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Supplemental Material to:

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The impact of cytokinin on jasmonate-salicylate antagonism in Arabidopsis immunity against infection with Pst DC3000

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Supplementary material

Methods

Generation of network topology and network simulations

The data for network setup was based on extensive literature research and data mining. Each well supported node as well as every inhibitory and activating edge of the plant hormone disease network was integrated into the network architecture. The network was created with the help of CellDesigner version 3.5.1 and compiled to SBML format (Systems Biology Markup Language).

For further analysis and Simulations the SBML files created by CellDesigner can be handled by SQUAD (Standardized Qualitative Dynamical Modeling Suite).[12] SQUAD automatically recognizes every single node and edge allowing an analysis of its interactions regarding steady states as well as dynamic simulations. For discrete dynamic analysis SQUAD uses generally validated assumptions: The presence of an activator can induce specific nodes whereas inhibitors are able to deactivate specific target nodes. Regarding more complex scenarios, different data was implemented into the network topology.

SQUAD identifies with a fast heuristic the total amount of steady states and calculates the activity of every single node. The simulations and equations of steady states are highlighting a systemic equilibrium and its impact due to signaling stimuli (pathogenic and/or hormonal signals). To set up an original equilibrium for continuous dynamic simulations all nodal activity values were adjusted to zero. Adjusting a single node value to 1 illustrates the systemic response towards either pathogenic or hormonal stimuli. Simultaneous adjustment of two or more stimuli allows the simulation of reciprocal effects between concerned nodes. Additionally, input values between 0 and 1 simulate partial activation of a node. Disabled states are transformed by SQUAD into time-dependent, sigmoid shaped graphs for every established node displaying their level of transcription. The original graphs are also transformed to heat maps for a better overview of the tendency of the datasets. By randomly adding and removing nodes the robustness of the complete network topology can be evaluated.

Analysis of micro array data

The Webtool GEO2R was used to analyze the original micro array data from GEO (Gene Expression Omnibus, http://www.ncbi.nlm.nih. gov/geo/geo2r/). GEO2R facilitates the user to compare two or more samples of GEO submitted micro array data sets. The webtool uses the Bioconducter R packages GEOquery und limma (Linear Models for Microarray Analysis). GEOquery parses the GEO-submitted array data into R data structure whereas limma utilizes multiple testing corrections for p-values to minimize the amount of false positives and identify differential expressed genes (p-value <0.05). Based on the amount of entries for each GEO-identifiers of micro array experiments mentioned above, the data was divided in either control or treated. The distribution of the selected values was calculated via value-distribution-option in GEO2R and rendered into boxplots to validate their applicability. By means of the testing procedure of the 'false discovery rate method' (FDR, [15] a multiple testing adjustment was applied. Hence GEO2R provides a limma-generated statistical analysis of data (corrected and raw p values, t and B values and fold changes).

References

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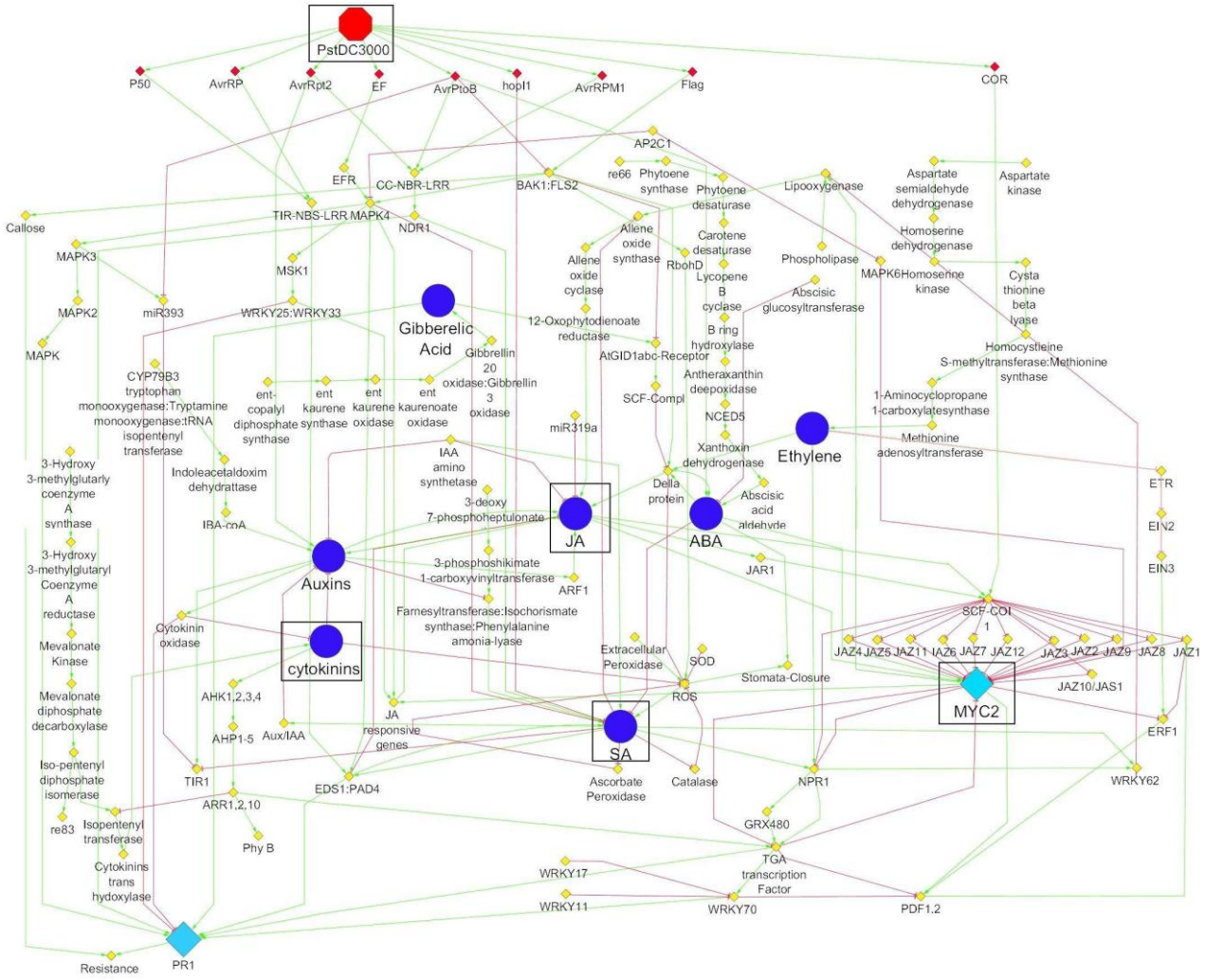
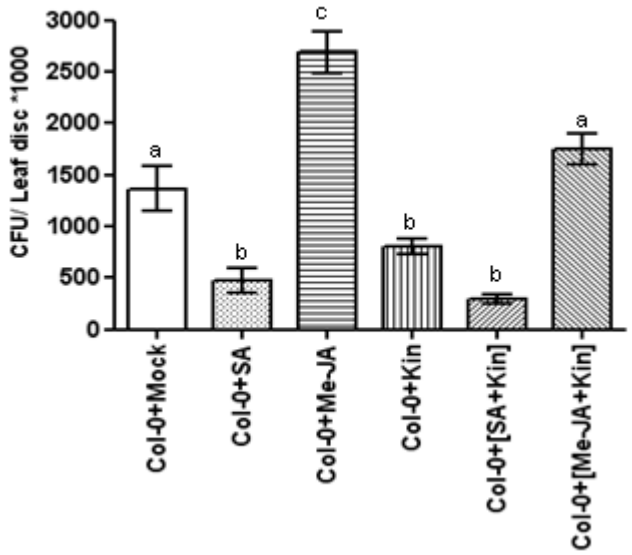
Supplementary Figure 1



S-Fig. 1. Integrated Boolean model on hormonal crosstalk in *Pst* DC3000-*Arabidopsis* Interaction. Phytohormones are small signaling molecules affecting almost all biological processes. The mutual interactions among hormone signaling pathways lead to crosstalk that eventually regulates gene expression. Information on hormonal crosstalk can be mined efficiently from public databases such as PubMed, Plant Interactome (STRING), PMN (Plant Metabolic Network) and KEGG. Moreover, pathogenic attributes of *Pst* DC3000 can be integrated from PPI (Plant Pathogen Interaction). All these databases can be utilized in constructing and integrating Boolean models. Starting from individual hormone biosynthesis to its signal transduction pathway inside the cell, model nodes (components of plant cells participating in hormone metabolic and signaling pathways: shown as round circles) and edges are assembled (functional interactions either activations or inhibitions: shown as green for activation and red for inhibition, respectively). Individual hormonal nodes (dark blue) are then integrated into networks nodes of *Pst* DC3000 (shown as red). *Pst* DC3000 injects effector proteins inside the cell through TTSS (red node). Nodes of *Pst* DC3000 are integrated to that of plant hormones regulatory networks. The network topology is designed in systems biology workbench, CellDesigner version 3.5.1. **PR1** (light blue) as important maker node is shown at the bottom of the network. In-put nodes used in the analysis such as *Pst* DC3000, SA, JA, MYC2 and cytokinin are boxed in rectangles. Functional evidence about behavior of selected edges as well as methods for network construction can further be studied in detail in Naseem et al. (2012).

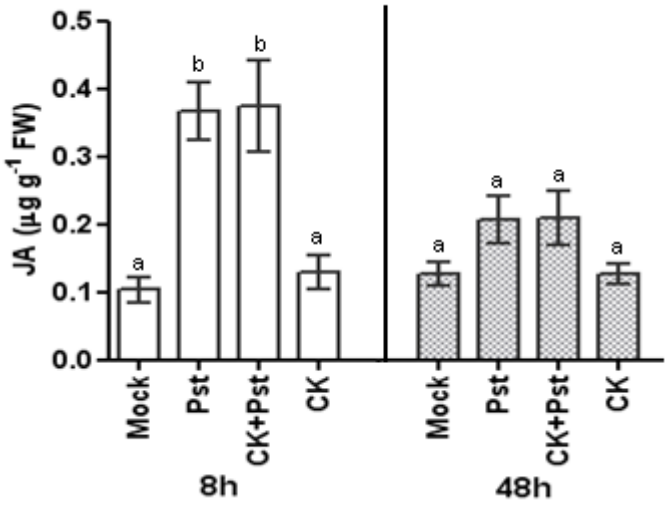
Supplementary Figure 2



S-Fig. 2. Growth quantification of *Pst* DC3000 in *Arabidopsis* leaves treated with different hormones.

4 weeks old Col-0 Arabidopsis leaves were syringe infiltrated with *Pst* DC3000 (10^3cfu/ml). 24h before pathogen inoculation leaves were treated with 10mM MgCl2 as control, 1mM SA, 10µM Kinetin, 1mM MeJA, combination of SA and kinetin and combination of MeJA and kinetin (hormonal treatments: x-axis). Bacterial spread was quantified as colony forming units (CFU/ml:y-axis) 3 days after pathogen infiltration. Similar results were obtained in three independent experiments. ($P < 0.05$, t test, and ±se, $n = 3$). Letters on the bars represent significant differences in response to pathogen spread.

Supplementary Figure3



S-Fig. 3. Accumulation of free JA in leaves of *Arabidopsis* Col-0 plants. Accumulation of free JA: Leaves of Arabidopsis Col-0 plants were compared with and without *Pst* and cytokinin feeding. The 8 and 72-h time points indicate differences in SA accumulation: Different letters denote statistically different values ($P < 0.05$, t test, and ±se, $n = 3$). The experiment was repeated twice with similar results. FW, fresh weight.

Supplemental Table 1

Node to node interaction					References
ATK	>	ASD			Yoshioka et al., 2001 and Plant Cyc Database
ASD	>	HSD			Curien et al., 2005 and Plant Cyc Database
HSD	>	HSK			Lee M and Leustek 1999 and Plant Cyc Database
HSK	>	CTL			Kim et al., 2002 and Plant Cyc Database
CTL	>	MTS/HMT			Ranocha et al., 2000 and Plant Cyc Database
MTS	>	MAT			Abel et al., 1995 and Plant Cyc Database
MAT	>	ACS			Lincoln 1991 and Plant Cyc Database
ACS	>	ET			Lincoln 1991 and Plant Cyc Database
PPS	>	PES			Lindgren et al., 2003 and AraCyc Database
PES	>	PED			Bartley et al., 1999 and AraCyc Database
PED	>	CED			Pogson et al., 1996 and AraCyc Database
CED	>	LBC			Cunningham et al., 199 and Plant Cyc Database
LBC	>	BRH			Kim and Dellapenna 2006 and AraCyc Database
BRH	>	ZEO			Hieber et al., 2000 and AraCyc Database
ZEO	>	AED			Frechilla et al., 1999 and AraCyc Database
AED	>	XDH			Nambara et al., 2005 and AraCyc Database
XDH	>	AAO			Gonzalez et al., 2002 and Plant Cyc Database
AAO	>	ABA			Seo et al., 2000 and AraCyc Database
AGT	|	ABA			Jackson et al., 2002 and AraCyc Database
IPT	>	CTH			Kakimoto et al., 2001 AraCyc Database
CTH	>	t-Zeatin (CK)			Takei et al., 2004 and AraCyc Database
CKX	|	CK			Werner et al. 2003
LOXs	>	AOS			Feussner and Wasternack 2002 and AraCyc Database
AOS	>	AOC			Feussner and Laudert et al., 1996 and AraCyc Database
AOC	>	OPRs			Hofmann et al., 2006 and Plant Cyc Database
OPRs	>	OPCs			Hooks et al., 1999 and AraCyc Database
OPCs	>	Jasmonate			Reymond and Farmer 1998 and AraCyc Database
EDS	>	EKS			Fleet et al., 2003 and AraCyc Database
EKS	>	EKOs			Helliwell et al., 2001 and AraCyc Database
EKOs	>	EUOs			Davidson et al., 2003 and AraCyc Database
EUOs	>	G20/3 Os			Lange et al., 1994 and AraCyc Database
GOs	>	GA			Lange et al., 1994 and AraCyc Database
TMO,TPM,IAD	>	IAN,IAO			Ouyang et al., 2000 and AraCyc Database
IAN,IAO	>	Auxin			Normanly et al., 1993 and AraCyc Database
IAA-Synthase	|	Auxin			Müller and Weiler 2000 and AraCyc Database
SKK	>	PCT			Singh et al., 2007 and Schmid et al., 1995
PCT	>	ICSs			Wildermuth et al., 2001 and AraCyc Database
ICS,PAL	>	SA			Shah 2003 and Mauch and Slusarenko 1996
ET	|	ETR			Kendrick and Chang 2008 and Kieber et al., 1993
ET	>	DELLA			Achard et al., 2003
ET	|	ETR	>	EIN2	Kendrick and Chang 2008 and Alonso et al., 1999
EIN2	|	SCFcomp	>	EIN3	Solano et al., 1998 and Kendrick and Chang 2008
ETR1	>	AHPs			Urao et al., 2000 and Müller and Sheen 2007
EIN2	>	NPR1			Leon-Reyes et al., 2009 and Pieterse et al., 2009
EIN3	>	ERF1			Solano et al., 1998 and Kendrick and Chang 2008
ERF1	>	PDF 1.2			Pré, M. et al 2008 and Pieterse et al., 2009
ABA	|	SA			Flors et al., 2007
ABA	>	OST1 Kinase.			Mustilli et al., 2002
OST1 K	>	Stom. Clos			Melotto et al. 2006
Stom. Clos	>	Resistance			Melotto et al. 2006 and Pieterse et al., 2009
ABA	>	MYC2			Anderson et al., 2004 and Abe et al., 2003
GA	>	GID1			Zentella et al., 2007
GID1	>	SCF	|	DELLA	Griffiths et al., 2006
GA	>	SA			Navarro et al., 2008 and Alonso-Ramirez et al, 2009
DELLA	|	JAZ			Hou et al., 2010 and Navarro et al., 2008
DELLA	>	ABA			Zentella et al., 2007
DELLA	|	GA			Zentella et al., 2007
DELLA	|	SA			Navarro et al., 2008 and Alonso-Ramirez et al, 2009
DELLA	|	ROS			Achard et al., 2008 and Grant and Jones 2009
Auxin	|	Cytokinin			Nordstrom et al., 2004 and Liu et al., 2010
Auxin	>	TIR1			Dharmasiri et al., 2005
AUX/IAA	|	ARFs			Benjamins and Scheres 2008 and Ulmasov et al., 1997
Auxin	>	SCFTIR1	|	AUX/IAA	Tiwari et al., 2001 and Santner and Estelle 2009

	Auxin	>	JA				Liu et al., 2006
	Auxin	>	AFB1	|	SA		Robert-Seilaniantz et al, 2011
	Auxin	>	Ethylene				Arteca and Arteca 2008
	JA	>	SCF-COI				Katsir et al., 2008
	JA	>	SCF-COI	|	JAZ		Pieterse et al., 2009 and Katsir et al., 2008
	JAZ	>	MYC2				Lorenzo and Solano 2005 and Pré et al. 2008
	JAZ	>	ERF1				Lorenzo and Solano 2005
	MYC2	>	LOX2				Mao et al., 2007 and Bari et al., 2009
	WRKY 62	|	LOX2				Pieterse et al., 2009 and Mao et al., 2007
	GRX480	|	PDF 1.2				Ndamukong et al., 2007 and Bari et al., 2009
	WRKY70	|	PDF1.2				Li et al., 2006
	MYC2	|	SA				Laurie-Berry et al., 2006
	MYC2	|	PR-1				Kazan and Manners 2008 and Laurie-Berry et al., 2006
	SA	>	NPR1				Mou et al., 2003 and Dong 2004
	NPR1	>	TGA-TF				Loake and Grant 2007 and Mou et al., 2003
	NPR1	>	GRX480	>	TGA	> PR1	Ndamukong et al., 2007
	NPR1	>	WRKY 62				Mao et al., 2007
	GRX480	>	TGA	|	PDF1.2		Ndamukong et al., 2007 and Bari et al., 2009
	NPR1	>	WRKY 70				Li et al., 2004
	SA	>	AUX/IAA				Wang et al., 2007
	WRKY 70	>	PR-1				Li et al., 2004, 2006
	WRKY 11	|	WRKY70				Journot-Catalino et al., 2006
	WRKY 17	|	WRKY 70				Journot-Catalino et al., 2006
	WRKY11 and 17	>	JA				Journot-Catalino et al., 2006
	WRKY 25	|	PR1				Zheng et al., 2007
	SA	|	AOS				Pan et al., 1998
	B ARRs	>	TGA	>	PR-1		Choi et al., 2010
	B ARRs	>	CKX				Müller and Sheen 2007
	CKX	|	PR1				Choi et al., 2010
	A ARRS	>	PhyB				Müller and Sheen 2007
	PhyB	>	SA				Genoud et al., 2001
	Pst DC3000	>	Flagellin				Zipfel et al., 2004
	Flagellin	>	FLS2				Zipfel et al., 2004
	Flag	>	FLS2	>	BAK1		Chinchilla et al., 2007
>	BAK1	>	MAPK1,2,3,4				Zipfel et al., 2006
	Pst DC3000	>	EF	>	EFR		Zipfel et al., 2006 and Nekrasov et al., 2009
>	EFR	>	MAPK4 and 6				Nekrasov et al., 2009
>	BAK1	>	....MAPK1	>	PR1		Gust et al., 2007 and Andreasson et al., 2005
	FLS2	>	BAK	>	NADPH-Oxi		Torres et al., 1998 and Mersmann et al., 2010
	BAK	>	NADPH-Oxi	>	ROS		Panstruga et al., 2009 and Torres et al., 1998
	ROS	>	SA				Torres et al., 1998 and Draper 1997
	SA	>	ROS				Klessig et al., 2000 and Torres et al., 1998
	FLS2	>	BAK	>	DELLA		Navarro et al., 2008 and Grant and Jones 2009
	DELLA	|	ROS				Grant and Jones 2009 and Achard et al., 2008
	FLS2	>	BAK	>	mirRNA393		Navarro et al., 2006
	miRNA 393	|	ARF1and TIR1				Pieterse et al., 2009 and Navarro et al., 2006
	AvrPtoB	|	mir393				Navarro et al., 2008
	MAPK4	>	MKS1				Andreasson et al., 2005
	MAPK4	|	PAD4 and EDS1				Andreasson et al., 2005 and Brodersen et al., 2006
	MSK1	|	WRKY 25 and 33				Andreasson et al., 2005
	WRKY25 and 33	|	PR1				Zhang et al., 2007 and loke and Grant 2007
	MAPK4	>	WRKY25				Loke and Grant 2007 and Andreasson et al., 2005
	PAD4 and EDS1	>	SA				Feys et al., 2001
	PAD4 and EDS1	|	JA				Brodersen et al., 2006 and Loke and Grant 2007
	MAPK4	|	SA				Petersen et al., 2000
	FLS2-BAK1	>	Callose				Luna et al., 2011
	FLS2, EFR	>	MAPK3,2,1				Panstruga et al., 2009
	PstDC3000	>	Avr PtoB				de toress-Zabala et al., 2007
	AvrPtoB	|	mir393				Navarro et al., 2008
	Pst DC	>	AvrPtoB	>	ABA		Zabala et al., 2007
	AvrPtoB	|	FLS2-BAK1				Shan et al., 2008
	T-LRRs	>	PAD4 and EDS1				Volt et al., 2009 and Aarts et al., 1998
	CC-NB-LRRs	>	NDR1	>	SA		Century et al., 1997 and Volt et al., 2009
	AvrPtoB	>	CC-NB-LRR				Collier and Moffett 2009

	AvrRpm1	>	CC-NB-LRR			Panstruga et al., 2009 and Collier and Moffett 2009
	Pst	>	Avr Rpt2	>	Auxin	Chen et al., 2007
	Avr Rpt2	>	CC-NB-LRR			Panstruga et al., 2009 and Collier and Moffett 2009
	Pst	>	HopAIA	>	TIRNB-LRR	Zhang et al., 2007
	Pst	>	Coronatine	>	COI | JAZ	Panstruga et al., 2009 and Block et al., 2005
	HopAI1	|	MAPK3 and MAPK6			Zhang et al., 2007
	SA	|	Catalase			Chen et al., 1993
	Catalase	|	ROS			Chen et al., 1993
	SA	|	Ascorbate Peroxidase			Durner and Klesssig 1995
	Ascorbate Peroxidase	|	ROS			Durner and Klesssig 1995
	extracellular Peroxidase	>	ROS			Kawano et al. 1998, Kawano 2003 and Kunihiro et al. 2011
	NADPH oxidase	>	ROS			Kawano et al. 1998, Kawano 2003 and Kunihiro et al. 2011
	Superoxide disumtase (SOD)	|	ROS			Mori et al. 2001, Khokon et al. 2011
	JA	>	JAR1			Farmer et al. 2010
	JAR1	>	SCFCOI/CSN			Farmer et al. 2010
	miR319a	|	JA			Schommer et al. 2008
	JA responsive genes	>	JA			Farmer et al. 2010
	NPR1	|	SCFCOI/CSN			Farmer et al. 2010
	SCFCOI/CSN	|	JAZ1			Chini et al. 2007, Katsir et al. 2008 and Thines et al. 2007
	SCFCOI/CSN	|	JAZ2			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ3			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ4			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ5			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ6			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ7			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ8			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ9			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ10/JAS1			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ11			Chini et al. 2007, Katsir et al. 2008
	SCFCOI/CSN	|	JAZ12			Chini et al. 2007, Katsir et al. 2008
	JAZ1	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ2	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ3	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ4	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ5	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ6	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ7	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ8	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ9	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ10/JAS1	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ11	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	JAZ12	|	MYC2			Chini et al. 2007, Katsir et al. 2008
	MYC2	>	JA responsive genes			Devoto et al. 2002, Reymond et al. 2004 and Zhou et al. 2005
	MAPK6	|	MYC2			Takahasi et al. 2007
	JA responsive genes	>	JA			Farmer et al. 2010
	SA	>	NPR1			Wu et al. 2012
	AP2C1	|	MAPK4 and 6			Farmer et al. 2010
	MAPK4	>	JA responsive genes			Petersen et al., 2000

> Activation, potentiation, stabilization, de-repression or other positive attribute

| Inhibition, degradation, repression or a negative attribute

Regulatory proteins, Receptors, Degradation complexes, Transcription factors, Response Regulators are shown as green letters

Pathogenic factors such as effectors are elicitors shown as red letters

Metabolic and phosphorylation enzymes are shown as black letters

Hormones are shown as blue letters

Phenotypes, metabolites, ions, genes during expression are shown as golden

Following are abbreviations and full names of all nodes presented in the network topology and Supplementary Table 1

JA-res.genes	Jasmonic acid responsive genes	IAD	Indoleacetaldoxime dehydrogenase
JAZ	jasmonate ZIM-domain	IAN	Indole-3-acetonitrile nitrilase
MYC2	a basic helix-loop helix transcription factor	IAO	Indole-3-acetaldehyde oxidase
JAZ-deg. Comp.	jasmonate ZIM-domain degrading complex	ICO	IBA-CoA oxidase
FLS2	flagellin sensitive 2	Aux	Auxin
Auxin		HMS	Hydroxy 3-methylglutaryl Co-A synthase
NADPH-Oxi	NADPH-Oxidase	HMR	Hydroxy 3-methylglutaryl Co-A synthase
NPR1	non-expressor of PR1	MNK	Melvonate kinase
CKX	cytokinin Oxidase	MDD	Melvonate Diphosphate decarboxylase
TIR1	transport inhibitor response1	IDI	Iso-pentenyl Diphosphate isomerase
ROS	reactive oxygen species	DPS	Diphosphate synthase
ABA	abscisic acid	PES	Phytoene synthase
JA	jasmonic acid	PED	Phytoene desaturase
MKS1	MAP Kinase substrate 1	CED	Carotene desaturase
Callose		LBC	Lycopene Beta cyclase
Della-Prot.	Della-Protein	BRH	Beta ring hydroxylase
MAPK	Mitogen activated protein kinase	ADO	Antheraxinthin deepoxidase
GRX480	Glutaredoxin	ZEO	Zeaxanthin epoxidase
PAD4	Phytoalexin deficient 4	AED	Antheraxanthin epoxidase
Resistance		Xanthoxin dehydrogenase	
WRKY22		AAO	Abscisic acid aldehyde oxidase
WRKY70 and WRKY62	transcription factors with W-box binding domain	ABA	Abscicic acid
miR393	microRNA 393	AGT	Abscisic acid glycosyltransferase
SA	salicylic acid	CTH	Cytokinin trans-hydroxylase
PR1	pathogenesis related protein	IPT	Isopentenyl transferase
Stom.Clos.	stomata closure	CK	Cytokinin
TGA-TF	TGACG motif binding [TGA] transcription factors	ICS	Isocharismate synthase
Aux/IAA	Auxin/Indole-3 acetic acid	PAL	Phenylalanine amonia layase
ET	ethylene	DPS	3-Deoxy 7-phosphoheptulonate synthase
ATK	Aspartate kinase	PCT	3-Phosphoshikimate 1-carboxyvinyl tranferase
ASD	Aspartate semialdehyde dehydrogenase	PSP	Phospholipase
HSD	homoserine dehydrogenase	LOX	Lipooxygenase
HSK	homoserine kinase	AOS	Allene oxide synthase
CTL	cystathionine beta-lyase	AOC	Allene oxide cyclase
MTS	Methionine synthase	OPR	Oxophytodienpate reductase
HMT	Homocysteine Smethyltransferase	JA	Jasmonic Acid
ACS	1-Aminocyclopropane 1-carboxylate synthase	EDS	ent-copalyl diphosphate synthase
MAT	Methionine adenosyltransferase	EKS	ent-kaurene synthase
TMO	CYP79B3 tryptophan monooyxygenase	EKO	entkaurene oxidase
TPM	tryptamine monooxygenase	EUO	ent-kaurenoate oxidase
RPT	tRNA isopentenyl transferase	G20O	gibberellin 20-oxidase
RbohD	respiratory burst oxidase homolog D	G3O	gibberellin 3-oxidase

Supplemental Table 2: Expression analysis (multiple comparisons) on the Impact of SA, JA and CK signaling on immunity in *Arabidopsis.* [1]

ID	P.Value	t- values SA	t-values JA	t-values CK	Gene.symbol	logFC SA	logFC CK	logFC JA	Annotation
259495_at	**9,61E-02**	**1,955**	-0,376	0,255	**AT1G15890**	**0,430**	1,320	1,320	**disease resistance protein (CC-NBS-LRR class), putative**
249264_s_at	**2,22E-03**	**4,959**	0,505	0,358	**AT5G41750/ AT5G41740**	**1,388**	2,540	2,540	**disease resistance protein (TIR-NBS-LRR class), putative/ disease resistance protein (TIR-NBS-LRR class), putative**
249561_at	**4,15E-02**	**2,552**	-0,069	0,369	**AT5G38340**	**0,277**	0,798	0,798	**disease resistance protein (TIR-NBS-LRR class), putative**
245233_at	**2,65E-01**	**1,222**	-5,355	0,499	**AT4G25580**	**0,125**	0,664	0,664	**stress-responsive protein-related**
248974_at	**2,19E-02**	**3,025**	0,225	0,773	**AT5G45060**	**0,555**	1,610	1,610	**disease resistance protein (TIR-NBS-LRR class), putative**
248875_at	**3,55E-02**	**2,666**	-2,828	0,808	**AT5G46470**	**0,517**	3,090	3,090	**disease resistance protein (TIR-NBS-LRR class), putative**
259925_at	**2,83E-01**	**1,174**	-1,208	0,836	**PR5**	**0,654**	9,060	9,060	**PR5 (PATHOGENESIS-RELATED GENE 5)**
266385_at	**9,25E-03**	**3,699**	-3,559	0,916	**PR1**	**3,019**	72,800	72,800	**PR1 (PATHOGENESIS-RELATED GENE 1)**
265588_at	**2,24E-02**	**3,005**	-2,755	1,051	**AT2G19970**	**0,599**	1,990	1,990	**pathogenesis-related protein, putative**
248847_at	**1,15E-01**	**1,829**	0,187	1,324	**AT5G46510**	**0,696**	3,500	3,500	**disease resistance protein (TIR-NBS-LRR class), putative**
248943_s_at	**5,42E-03**	**4,147**	-0,273	1,571	**AT5G45490/ AT5G45440**	**1,213**	7,630	7,630	**disease resistance protein-related/ disease resistance protein-related**
252684_at	**5,49E-03**	**4,135**	-0,310	1,681	**AT3G44400**	**1,511**	3,760	3,760	**disease resistance protein (TIR-NBS-LRR class), putative**
265586_at	**3,64E-01**	**0,977**	-2,736	2,031	**PR-1-LIKE**	**0,147**	8,450	8,450	**PR-1-LIKE (PATHOGENESIS-RELATED PROTEIN-1-LIKE)**
259443_at	**1,11E-02**	**3,549**	-0,099	2,086	**AT1G02360**	**1,380**	8,800	8,800	**chitinase, putative**
261914_at	**1,71E-01**	**1,546**	-3,332	2,557	**AT1G65870**	**0,461**	14,700	14,700	**disease resistance-responsive family protein**
256781_at	**4,08E-01**	**0,885**	-0,744	5,422	**AT3G13650**	**0,398**	26,800	26,800	**disease resistance response**
266333_at	**2,23E-01**	**-1,352**	2,340	-1,352	**AXL**	**-0,127**	-0,127	-0,127	**AXL (AXR1-LIKE); binding / catalytic**
261713_at	**9,50E-02**	**-1,963**	10,474	-2,818	**MYC2**	**-0,676**	-20,200	-20,200	**MYC2; DNA binding / transcription activator/ transcription factor**
247025_at	**6,75E-01**	**-0,440**	1,946	-0,048	**ABA1**	**-0,120**	-2,680	-2,680	**ABA1 (ABA DEFICIENT 1); zeaxanthin epoxidase**
246432_at	**2,00E-01**	**-1,432**	7,409	-1,229	**RGL3**	**-0,159**	-2,300	-2,300	**RGL3 (RGA-LIKE PROTEIN 3); transcription factor**
247549_at	**0,00133**	**-6,503**	-1,116	-6,503	**MYB28**	**-145,0**	-145,0	-145,0	**MYB28 (myb domain protein 28); DNA binding / transcription factor**

[1]GEO experiments as given in legend to Figure 1C; significant differences from network analysis are shown in Figure 1C. p-values = individual level of significance for gene expression comparison from described GEO experiment, t-values = difference in mean of gene expression between wild type and treated plants, logFC= log fold changes, again according to the GEO experiment.