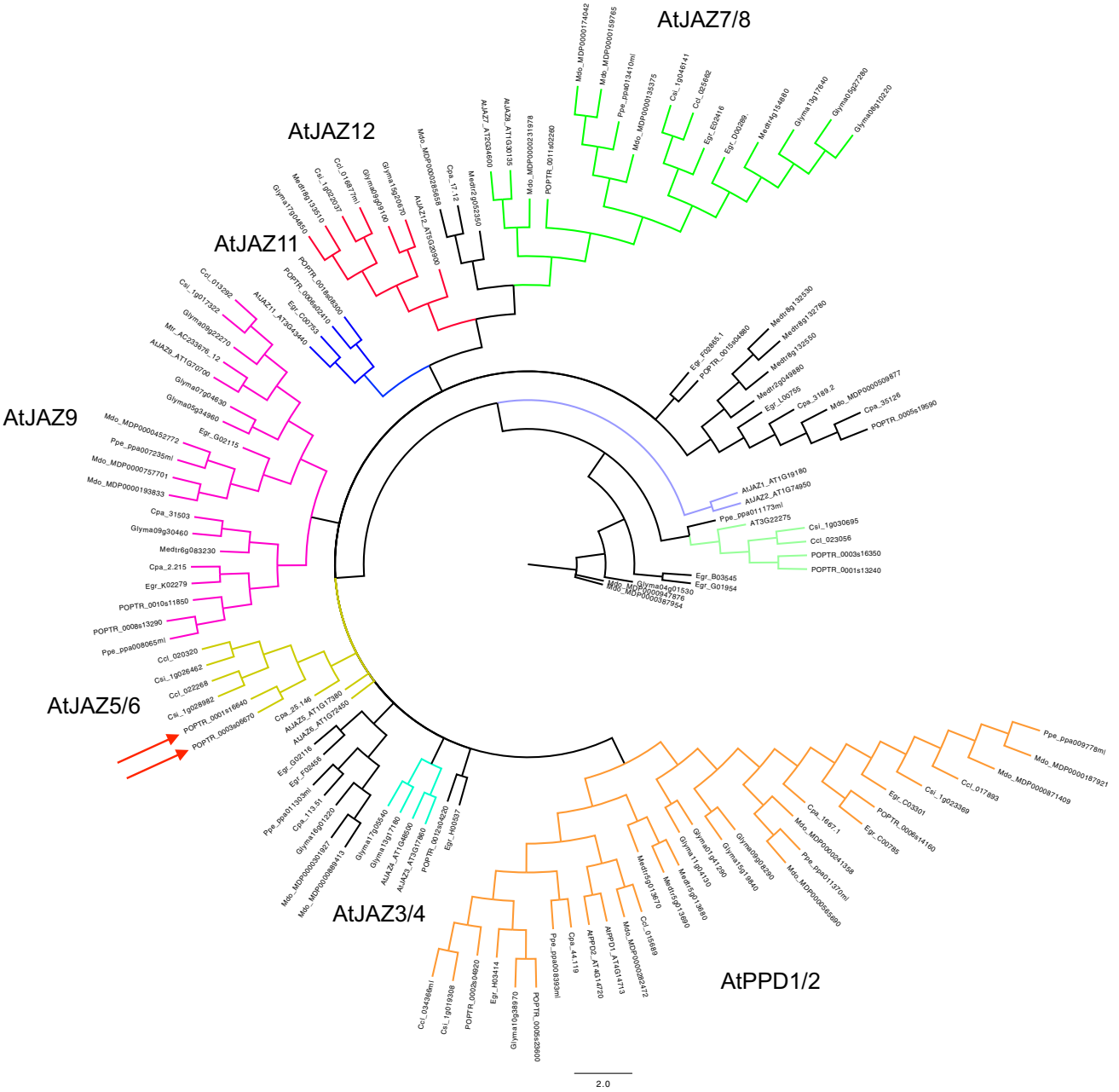

Fig. S2. Phylogenetic tree of JASMONATE ZIM-DOMAIN (JAZ) proteins from 10 different plant species. The evolutionary history was inferred by using the maximum-likelihood method based on the JTT matrix-based model (1). The bootstrap consensus tree inferred from 500 replicates (2) is taken to represent the evolutionary history of the taxa analyzed (3). Branches corresponding to partitions reproduced in less than 30% bootstrap replicates are collapsed. Evolutionary analyzes were conducted in MEGA5 (3). Colored branches indicate groups of proteins homologous to a known *Arabidopsis thaliana* JAZ protein or the closely related TIFY domain-containing proteins PPD1 and PPD2. Red arrows indicate the placement of the two poplar JAZ proteins, PtJAZ5 and PtJAZ6, within this tree. All proteins are identified by either published name (for *Arabidopsis thaliana*) or by Phytozome annotation. POPTR, *Populus trichocarpa*; AT, *Arabidopsis thaliana*; Ccl, *Citrus clementina*; Cpa, *Carica papaya*; Csi, *Citrus sinensis*; Egr, *Eucalyptus grandis*; Glyma, *Glycine max*; Mdo, *Malus domestica*; Medtr, *Medicago truncatula;* Ppe, *Prunus persica*.

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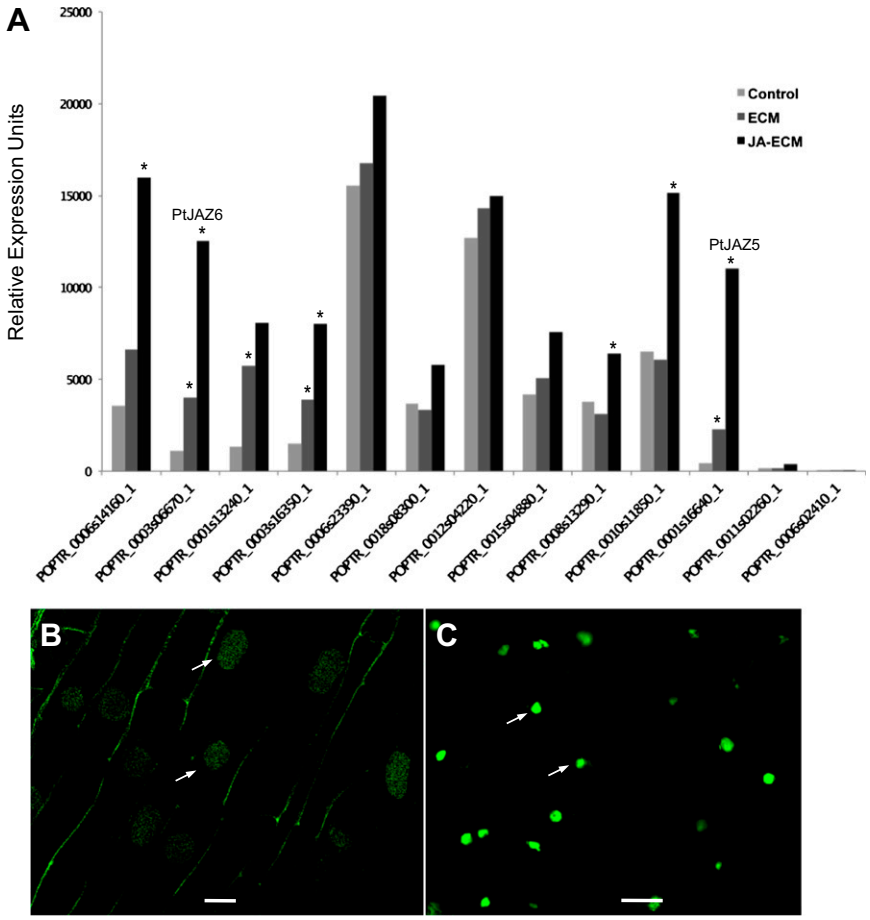

Fig. S3. Expression of different JAZ domain-containing genes are induced during *L. bicolor* colonization and by 1×10^{-8} M JA treatment whereas the localization of MiSSP7 and PtJAZ6 is to plant nucleus. (*A*) Relative expression of the 13 JAZ domain containing genes in the *P. trichocarpa* genome in fine roots, in mature ectomycorrhizal (ECM) root tips and in 1×10^{-8} M JA-treated ECM root tips as measured by whole-genome oligo-arrays. All tissues were grown under the same conditions and harvested after 2 wk postcontact between roots and *L. bicolor*. All values are the mean of three biological replicates. Gene annotations can be found in Table S1. The asterisks represent significant difference from control conditions ($P < 0.05$). (*B*) Root cells treated with 15 μM MiSSP7-FAM exhibit uptake of the fluorescent molecule and localization of the protein in the plant nucleus (examples indicated with arrows). (Scale bar, 10 μm.) (*C*) Transient transformation of *N. benthamiana* leaves with *35S::PtJAZ6-GFP* contruct via agroinfiltration results in production of GFP-tagged PtJAZ6, which localizes predominantly in the nucleus (examples indicated with arrows). (Scale bar, 40 μm.)

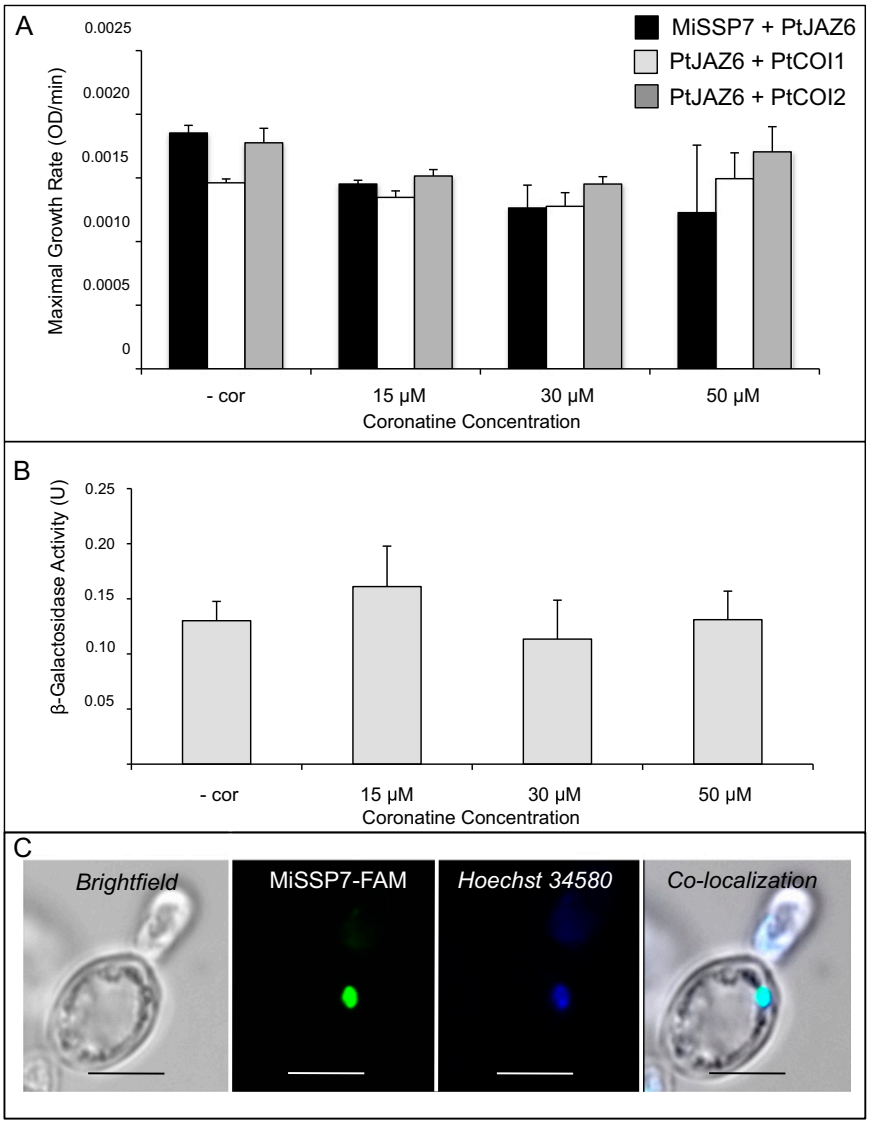

Fig. S4. Coronatine does not affect yeast growth nor does it alter the interaction between proteins unrelated to the JA pathway. (*A*) A comparison of maximal growth rate of yeast expressing MiSSP7+PtJAZ6 (black bars), PtJAZ6+PtCOI1 (white bars) or PtJAZ6+PtCOI2 (gray bars). (*B*) β-Galactosidase activity of yeast cells grown on differing concentrations of coronatine and expressing the control Krev1/RalGDS-*wt* interacting proteins of the ProQuest Yeast Two-Hybrid System (Life Technologies; ± SEM). (*C*) MiSSP7 is taken up into yeast cells and localizes to the nucleus. Fluorescently labeled MiSSP7 (MiSSP7-FAM; green signal) enters the cell and colocalizes with Hoechst 34580 (nucleic acid stain; blue signal) in the nucleus. (Scale bars, 5 μm.)

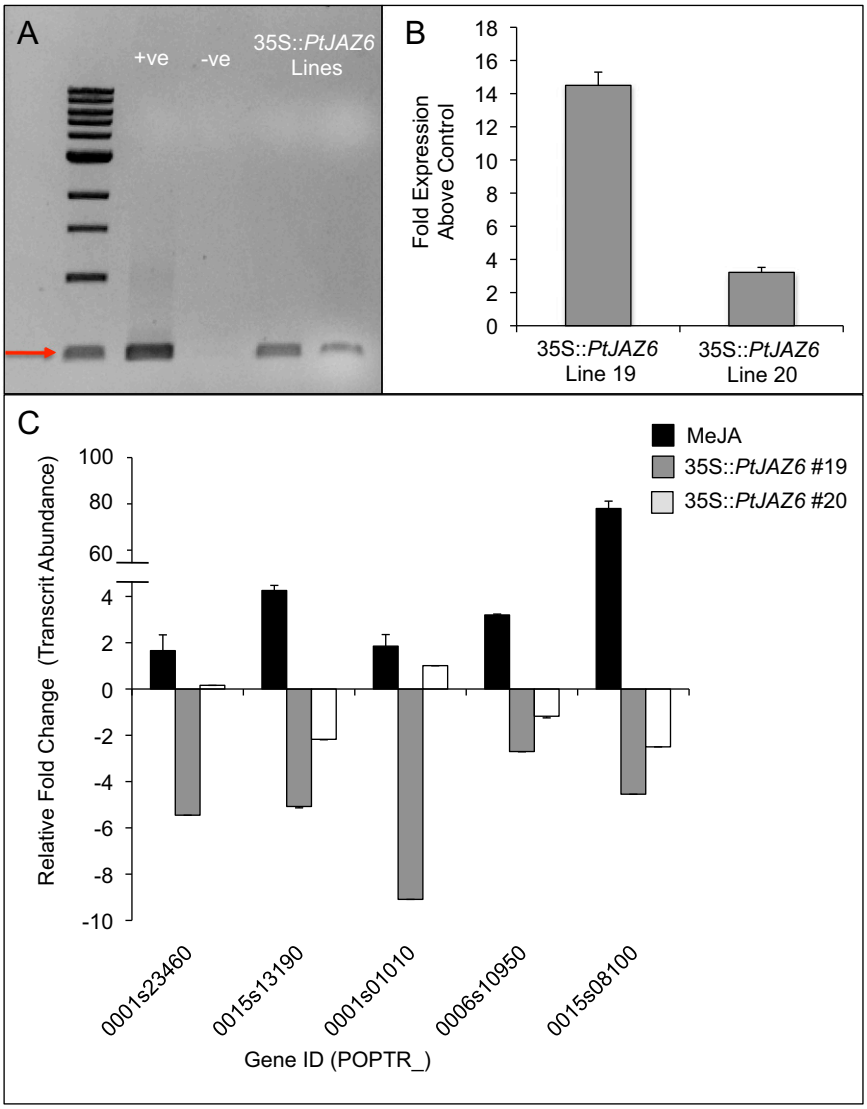

Fig. S5. *PtJAZ6* expression represses the transcription of JA-marker genes. (*A*) PCR proof of gDNA insertion of the *35S::PtJAZ6* T-DNA construct into two independent transformant *Populus* lines (red arrow indicates product). (*B*) Quantitative PCR proof of overexpression of *PtJAZ6* in both transgenic lines. (*C*) Repression of five JA-marker genes compared with transcript levels in roots with normal levels of *PtJAZ6* expression. Black bars represent gene induction by MeJA, gray and white bars represent gene expression in lines 19 and 20 of *35S::PtJAZ6,* respectively. Gene annotations can be found in Table S1 (± SEM).

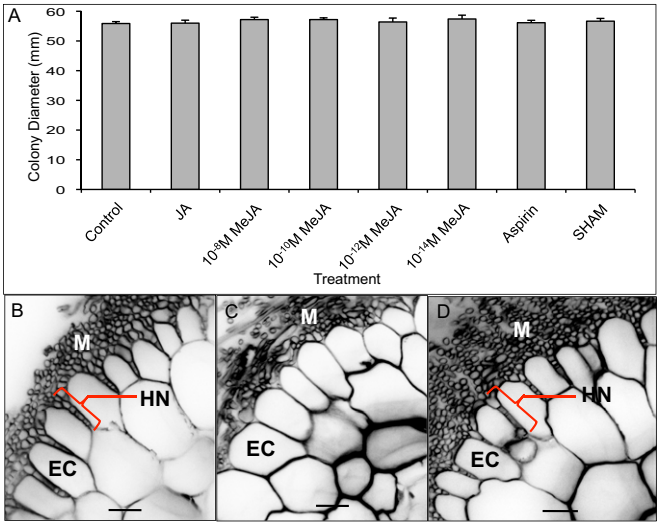

Fig. S6. Treatment of *L. bicolor* with either JA, MeJA or JA signaling inhibitors (Asp and SHAM) does not affect fungal growth while variation of *PtJAZ6* expression alters *L. bicolor*'s ability to form a Hartig net. (*A*) Effect of different treatments on *L. bicolor* growth. (*B*) Transverse cross-section of control ECM roots with no altered expression of *PtJAZ6* exhibit normal mantle formation (M) and formation of a Hartig net (HN). (*C*) Transverse cross-section of *PtJAZ6-RNAi* ECM root with no visible Hartig net. (*D*) Transverse cross-section of 35S::*PtJAZ6* ECM root with normal Hartig net development. (Scale bars, 15 μm.) Parentheses show the depth of the Hartig net in *B* and *D*.

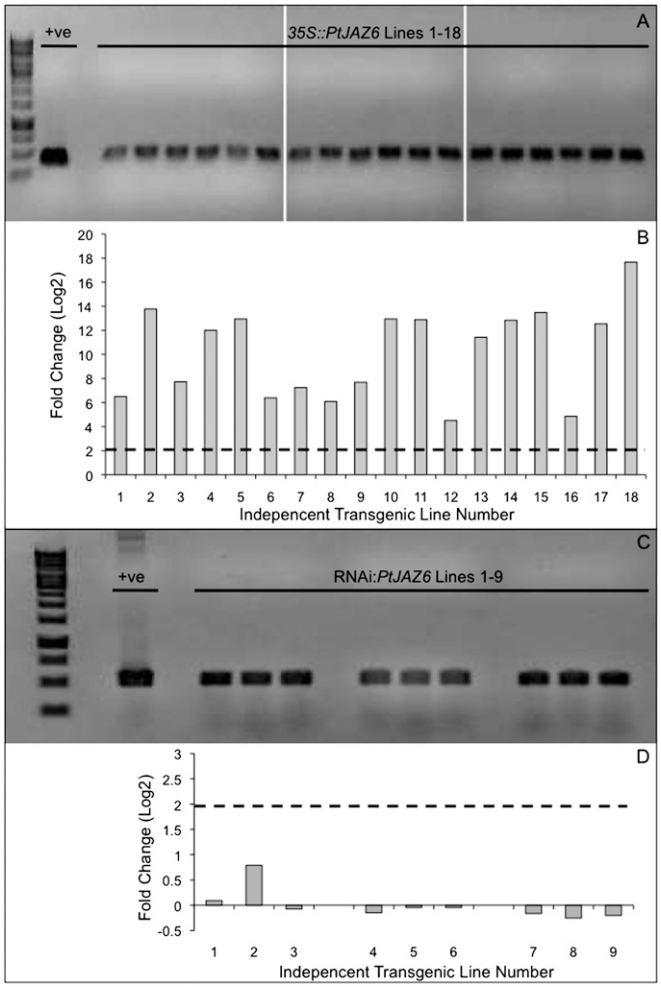

Fig. S7. Proof of gDNA insertion of PtJAZ6 T-DNA constructs and mis-regulation of *PtJAZ6*. (*A*) PCR proof of gDNA insertion of the *35S::PtJAZ6* T-DNA construct into 18 independent transformant *Populus* lines (denoted in main text as *35S::PtJAZ6* lines 1–18) and (*B*) subsequent quantitative PCR proof of overexpression of *PtJAZ6*. This graph is the expression of *PtJAZ6* in colonized mutant root tissues compared with uncolonized control root tissues. (*C*) PCR proof of gDNA insertion of the *PtJAZ6-RNAi* T-DNA construct into nine independent transformant lines (denoted in main text as *PtJAZ6-RNAi* line 1–9) and (*D*) subsequent quantitative PCR analysis of the levels of *PtJAZ6*. This graph is the expression of *PtJAZ6* in colonized mutant root tissues compared with uncolonized control root tissues. In *B* and *D* the dashed line represents the normal expression of *PtJAZ6* in wild-type roots of poplar colonized by *L. bicolor*. Expression values over this line represent overexpression of the gene and expression values under the line represent reduced expression of the gene. +ve, PCR of the hygromycin resistance gene in the transformation vector.

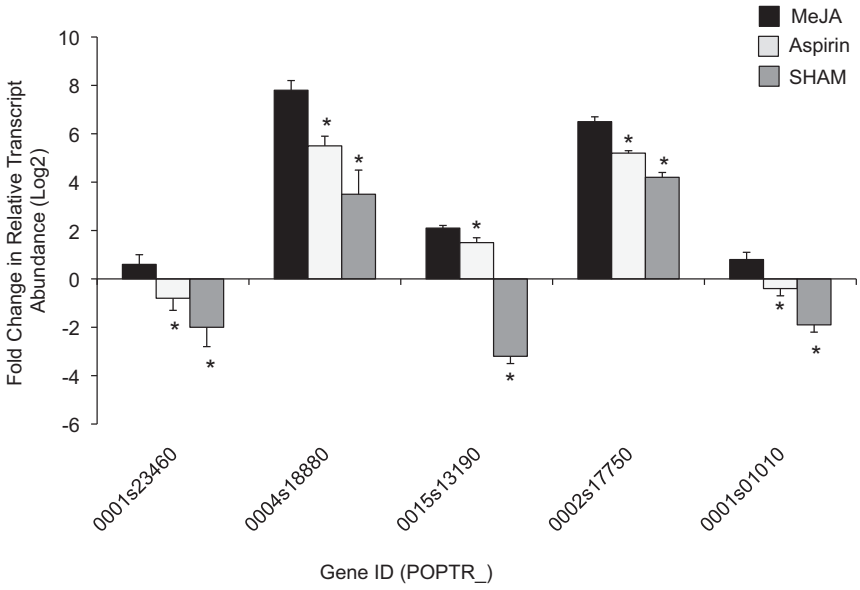

Fig. S8. SHAM and Aspirin treatment of poplar root cells results in a repression of JA marker gene transcription. Expression of 5 JA-marker genes as induced by MeJA (black bars) over transcript abundance in untreated control roots. Expression of these same genes after cotreatment with MeJA + Aspirin (light gray bars) or with MeJA + SHAM (dark gray bars). Treatment with either Aspirin or SHAM significantly repressed the expression of these genes compared with MeJA treatment alone (*$P < 0.05 \pm$ SEM). Gene annotations can be found in Table S1.

Table S1. Correspondence between *P. trichocarpa* gene numbers and their homologs in *A. thaliana* used in this study

Poplar gene	*A. thaliana* gene	Closest *A. thaliana* homolog functional definition
POPTR_0004s18880	AT3G12500.1	ATHCHIB (*ARABIDOPSIS THALIANA* BASIC CHITINASE); chitinase
POPTR_0013s07840	AT4G24340.1	Phosphorylase family protein
POPTR_0092s00200	AT3G25810.1	Myrcene/ocimene synthase, putative
POPTR_0001s31570	AT3G25810.1	Myrcene/ocimene synthase, putative
POPTR_0013s04880	AT3G05950.1	Germin-like protein, putative
POPTR_0001s36520	AT1G17020.1	SRG1 (SENESCENCE-RELATED GENE 1)
POPTR_0001s21010	N/A	
POPTR_0015s15750	AT1G31260.1	ZIP10 (ZINC TRANSPORTER 10 PRECURSOR)
POPTR_0015s15730	AT1G31260.1	ZIP10 (ZINC TRANSPORTER 10 PRECURSOR)
POPTR_0003s21660	AT5G19890.1	Peroxidase, putative
POPTR_0017s01230	AT4G02270.1	Pollen Ole e 1 allergen and extensin family protein
POPTR_0019s14550	AT1G73325.1	Trypsin and protease inhibitor family protein/Kunitz family protein
POPTR_0001s01010	AT4G27870.1	Integral membrane family protein
POPTR_0001s22610	AT5G22410.1	Peroxidase, putative
POPTR_0010s25380	AT3G10710.1	Pectinesterase family protein
POPTR_0001s23460	AT2G44480.1	BGLU17 (BETA GLUCOSIDASE 17)
POPTR_0014s12130	AT2G47540.1	Pollen Ole e 1 allergen and extensin family protein
POPTR_0002s20290	AT4G02270.1	Pollen Ole e 1 allergen and extensin family protein
POPTR_0002s17750	AT1G32640.1	MYC2; DNA binding/transcription activator/ transcription factor
POPTR_0014s12100	N/A	
POPTR_0001s23440	AT2G44480.1	BGLU17 (β-GLUCOSIDASE 17)
POPTR_0015s13190	AT5G52260.1	AtMYB19 (myb domain protein 19); DNA binding/transcription factor
POPTR_0010s24030	AT5G03760.1	ATCSLA09; mannan synthase/ transferase, transferring glycosyl groups
POPTR_0006s10950	AT2G40750.1	WRKY54 DNA Binding Protein
POPTR_0015s08100	AT3G48090.1	EDS (ENHANCED DISEASE SUSCEPTIBILITY)
POPTR_0006s14160	AT1G19180.1	JAZ1 (JASMONATE-ZIM-DOMAIN PROTEIN 1)
POPTR_0003s06670	AT1G72450.1	JAZ6 (JASMONATE-ZIM-DOMAIN PROTEIN 6)
POPTR_0001s13240	AT5G13220.1	JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10)
POPTR_0003s16350	AT5G13220.1	JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10)
POPTR_0006s23390	AT5G20900.1	JAZ12 (JASMONATE-ZIM-DOMAIN PROTEIN 12)
POPTR_0018s08300	AT3G43440.1	JAZ11 (JASMONATE-ZIM-DOMAIN PROTEIN 11)
POPTR_0012s04220	AT3G17860.1	JAZ3 (JASMONATE-ZIM-DOMAIN PROTEIN 3)
POPTR_0015s04880	AT3G17860.1	JAZ3 (JASMONATE-ZIM-DOMAIN PROTEIN 3)
POPTR_0008s13290	AT1G70700.1	JAZ9 (JASMONATE-ZIM-DOMAIN PROTEIN 9)
POPTR_0010s11850	AT1G70700.1	JAZ9 (JASMONATE-ZIM-DOMAIN PROTEIN 9)
POPTR_0001s16640	AT1G17380.1	JAZ5 (JASMONATE-ZIM-DOMAIN PROTEIN 5)
POPTR_0011s02260	AT1G30135.1	JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8)
POPTR_0006s02410	AT3G43440.1	JAZ11 (JASMONATE-ZIM-DOMAIN PROTEIN 11)