Supplemental Table 1. Gene names and IDs used for the Phylogenetic analysis

SPCHMUTEFAMA tree	**gene name ID**
At SPCH	At5g53210
At MUTE	At3g06120
At FAMA	At3g24140
Pt SPCH1	fgenesh4_pm.C_LG_XII000063
Pt SPCH2	gw1.197.14.1
Os SPCH1	Os06g33450
Os SPCH2	Os02g15760
Pt MUTE	gw1.VIII.81.1
Os MUTE	Os05g51820
Pt FAMA1	gw1.I.3509.1
Pt FAMA2	gw1.XVII.460.1
Os FAMA	Os05g50900
Pp FAMA1	estExt_gwp_gw1.C_710125
Pp FAMA2	e_gw1.519.9.1
outgroup	At4g01460
outgroup	At5g46690

TMM tree	**gene name ID**
At TMM	At1g80080
Pt TMM	eugene3.00970008
Os TMM	Os01g43440
Pp TMM	gw1.1.550.1
At outgroup	At2g42800
Pt outgroup	gw1.77.132.1
Os outgroup	Os01g52880
Os outgroup	Os05g45430
At outgroup	At4g28560
Pt outgroup	gw1.V.1354.1
Os outgroup	Os06g42220
Pt outgroup	gw1.VIII.2940.1
Os outgroup	Os01g02060
Pp outgroup	gw1.49.40.1
Pp outgroup	gw1.387.50.1
Pp outgroup	gw1.184.16.1

YODA N term regulatory region	**gene name ID**
At YODA	At1g63700
Pt YODA1	estExt_Genewise1_v1.C_LG_I8903
Pt YODA2	FGENESH4_PM.C_LG_III000419
Os YODA1	Os04g47240
Os YODA2	Os02g44642
Pp YODA	gw1.44.79.1
At YODA outgroup (supplement)	At1g53570
At YODA outgroup (supplement)	At5g66850
At YODA outgroup (supplement)	At1g09000
At YODA outgroup (supplement)	At1g54960
At YODA outgroup (supplement)	At3g06030

genome sources	
Populus trichocarpa v1.1	Poplar
TAIR	Arabidopsis
GRAMENE	Rice
Physcomitrella patens v1.1	Moss

Supplemental Methods

Bioinformatic/Phylogenetic Methods

BLAST searches using Arabidopsis amino acid sequences were performed using GRAMENE, Populus trichocarpa v1.1, Physcomitrella patens v1.1 genome websites to identify putative orthologs for SPCH, MUTE, FAMA, TMM, and YODA. All high scoring matching genes were used in initial phylogenetic analyses to identify true orthologs. Non-orthologous genes were then discarded, and the dataset was realigned and analyzed as described below. Outgroup sequences used for the analyses were identified in previously published comprehensive analyses of Arabidopsis bHLH and receptor like protein gene families (Toledo-Ortiz, 2003; Wang et al. 2008). Identification of the putative N terminal regulatory region of *Physcomitrella patens* YODA, was first identified using BLAST searches, and then additional unannotated sequence were found by identifying open reading frames towards the N terminal end.

Amino acid sequences for the bHLH and ACT domains from SPCH, MUTE, FAMA, and their orthologs were aligned with CLUSTAL X (Jeanmougin et al., 1998). The full-length amino acid sequences from TMM and its orthologs were also aligned with CLUSTAL X. Default CLUSTAL X alignment parameters were used, which include pairwise alignment gap opening penalty of 10 and extension of 0.1, multiple alignment gap opening penalty of 10 and extension of 0.2, and a gonnet series matrix. Neighbor-joining trees were constructed using Phylip 3.68 (Felsenstein, 2005) (Dayhoff PAM matrix) and nodal support was assessed using 100,000 bootstrap replicates. Tree topologies were also computed using Bayesian methods (MrBayes 3.1.2) (Ronquist and Huelsenbeck,2003) based on a mixed model of amino acid substitution and also

allowed for invariant sites and rate heterogeneity using the gamma distribution. For the TMM tree, the analysis was run for 435,500 generations in 2 separate analyses, and the first 1000 generations were discarded as burnin. The SPCH, MUTE, FAMA analysis was run for 1,000,000 generations in 2 separate analyses and the first 600 generations were discarded as burnin. To ensure adequate mixing had occurred in the Bayesian analyses, each or the 2 separate analyses were analyzed separately to compare clade recovery and posterior probability support values. For both the TMM, and SPCH, MUTE, and FAMA analyses, independent run tree topologies were identical, and posterior probability values varied by no more than 2%. Trees shown in Figure 6 are of the two separate runs combined.

Supplemental References

Felsenstein, J. (2005). PHYLIP (Phylogeny Inference Package) (Department of Genome Sciences, University of Washington, Seattle: Distributed by the author).

Jeanmougin, F., Thompson, J.D., Gouy, M., Higgins, D.G., and Gibson, T.J. (1998). Multiple sequence alignment with Clustal X. Trends in Biochemical Sciences **23,** 403–405. **Ronquist, F., and Huelsenbeck, J.P.** (2003). MRBAYES 3: Bayesian phylogenetic inference under mixed models. Bioinformatics **19,** 1572- 1574.

Ichimura, K., Shinozaki, K., Tena, G., Sheen, J., Henry, Y., Champion, A., Kreis, M., Zhang, S., Hirt, H., Wilson, C., Heberle-Bors, E., Ellis, B.E., Morris, P.C., Innes, R.W., Ecker, J.R., Scheel, D., Klessig, D.F., Machida, Y., Mundy, J., Ohashi, Y., and Walker, J.C. (2002). Mitogen-activated protein kinase cascades in plants: a new nomenclature. Trends in Plant Science 7, 301-308.

Toledo-Ortiz, G., Huq, E., and Quail, P.H. (2003). The Arabidopsis Basic/Helix-Loop-Helix Transcription Factor Family. Plant Cell **15,** 1749-1770.

Wang, G., Ellendorff, U., Kemp, B., Mansfield, J.W., Forsyth, A., Mitchell, K., Bastas, K., Liu, C.-M., Woods-Tor, A., Zipfel, C., de Wit, P.J.G.M., Jones, J.D.G., Tor, M., and Thomma, B.P.H.J. (2008). A Genome-Wide Functional Investigation into the Roles of Receptor-Like Proteins in Arabidopsis. Plant Physiol. **147,** 503-517.