Supporting Information

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SI Text

Cloning of Transcription Factor *BoMYC* as an Example in the Study. A partial sequence (575 bp) of the cabbage transcription factor (*MYC)* was constructed after sequencing fragments were obtained by RT-PCR. In the RT-PCR we used degenerate oligonucleotide primers that were derived from *MYC* sequences of other plant species (Tables S6 and S7). A full-length cDNA of 2,071-bp nucleotides was isolated using rapid amplification of cDNA ends (5′-RACE and 3′-RACE). This cDNA clone contained an ORF starting with an ATG codon preceded by an in-frame stop codon, indicating that it contains the complete coding region. The ORF of 1,833 nucleotides (from 61 to 1893) encoded a predicted protein of 610 amino acids. This cDNA clone was designated as the *Brassica oleracea MYC* gene, and we use *BoMYC* as the abbreviated term referring to this gene.

BoMYC contains a helix–loop–helix domain found in specific DNA-binding proteins that act as transcription factors. In the GenBank database, the deduced protein matches well with other bHLH-like proteins. The full-length cDNA sequence of *BoMYC* has been deposited to the GenBank database under accession no. EF423803. The deduced protein sequence of *BoMYC* contains a bHLH-type DNA-binding/dimerization domain in the C-terminal region. Sequence alignment and phylogenetic tree analysis showed that *BoMYC* shared an overall identity of 87% at the amino acid level with the *Arabidopsis AtMYC2* protein (Figs. S1 and S2). We used the same method to clone the other genes used in this study (for accession numbers see Table S6).

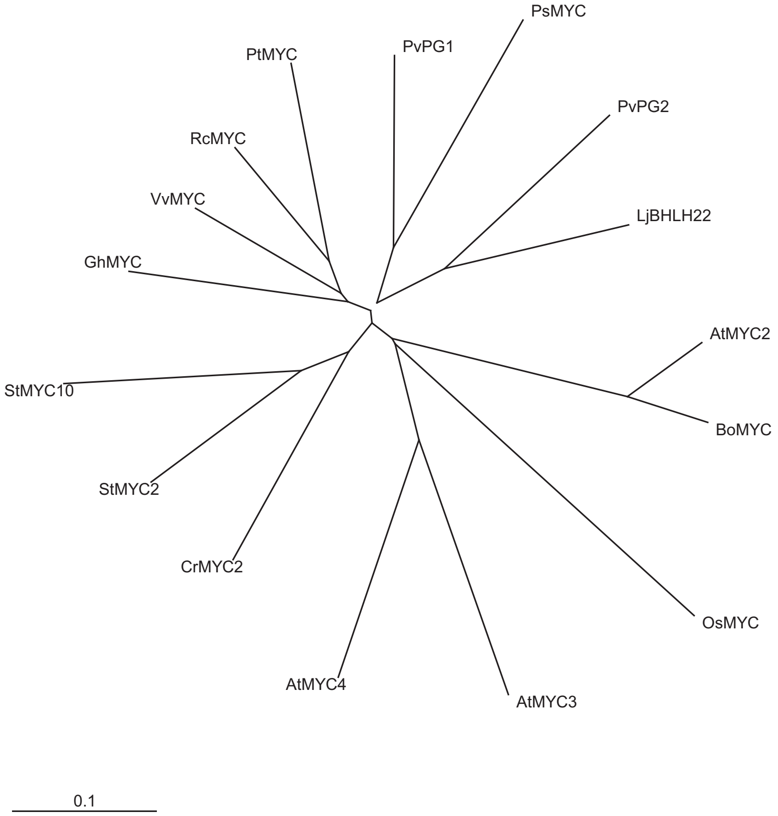

Fig. S1. Phylogenetic tree of *MYC* genes from different plant species. Accessions for *MYC* amino sequences represented in this tree are *Arabidopsis thaliana AtMYC2* (At1g32640); *A. thaliana AtMYC3* (At5g46760); *A. thaliana AtMYC4* (At4g17880); *B. oleracea BoMYC* (EF423803); *Oryza sativa OsMYC* (AY536428); *Catharanthus roseus CrMYC2* (AF283507); *Solanum tuberosum StMYC2* (AJ630505); *S. tuberosum StMYC10* (AJ630506); *Gossypium hirsutum GhMYC* (FJ358540); *Vitis vinifera MYC* (XM_002280217); *Ricinus communis RcMYC* (XM_002519768); *Populus trichocarpa PtMYC* (XM_002326688); *Phaseolus vulgaris PvMYC* (U18348); *P. vulgaris PvMYC* (U18349); *Pisum sativum* PsMYC (DQ399528); and *Lotus japonicus LjBHLH22* (FJ379754).

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AtMYC2          MTDYRLQPTMNLWTTDDNASMMEAFMSSS-DISTLWPPASTTTTTATTETTPTPAMEIPA
BoMYC           MT----EPTMNLWTTDDNASMMEAFMSSSSDISALWPPVTTTATASTTA---------PA
                **    :********************** ***:****.:**:*::**          **

AtMYC2          QAGFNQETLQQRLQALIEGTHEGWTYAIFWQPSYDFSGASVLGWGDGYYKGEEDKANPRR
BoMYC           PAGFNEETLQQRLQALIEGTNEGWTYAIFWQPSYDFSGASVLGWGDGYYKGEEDKAKPRQ
                 ****:**************:***********************************:**:

AtMYC2          RSSSPPFSTPADQEYRKKVLRELNSLISGGVAPSDDAVDEEVTDTEWFFLVSMTQSFACG
BoMYC           RTSPPPFSTPADQEYRKKVLRELNSLISGGGGPTDDAVDEEVTDTEWFFLVSMTQSFACG
                *:*.************************** .*:**************************

AtMYC2          AGLAGKAFATGNAVWVSGSDQLSGSGCERAKQGGVFGMHTIACIPSANGVVEVGSTEPIR
BoMYC           SGLAGKAFSTGNAVWVYGSDQLTGSGCERAKQGGVFGMQTIACIPSANGVVELGPTEQIR
                :*******:******* *****:***************:*************:*.** **

AtMYC2          QSSDLINKVRILFNFDGGAGDLSGLNWNLDPDQGENDPSMWINDPIGTPGSNEPGNGAPS
BoMYC           QSSDLMNKVRVLFNFNGGAGDLSCLNWNLDPDQGENDPSMWINDPIGVP---EQGNGAPS
                *****:****:****:******* ***********************.*   * ******

AtMYC2          SSSQLFSKSIQFENG-SSSTITENPNLDPT--PSPVHSQTQNPKFNNTFSRELNFSTSSS
BoMYC           SSSQLFAKSIQFENGGSSSTIIENPNPDPAPAPSPVHSQTQNPKFSNNFSRELNFSTSST
                ******:******** ***** **** **:  *************.*.***********:

AtMYC2          TLVKPRSGEILNFGDEGKRSSGNPDPSSYSGQTQFENKRKRSMVLNEDKVLSFGDKTAGE
BoMYC           TLVKPRPAEILSFGDEGKRSSVNPDPSSYSGQTQFENKRKKSIGMSDDKVLTFG-TGGGE
                ******..***.********* ******************:*: :.:****:** . .**

AtMYC2          SDHSDLEASVVKEVAVEKRPKKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAVVP
BoMYC           SDHSDLEASVVKEIP-EKRPKKRGRKPANGREEPLNHVEAERQRREKLNQRFYALRAVVP
                *************:. ********************************************

AtMYC2          NVSKMDKASLLGDAIAYINELKSKVVKTESEKLQIKNQLEEVKLELAGRKASASGGDMSS
BoMYC           NVSKMDKASLLGDAIAYINELKSKVTKTESEKTQIKTQLEEVKMELAGRKASA-GGDLSS
                *************************.****** ***.******:********* ***:**

AtMYC2          SCS--SIKPVGMEIEVKIIGWDAMIRVESSKRNHPAARLMSALMDLELEVNHASMSVVND
BoMYC           SCSLTAIKPVGMEIEVKIIGWDAMIRVESSKRNHPAARLMSALMDLELEVNHASMSVVND
                ***  :******************************************************

AtMYC2          LMIQQATVKMGFRIYTQEQLRASLISKIG
BoMYC           LMIQQATVKMGFRIYTQEQLRASLISKIG
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Fig. S2. Clustal X (1.83) alignment of deduced amino acid sequence of *B. oleracea MYC* (*BoMYC*) with *Arabidopsis thaliana AtMYC2*. They share an overall identity of 87% at the amino acid level. The bHLH-ZIP domain is indicated in red. The acidic region is underlined with blue.

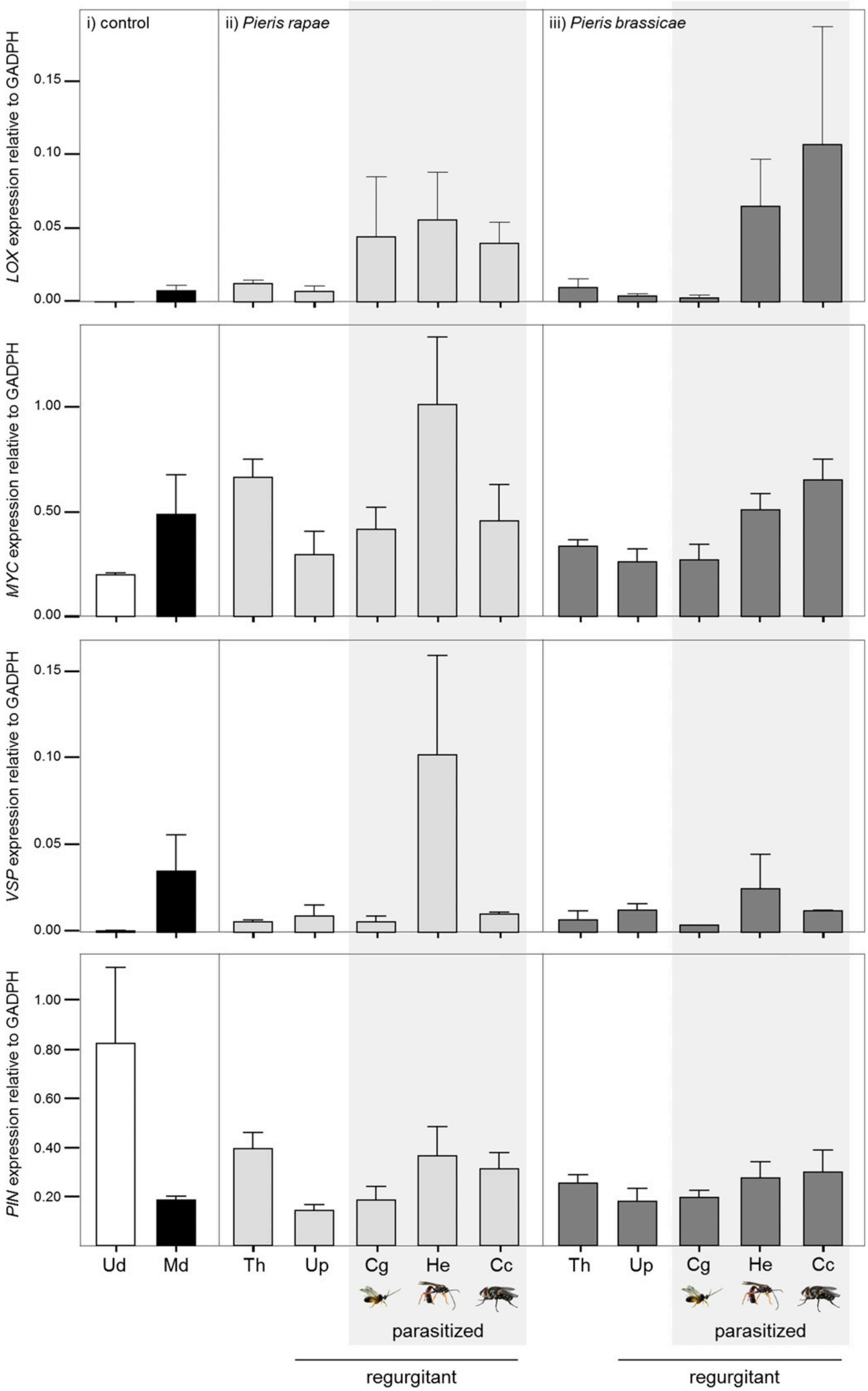

Fig. S3. Expression levels of *BoLOX, BoMYC, BoVSP*, and *BoPIN* 6 h after treatments were applied to *B. oleracea* plants. Treatments: undamaged plants (Ud, white bars); mechanical damage consisting of three needle punctures (Md, black bars); herbivore treatments with *Pieris rapae* (light gray) or *Pieris brassicae* (dark gray): true herbivory (Th), mechanical damage plus regurgitant from unparasitized caterpillars (Up) or caterpillars parasitized by *Cotesia glomerata* (Cg), *Hyposoter ebeninus* (He), or *Compsilura concinnata* (Cc).

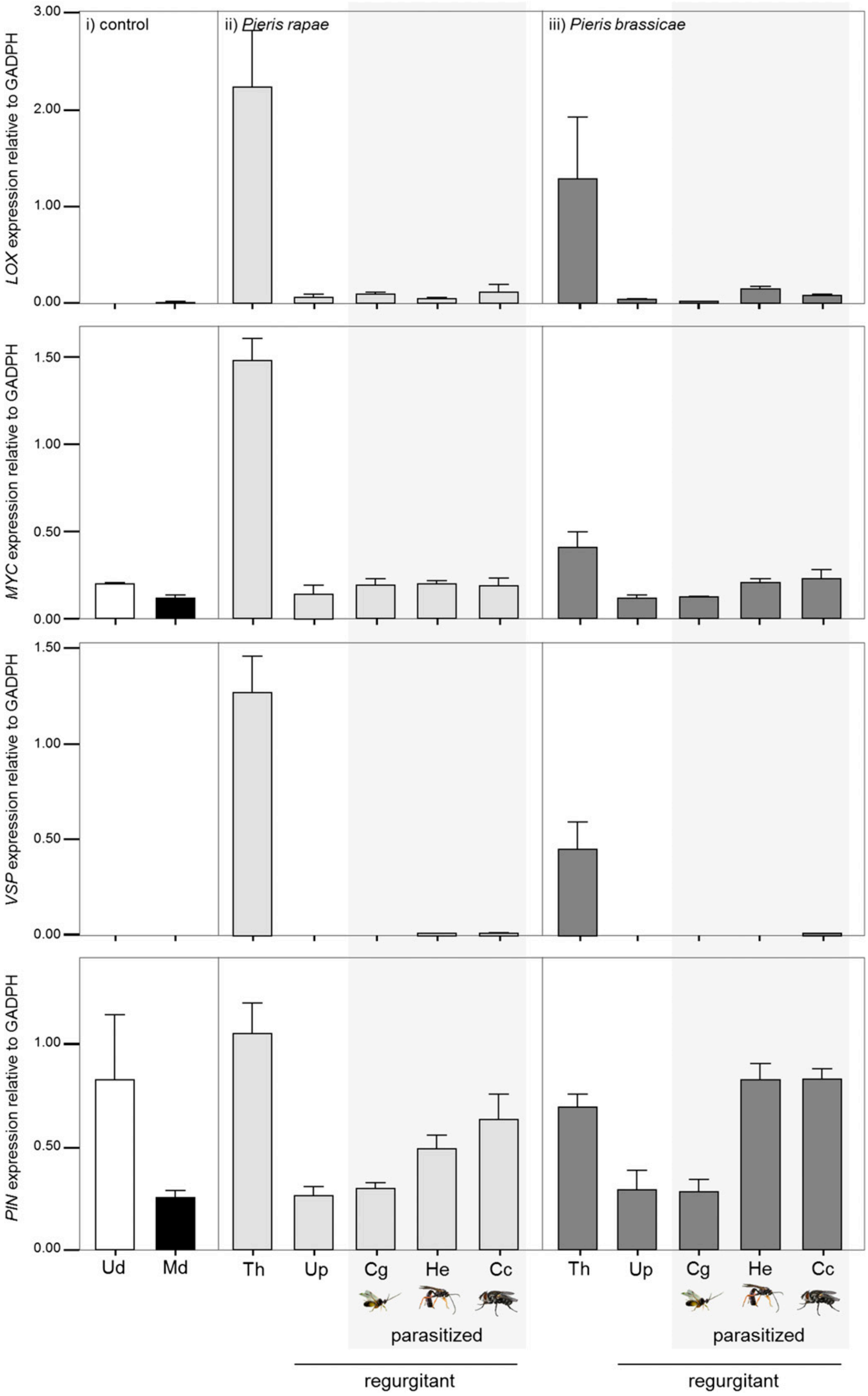

Fig. S4. Expression levels of *BoLOX, BoMYC, BoVSP*, and *BoPIN* 24 h after treatments were applied to *B. oleracea* plants. Treatments: undamaged plants (Ud, white bars); mechanical damage consisting of three needle punctures (Md, black bars); herbivore treatments with *Pieris rapae* (light gray) or *Pieris brassicae* (dark gray): true herbivory (Th), mechanical damage plus regurgitant from unparasitized caterpillars (Up) or caterpillars parasitized by *Cotesia glomerata* (Cg), *Hyposoter ebeninus* (He), or *Compsilura concinnata* (Cc).

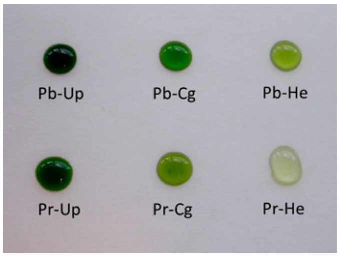

Fig. S5. Regurgitant of *Pieris brassicae* (Pb) and *Pieris rapae* (Pr) collected from unparasitized (Up), *Cotesia glomerata*-parasitized (Cg), and *Hyposoter ebeninus*-parasitized (He) caterpillars.

Table S1. Lists of different treatments in plant leaves for gene expression studies

	Treatment											
Parameter	WT	MD	Pb	U-Pb	Cg-Pb	He-Pb	Cc-Pb	Pr	U-Pr	Cg-Pr	He-Pr	Cc-Pr
Description	Undamaged	Mechanical damage by needle punching	First-instar *P. brassicae* feeding	Regurgitant from unparasitized *P. brassicae*	Regurgitant from *C. glomerata* parasitized *P. brassicae*	Regurgitant from *H. ebeninus* parasitized *P. brassicae*	Regurgitant from *C. concinnata* parasitized *P. brassicae*	First-instar *P. rapae* feeding	Regurgitant from unparasitized *P. rapae*	Regurgitant from *C. glomerata* parasitized *P. rapae*	Regurgitant from *H. ebeninus* parasitized *P. rapae*	Regurgitant from *C. concinnata* parasitized *P. rapae*
Time point (h)		2 6 24	2 6 24	2 6 24	2 6 24	2 6 24	2 6 24	2 6 24	2 6 24	2 6 24	2 6 24	2 6 24
Symbol	🍃	🍃	🍃	🍃+💧	🍃+💧	🍃+💧	🍃+💧	🍃	🍃+💧	🍃+💧	🍃+💧	🍃+💧

Table S2. Multiple ANOVA analyses of gene expression over time (2, 6, 24 h) after plants were induced with different types of damage (undamaged, mechanical damage, mechanical damage plus regurgitant, true herbivory)

	Time (df = 2)		Treatment (df = 3)		Time × Treatment (df = 6)		
Variable	*F*	*P*	*F*	*P*	*F*	*P*	Post hoc treatment*
Pillai's trace	3.285	**<0.001**	6.202	**<0.001**	2.546	**<0.001**	
Gene							
BoLOX (JA)	16.859	**<0.001**	15.553	**<0.001**	15.439	**<0.001**	(a = 1, 2, 3) (b = 4)
BoMYC (JA)	0.091	0.913	5.466	**0.002**	7.481	**<0.001**	(a = 1, 2) (ab = 3) (b = 4)
BoVSP (JA)	15.057	**<0.001**	16.005	**<0.001**	16.599	**<0.001**	(a = 1, 2, 3) (b = 4)
BoDEF (JA)	0.900	0.412	14.023	**<0.001**	1.297	0.273	(a = 2, 3, 4) (b = 1)
BoPAL (SA)	4.277	**0.018**	3.624	**0.018**	7.425	**<0.001**	(a = 1) (ab = 2, 4) (b = 3)
BoPR1 (SA)	2.127	0.128	4.793	**0.005**	4.341	**0.001**	(a = 1, 2) (ab = 4) (b = 3)
BoACS (ET)	1.327	0.273	2.216	0.096	3.425	**0.006**	—
BoMYR	0.047	0.954	0.694	0.559	3.160	**0.009**	—
BoPIN	3.366	**0.041**	22.202	**<0.001**	1.838	0.107	(a = 2, 3) (b = 4) (c = 1)

Values in bold indicate significant effects at $P < 0.05$.

*Post hoc classes for the factor Treatment based on Tukey: (1) undamaged plants, (2) mechanical damage, (3) mechanical damage plus regurgitant, (4) true herbivory. Classes are indicated with a, b, and c.

Table S3. MANOVA analysis of gene expression over time (2, 6, 24 h) after plants were manually damaged and regurgitant of either *Pieris rapae* or *Pieris brassicae* caterpillars was applied, which originated from unparasitized caterpillars or caterpillars parasitized by different parasitoids (*Cotesia glomerata*, *Hypersoter ebeninus*, *Compsilura concinnata*)

	Time (df = 2)		Herbivore (df = 1)		Parasitoid (df = 3)		Time × herbivore (df = 2)		Time × parasitoid (df = 6)		Herbivore × parasitoid (df = 3)		Time × herbivore × parasitoid (df = 6)	
Variable	*F*	*P*	*F*	*P*	*F*	*P*	*F*	*P*	*F*	*P*	*F*	*P*	*F*	*P*
Pillai's trace	11.907	**<0.001**	1.686	0.125	2.764	**<0.001**	1.759	**0.045**	1.935	**<0.001**	1.482	0.077	1.077	0.344
Gene														
BoLOX (JA)	9.279	**<0.001**	0.004	0.947	4.318	**0.009***	0.135	0.874	0.354	0.904	2.211	0.099	1.205	0.320
BoMYC (JA)	40.231	**<0.001**	1.523	0.223	11.604	**<0.001**[†]	0.321	0.727	2.389	**0.042**	1.752	0.169	0.849	0.539
BoVSP (JA)	3.354	**0.043**	0.785	0.380	3.868	**0.015**[‡]	1.923	0.157	2.672	**0.026**	2.055	0.119	1.336	0.260
BoDEF (JA)	23.552	**<0.001**	1.726	0.195	1.920	0.139	0.026	0.975	5.501	**<0.001**	5.771	**0.002**	0.816	0.563
BoPAL (SA)	12.936	**<0.001**	0.050	0.825	1.446	0.241	0.938	0.398	0.989	0.443	0.821	0.489	0.521	0.789
BoPR1 (SA)	0.412	0.665	0.805	0.374	0.296	0.828	0.900	0.413	0.528	0.784	0.479	0.698	0.539	0.776
BoACS (ET)	5.490	**0.007**	1.735	0.194	0.491	0.690	2.142	0.129	0.225	0.967	0.914	0.441	0.629	0.706
BoMYR	0.907	0.411	0.894	0.349	2.648	0.059	2.546	0.089	0.713	0.641	1.534	0.218	0.469	0.828
BoPIN	26.174	**<0.001**	1.591	0.213	27.871	**<0.001**[§]	3.521	**0.037**	3.509	**0.006**	0.965	0.417	1.372	0.345

Values in bold indicate significant effects at $P < 0.05$.

*Post hoc classes based on Tukey (a = unparasitized) (ab = *C. glomerata*, *C. concinnata*) (b = *H. ebeninus*).

[†] Post hoc classes based on Tukey (a = unparasitized) (ab = *C. glomerata*) (b = *C. concinnata*) (c = *H. ebeninus*).

[‡] Post hoc classes based on Tukey (a = unparasitized, *C. glomerata*) (ab = *C. concinnata*) (b = *H. ebeninus*).

[§] Post hoc classes based on Tukey (a = unparasitized, *C. glomerata*) (b = *C. concinnata*, *H. ebeninus*).

Table S4. Amount of feeding damage on leaves of the different induction treatments that entered the oviposition experiments

Herbivore*	Parastism[†]	No. of leaves	Mean damage (mm^2)	SD
Pieris rapae (Pr)	Unparasitized (Up)	135	64.96	28.02
Pieris rapae (Pr)	*Cotesia glomerata* (Cg)	145	40.15	19.90
Pieris rapae (Pr)	*Hyposoter ebenius* (He)	125	23.38	9.78
Pieris brassicae (Pb)	Unparasitized (Up)	135	74.77	30.11
Pieris brassicae (Pb)	*Cotesia glomerata* (Cg)	123	49.42	24.22
Pieris brassicae (Pb)	*Hyposoter ebeninus* (He)	137	30.44	15.29

*Herbivore species significantly differed in the amount of damage inflicted to the plants (ANOVA, $F = 30.11$, $P < 0.001$).

[†] Parasitoid species significantly affected the amount of leaf damage (ANOVA, $F = 246.66$, $P < 0.001$). The interaction between the factors "herbivore" and "parasitism" was not significant (ANOVA, $F = 0.28$, $P = 0.76$).

Table S5. Pearson's correlations between relative leaf damage and relative number of eggs oviposited on treatment A for each of the two choice tests offered to diamondback moth to study oviposition preference

Treatment A*	Treatment B	Pearson's correlation	*n*	*P*
Up Pr	He Pr	−0.06	28	0.76
Up Pr	Cg Pr	−0.23	43	0.14
He Pr	Cg Pr	−0.08	30	0.69
Up Pb	He Pb	−0.09	34	0.59
Up Pb	Cg Pb	−0.22	31	0.23
He Pb	Cg Pb	−0.07	31	0.71
Up Pr	Up Pb	−0.16	30	0.93
He Pr	He Pb	0.28	31	0.13
Cg Pr	Cg Pb	−0.13	30	0.49

*Unparasitized (Up), *Hyposoter ebeninus*-parasitized (He), and *Cotesia glomerata*-parasitized (Cg) caterpillars of *Pieris rapae* (Pr) and *Pieris brassicae* (Pb).

Table S6. Cloning specific genes from different signal pathways in cabbage plants (*B. oleracea*) by using degenerate primers that were derived from sequences of other plant species

			GenBank accessions of different plant species whose sequences were used for designing degenerate primers						
GenBank accession no.	Gene	Function	*Arabidopsis*	*Brassica*	Rice	Tomato	Potato	Tobacco	Soybean
EU921648	*BoACS*	1-Aminocyclopropane-1-carboxylate synthase	U73786	X82273					
EF423802	*BoDEF*	Plant defensin	AY063779	U59459					
EF123055	*BoGAPDH*	Glyceraldehyde-3-phosphate dehydrogenase	M64116	X04301		U93208	U17005		
EF123056	*BoLOX*	Lipoxygenase	NM104376, L23968	AY16214, AY162143		U37839, U37840	X96405, X96406	AY254349	X13302
EF423803	*BoMYC*	JA-responsive transcription factor	NM_102998		AY536428	AF011557	AJ63050, AJ630506		
DQ456999	*BoMYR*	Myrosinase	AY113880	X60214					
EF423804	*BoPAL*	Phenylalanine ammonia-lyase	AY303128	AY795078					
EF423805	*BoPIN*	Cysteine proteinase inhibitor	AB04405	DQ539645		X94946	U45450		
EF423806	*BoPR1*	Pathogenesis-related protein-1	AY117187	U70666		X68738		X05959	AF136636
EU921650	*BoVSP*	Vegetative storage protein	AY092991, AY114606						

Table S7. Specific primers used for quantitative PCR

Gene	Forward (from 5′ to 3′)	Reverse (from 5′ to 3′)
BoLOX	ACTTTCCCGTCCCGTTCTTGG	GATTGTCGTGCCCGTGAATGC
BoMYC	GGCTGGACCTACGCTATATTCTGG	GCTCACGCAACACCTTCTTACG
BoVSP	GACTACCTCACTTCCCCACAG	CGGGTCTATCTTCTCTGTCC
BoDEF	GTTTGCTTCCATCATCACCCTTCTC	CACTTGACCTCTCGCACAACTTAG
BoPAL	TCGCTATGGCTTCTTACTGCTCTG	GAGGTCTTACGAGATGAGATGAGTCC
BoPR1	GTCAACGAGAAGGCTAACTATAACTACG	TTACACCTTGCTTTGCCACATCC
BoACS	ACTACGGTTGGCTGAAAGAC	GAGAAACGTTCAGCTTCACC
BoMYR	GTTTCTTAGACCGCCAGATCATACAAG	CAGTGCTTTACCTTTCCACCAAATTC
BoPIN	TTCAAGAACATAACAACAAAGAGAACAAGG	GAGTTAGGTAGTACATCATTCCAGCAAC
BoGAPDH	GCTACGCAGAAGACAGTTGATGG	TGGGCACACGGAAGGACATAC