

Supplementary material

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Figure S1 Amino acid alignment of a *Plutella xylostella* defensin-like protein with its homologues from other lepidopteran species. Amino acid sequences were aligned using the ClustalW multiple alignment program. All identical amino acid residues are shaded. Conserved amino acid residues are shaded. The defensin family motif and six highly conserved cysteine residues are highlighted in boxes. Pxyl, *Plutella xylostella*; Tni, *Trichoplusia ni* (ABV68852); Msex, *Manduca sexta* (ACX49766); Bmor, *Bombyx mori* (NP_001037370); Sfru, *Spodoptera frugiperda* (AAM96925); Aass, *Antheraea assama* (not available, from reference [15]); Bany, *Bicyclus anynana* (not available, sequence obtained from [15]); Dple, *Danaus plexippus* (EHJ63539).

Figure S2 Amino acid sequence alignment of a *Plutella xylostella* lysozyme-like protein with its homologues from other lepidopteran species. Amino acid sequences were aligned using the ClustalW multiple alignment program. Conserved amino acid residues are shaded. The alpha-lactalbumin/lysozyme C signature motif is highlighted in a box. The predicted catalytic nucleophiles are denoted with an asterisk. Pxyl, *Plutella xylostella*; Msex, *Manduca sexta* (ACX49765); Amyl, *Antheraea mylitta* (ABP52098); Bmor, *Bombyx mori* (NP_001093293); Tni, *Trichoplusia ni* (AAB41353).

Figure S3 Amino acid sequence alignment of a *Plutella xylostella* chitin synthase with its homologues from other lepidopteran species. Amino acid sequences were aligned using the ClustalW multiple alignment program. Conserved amino acid residues are shaded. The putative catalytic domain is marked with bidirectional arrows. The signature motifs are highlighted in boxes. Pxyl, *Plutella xylostella* (BAF47974); Cfum, *Choristoneura fumiferana* (ACD84882); Ofur, *Ostrinia furnacalis* (ABX46067); Msex, *Manduca sexta* (AAX20091); Sfru, *Spodoptera frugiperda* (AAS12599).

Figure S1

Pxyl_defensin	L L F V F V I A F V F V P S A L C Y P R D V A V Q R T E E V K A Q I I E T E A K P Q P T T V V E P Q Q E T V V E P P Q Q E	60
<i>Tri_defensin</i>	M E L K T V N L F L I A L S I C F V Q N A I A M P - - R D S A A I H D E S V V P I S E A L A A K E D - I T K L E K -	56
<i>Msex_defensin-like-1</i>	- M G S K V Y Y V L M A L S F Y V V Q - L C A F P - - R N S V A F E K Q H E S L P H - A D Y I V T Q K - I E S H E - -	52
<i>Bmor_defensin-like</i>	M A H Q R K S L V I F I F L T V - L V F - V F A L P - - R D A T - V F D N Q H S - - - - - E V A I E - K S T S K - -	45
<i>Sfru_defensin</i>	M G V K V I N V E L L I A V S A C L I H A V A G K P N P R D S S V V E E Q S L G P I H N E D L E V K - - - - V K P E T -	55
<i>Aass_defensin-like-1</i>	- D L K L V N L I V E I L F S I H F V N - I F A L P - - R D S T A V I K S A E S P - - - - - F E K K L E - I S S K T - -	48
<i>Bany_defensin-like-1</i>	M N Y K A I C - - I V F T L T V C I M R - T D A L P - - R D N S V T K S E A C L I N S - K E D A G K I R - - L A P K - -	50
<i>Dple_defensin-like-1</i>	M A R D S I Y T L L V F T V I C S I N F - T V A F P - - R D S S V I R T E P L T S N N - D D V A S K V K - E I S P Q T I	55
Pxyl_defensin	T V V E E S T E P L N I E H V H G R I P C Q Y E D A T E D T I C Q E H L P K G Y S Y G I C V S Y R C S C V	114
<i>Tri_defensin</i>	- - - S I I - E L T - - - - I P G R I S C K Y E E P T D D T I C Q E H C L P K G Y N Y G I C V S Y T C S C I	102
<i>Msex_defensin-like-1</i>	- - - K I I A E P K - - - - L P G R I W C Q Y E E V T E D A I C Q E H C I P K G Y S Y G L C I S N T C S C I	99
<i>Bmor_defensin-like</i>	- - - I D S S D V K - - - - I P G R I W C F E E A T E T A I C Q E H C L P K G Y S Y G I C V S N T C S C I	92
<i>Sfru_defensin</i>	- - - T I T P E P R - - - - I P G R V S C D F E E A N E D A V C Q E H C L P K G Y T Y G I C V S H T C S C I	102
<i>Aass_defensin-like-1</i>	- - - E L A S E I K - - - - I P G R T W C Q H E E A T E D V I C Q E H C L P K G Y S Y G I C V S N T C S C I	95
<i>Bany_defensin-like-1</i>	- - - E T G S Q F G - - - - I P G R V T C P Y E E A T E D S S C Q E H C L P K G Y S Y G I C V S G T C S C I	97
<i>Dple_defensin-like-1</i>	T V S D S V N E F K - - - - I P G R I S C P H E E A T E D P S C L E H C L P K G Y S Y G L C V S H I C S C I	105

Defensin family motif with six conservative cysteine residues

Figure S2

	The catalytic residue Glu	The catalytic residue Asp
<i>PxyI_LLP_1</i>	MRNGRVL [*] SLFVFSFCFLNFASSK [*] FDTRCRLVREFMPIGVFNDFLGGWVCLAKVSDRD [*] GALHVT [*] P-SCKKYYGLFQI [*] P-TP	83
<i>Msex_LLP_1</i>	MANGRVLIALVIFL [*] LNTNID [*] AKVYTRCQLTR [*] ELKNGFS-KTFMSNWCLIEQESLRNTSALVEKN-ARRKYYGLFQI [*] G-SE	80
<i>AmyI_LLP-1</i>	MAYGRVLLSIFVSLF-LNTEA--RIYTRCQLTR [*] ELLKNFS-RTFLSNWCLIEQESDRNTSALVVK [*] S-SRRKYYGLFQI [*] G-SE	79
<i>Bmor_LLP_1</i>	MVQSPHGLFLAVT [*] L VHSSEGHAKV [*] FTRCQLSRELLRYNFP-RALIP [*] TWCLIEHMSRTTEK [*] ITNHN-NSYSSYGLFQI [*] NNKD	83
<i>Tri_lysozyme</i>	--MQKLRVFLALAA [*] CISCEAK-YFA [*] NCELVHE [*] RRQGF [*] P-EDKMRD [*] WVCLIQNESGRNTSKMGTI [*] NKNSRDYGLFQI [*] NDKY	81
<i>PxyI_LLP_1</i>	WCKEGRVCGE-CNVACESL [*] DDDI [*] RDDV [*] KCAV [*] IEQREGFKFVTQ [*] TARC [*] KNDNFI [*] TNEI [*] YKCP [*] PLSI [*] SP-ESSPER	138
<i>Msex_LLP_1</i>	WCKEGRKGGK-CDIACEALL [*] DEDI [*] RDDGAC [*] QK [*] VQMEGFKY [*] WPK [*] W [*] SRCKG--QVLPD [*] VQ [*] CPDW [*] QNP [*] PSR [*] ASPPR	154
<i>AmyI_LLP-1</i>	WCKEGRKGGK-CDISCEALL [*] DEDL [*] KDDGNC [*] ALK [*] V [*] ELLEGFKY [*] WPK [*] W [*] ARCKG--QLLPDI [*] E [*] KCPDW [*] QNP [*] PSR [*] ASPPR	153
<i>Bmor_LLP_1</i>	WCKGRKGGN-CNMK [*] CE [*] DL [*] NE [*] DL [*] AD [*] VRCA [*] KRVYDRI [*] GFK [*] AW [*] SSYSYCKQ--KNLPDI [*] SRC	148
<i>Tri_lysozyme</i>	WCKS [*] KTS [*] TP [*] CK [*] DC [*] N [*] VT [*] CAEM [*] L [*] DD [*] IT [*] KASK [*] CA [*] KKI [*] YK [*] RHK [*] Q [*] AV [*] YGR [*] NHC [*] Q--TLLPDI [*] SKC	141

Alpha-lactalbumin / lysozyme C signature

Figure S3

- Pyl.chitin_synthase*
 - Pyl.chitin_synthase_1*
 - Chr.chitin_synthase_1*
 - Chr.chitin_synthase_2*
 - Str.chitin_3_synthase*
-
- Pyl.chitin_synthase*
 - Am.chitin_synthase_1*
 - Chr.chitin_synthase_1*
 - Chr.chitin_synthase_2*
 - Str.chitin_3_synthase*
-
- Pyl.chitin_synthase*
 - Pyl.chitin_synthase_1*
 - Chr.chitin_synthase_1*
 - Chr.chitin_synthase_2*
 - Str.chitin_3_synthase*
-
- Pyl.chitin_synthase*
 - Pyl.chitin_synthase_1*
 - Chr.chitin_synthase_1*
 - Chr.chitin_synthase_2*
 - Str.chitin_3_synthase*

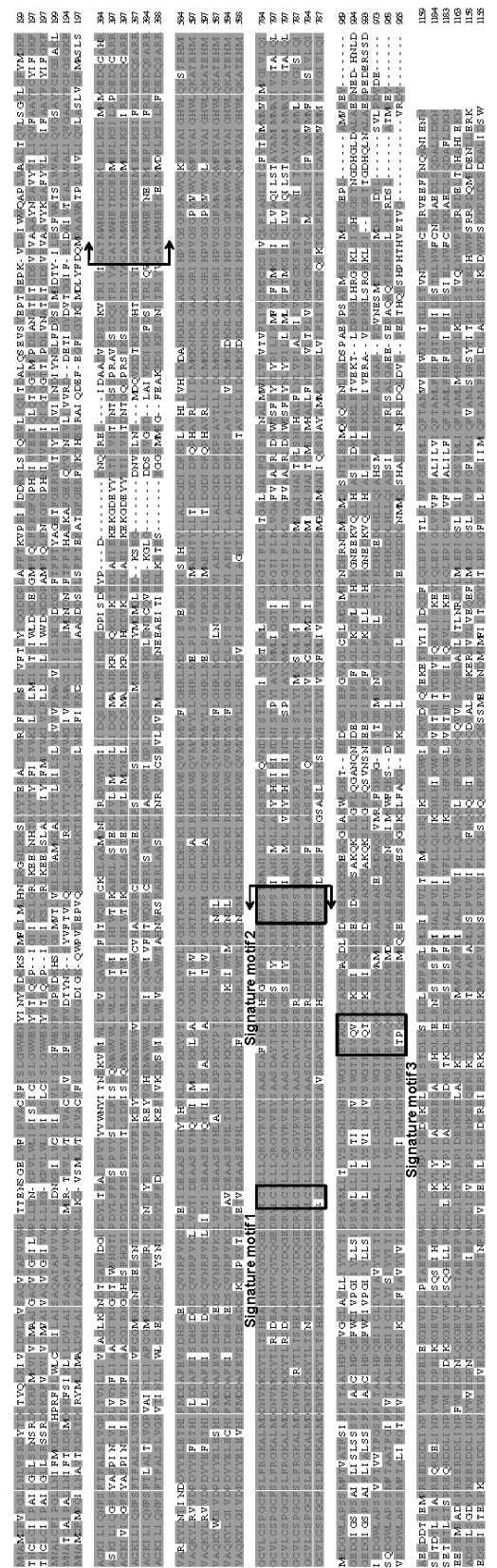


Table S8 Putative Chymotrypsin genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene17880_mk	969	NP_001040430.1	chymotrypsin-like serine protease	Bombyx mori	3.00E-64	304
Unigene35038_mk	505	NP_001040178.1	chymotrypsinogen	Bombyx mori	3.00E-50	159
Unigene25000_mk	320	EFN82637.1	chymotrypsin-1	Harpegnathos saltator	1.00E-08	107
Unigene26742_mk	364	CAM84318.1	chymotrypsinogen-like protein 3	Manduca sexta	1.00E-28	111
Unigene26453_mk	624	CAM84317.1	chymotrypsinogen-like protein 2	Manduca sexta	5.00E-30	167
Unigene36021_mk	248	CAA72959.1	chymotrypsin-like protease	Helicoverpa armigera	1.00E-25	82
Unigene35479_mk	390	CAA72958.1	chymotrypsin-like protease	Helicoverpa armigera	2.00E-13	76
Unigene9816_mk	1095	ADI32880.1	chymotrypsin	Helicoverpa armigera	9.00E-87	296
Unigene35969_mk	1133	ACU00133.1	chymotrypsin-like protein precursor	Spodoptera litura	1.00E-76	288
Unigene36_mk	768	ABR88239.1	chymotrypsin-like protease C9	Heliothis virescens	1.00E-84	258
Unigene5826_mk	898	ABR88231.1	chymotrypsin-like protease C1	Heliothis virescens	1.00E-87	261
Unigene34257_mk	940	AAX35812.1	midgut chymotrypsin	Spodoptera exigua	2.00E-43	231
Unigene35_mk	605	AAV33657.1	chymotrypsin-like	Helicoverpa punctigera	1.00E-34	153
Unigene26947_mk	350	AAV33656.1	chymotrypsinogen	Helicoverpa punctigera	8.00E-06	32
Unigene4900_mk	378	AAF71515.1	AiC2 chymotrypsinogen	Agrotis ipsilon	7.00E-07	32
Unigene5172_mk	365	AAD21824.1	chymotrypsin-like serine protease	Ctenocephalides felis	2.00E-18	83
Unigene649_mk	408	AAC36150.1	chymotrypsinogen-like protein	Plodia interpunctella	1.00E-39	135
Unigene14688_mk	150	AAA58743.1	chymotrypsinogen	Manduca sexta	4.00E-15	49

Table S9 Putative ABC transporter genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene37779_mk	862	XP_974441.2	ABC transporter	Tribolium castaneum	3.00E-71	241
Unigene8904_mk	556	XP_973526.1	ABC transporter	Tribolium castaneum	1.00E-55	185
Unigene55092_mk	346	XP_973458.1	ABC transporter	Tribolium castaneum	7.00E-48	116
Unigene1106_mk	990	XP_971735.1	ABC transporter	Tribolium castaneum	1.00E-107	331
Unigene28602_mk	406	XP_001951744.1	ABC transporter G family	Acyrtosiphon pisum	2.00E-08	39
Unigene2977_mk	491	XP_001945213.1	ABC transporter G family	Acyrtosiphon pisum	1.00E-52	163
Unigene47310_mk	169	XP_001862847.1	ABC transporter	Culex quinquefasciatus	7.00E-19	56
Unigene24195_mk	212	XP_001847679.1	ABC transporter	Culex quinquefasciatus	1.00E-10	59
Unigene39003_mk	213	XP_001845787.1	ABC transporter	Culex quinquefasciatus	3.00E-28	70
Unigene34723_mk	759	XP_001659406.1	ABC transporter	Aedes aegypti	6.00E-83	179
Unigene4017_mk	2389	XP_001653364.1	ABC transporter	Aedes aegypti	0	596
Unigene14639_mk	1127	XP_001653358.1	ABC transporter	Aedes aegypti	7.00E-35	180
Unigene13664_mk	339	XP_001650571.1	ABC transporter	Aedes aegypti	5.00E-32	117
Unigene27087_mk	528	XP_001607392.1	ABC transporter	Nasonia vitripennis	2.00E-47	177
Unigene38109_mk	226	XP_001605664.1	ABC transporter	Nasonia vitripennis	3.00E-28	75
Unigene28036_mk	271	XP_001605437.1	ABC transporter	Nasonia vitripennis	6.00E-17	89
Unigene1003_mk	433	XP_001605354.1	ABC transporter	Nasonia vitripennis	4.00E-61	144
Unigene39004_mk	243	XP_001604973.1	ABC transporter	Nasonia vitripennis	3.00E-30	79
Unigene33953_mk	176	XP_001602429.1	ABC transporter	Nasonia vitripennis	2.00E-07	53
Unigene18349_mk	571	EFN84917.1	ABC transporter G family	Harpegnathos saltator	6.00E-34	179
Unigene16134_mk	715	BAH03523.1	ABC transporter	Bombyx mori	1.00E-120	230
Unigene51050_mk	436	ADH16745.1	ABC transporter family C protein	Heliothis subflexa	3.00E-30	69
Unigene16611_mk	580	ADH16744.1	ABC transporter family C protein	Heliothis subflexa	1.00E-44	189
Unigene38785_mk	1329	ADH16743.1	ABC transporter family C protein	Heliothis subflexa	1.00E-139	388
Unigene9793_mk	3097	ADH16740.1	ABC transporter family C protein	Heliothis virescens	0	502
Unigene14636_mk	438	ABW74848.1	atet-like ABC transporter	Heliconius melpomene	6.00E-60	143
Unigene59262_mk	177	AAF63207.1	ABC transporter protein	Bombyx mori	2.00E-14	57

Table S10 Putative Glutamate receptor genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene37918_mk	414	XP_391854.1	glutamate receptor	<i>Apis mellifera</i>	3.00E-31	101
Unigene31125_mk	777	XP_001655460.1	glutamate receptor subunit ia	<i>Aedes aegypti</i>	4.00E-77	241
Unigene49552_mk	218	XP_001606376.1	glutamate receptor	<i>Nasonia vitripennis</i>	3.00E-28	70
Unigene27605_mk	824	NP_001080331.1	glutamate receptor	<i>Xenopus laevis</i>	7.00E-06	118
Unigene35747_mk	980	NP_001040129.2	glutamate receptor Gr1	<i>Bombyx mori</i>	2.00E-96	271
		EFN81954.1	glutamate receptor subunit			
Unigene22705_mk	175		epsilon-2	<i>Harpegnathos saltator</i>	2.00E-16	51
Unigene1787_mk	280	EFN63444.1	glutamate receptor	<i>Camponotus floridanus</i>	2.00E-16	92
Unigene8465_mk	339	ABD36126.1	glutamate receptor Gr3	<i>Bombyx mori</i>	8.00E-44	112

Table S11 Putative Ryanodine receptor genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene48810_mk	186	XP_001657320.1	ryanodine receptor 3	Aedes aegypti	7.00E-15	56
Unigene21732_mk	230	XP_001602231.1	ryanodine receptor domain	Nasonia vitripennis	4.00E-14	75
Unigene31176_mk	344	EFN78897.1	ryanodine receptor 44F	Harpegnathos saltator	6.00E-54	115
Unigene20326_mk	214	EFN67324.1	ryanodine receptor 44F	Camponotus floridanus	2.00E-32	71
Unigene47756_mk	281	BAA04212.1	ryanodine receptor homologue	Drosophila melanogaster	9.00E-43	93
Unigene45552_mk	248	ADO33053.1	ryanodine receptor	Biston betularia	1.00E-43	82
Unigene34415_mk	471	ABV44719.1	ryanodine receptor-like protein	Phlebotomus papatasi	5.00E-46	118
Unigene17283_mk	470	AAD01425.1	ryanodine receptor	Heliothis virescens	7.00E-75	134
Unigene22501_mk	359	AAD01424.1	ryanodine receptor	Heliothis virescens	6.00E-60	119

Table S12 Putative Trehalase receptor genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene18161_mk	1023	ABU95354.1	trehalase-2	Spodoptera exigua	1.00E-120	261
Unigene18756_mk	327	ABO20846.1	trehalase-1	Omphisa fuscidentalis	2.00E-29	89
Unigene1956_mk	399	ACY02267.1	trehalase 1a	Heliconius melpomene rosina	3.00E-52	132
Unigene22148_mk	185	ACF94698.1	trehalase	Spodoptera frugiperda	3.00E-22	61
Unigene23801_mk	385	ACY02228.1	trehalase 1b	Heliconius melpomene rosina	6.00E-46	115
Unigene37322_mk	178	CBH09243.1	trehalase-1B	Heliconius melpomene	6.00E-10	57
Unigene52836_mk	253	ACY02247.1	trehalase 1b	Heliconius melpomene amaryllis	4.00E-23	83
Unigene7874_mk	893	ABE27189.1	trehalase	Spodoptera frugiperda	5.00E-74	228

Table S13 Putative Serine protease inhibitor (Serpin) genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene27721_mk	511	XP_974450.1	serine protease inhibitor	Tribolium castaneum	1.00E-39	164
Unigene1119_mk	675	NP_001139706.1	serine protease inhibitor 14	Bombyx mori	9.00E-31	225
Unigene5053_mk	1533	NP_001139705.1	serine protease inhibitor 13	Bombyx mori	1.00E-113	400
Unigene10463_mk	788	NP_001139704.1	serine protease inhibitor 11	Bombyx mori	4.00E-71	222
Unigene6863_mk	1110	NP_001139703.1	serine protease inhibitor 10	Bombyx mori	1.00E-125	369
Unigene10121_mk	1146	NP_001139701.1	serine protease inhibitor 7	Bombyx mori	4.00E-81	335
Unigene42197_mk	358	NP_001103823.1	serine protease inhibitor 6	Bombyx mori	3.00E-36	91
Unigene15109_mk	989	NP_001037205.1	serine protease inhibitor 5	Bombyx mori	1.00E-97	276
Unigene34550_mk	1036	NP_001037090.1	serine protease inhibitor 4	Bombyx mori	1.00E-102	285
Unigene10582_mk	907	NP_001037021.1	serine protease inhibitor 2	Bombyx mori	1.00E-58	260
Unigene11307_mk	658	NP_001036857.1	serine protease inhibitor 12	Bombyx mori	9.00E-49	219
Unigene33980_mk	158	CAB63098.1	serpin-3	Drosophila melanogaster	2.00E-08	45
Unigene35662_mk	425	BAF48335.1	serpin 1c	Plutella xylostella	2.00E-46	97
Unigene34903_mk	1017	BAF48334.1	serpin 1b	Plutella xylostella	1.00E-162	295
Unigene16002_mk	554	BAF36821.1	pxSerpin 3	Plutella xylostella	2.00E-63	124
Unigene2668_mk	923	BAF36820.1	pxSerpin 2	Plutella xylostella	1.00E-154	297
Unigene35476_mk	278	BAD52261.1	serpin 1a	Plutella xylostella	2.00E-19	48
Unigene42610_mk	181	ACZ81437.1	serpin-4	Bombyx mori	5.00E-16	59
Unigene25013_mk	231	AAV91429.1	serpin 2	Lonomia obliqua	7.00E-15	77
Unigene8716_mk	691	AAV91026.1	serpin-6	Manduca sexta	2.00E-90	230
Unigene2425_mk	597	AAS68504.1	serpin-4B	Manduca sexta	3.00E-09	77

Table S14 Putative Peptidoglycan recognition protein genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene32038_mk	612	XP_001848057.1	peptidoglycan recognition protein-lc	Culex quinquefasciatus	1.00E-18	137
Unigene19483_mk	1166	XP_001603488.1	peptidoglycan recognition protein-SC2	Nasonia vitripennis	3.00E-26	170
Unigene10601_mk	631	BAF74637.1	peptidoglycan recognition protein-D	Samia cynthia ricini	1.00E-21	84
Unigene59547_mk	237	BAF36823.1	pxPeptidoglycan recognition protein	Plutella xylostella	4.00E-33	69
Unigene6491_mk	288	BAF03520.1	peptidoglycan recognition protein B	Samia cynthia ricini	2.00E-27	91
Unigene10558_mk	318	ACB32179.1	peptidoglycan recognition protein	Plutella xylostella	2.00E-52	100

Table S15 Putative Lysozyme genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene36037_mk	358	XP_643144.1	lysozyme 3	Dictyostelium discoideum AX4	5.00E-14	119
Unigene12726_mk	624	XP_309527.3	lysozyme i-1	Anopheles gambiae str. PEST	9.00E-43	144
Unigene22894_mk	157	XP_001850854.1	lysozyme i-1	Culex quinquefasciatus	3.00E-11	49
Unigene34777_mk	656	ACR82289.1	lysozyme	Papilio xuthus	3.00E-49	137
Unigene58181_mk	542	ABP52098.1	lysozyme-like protein 1	Antheraea mylitta	3.00E-39	159

Table S16 Putative Chitin synthase genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene23722_mk	378	BAF47974.1	chitin synthase 1	Plutella xylostella	4.00E-69	125
Unigene60458_mk	221	ACD84882.1	chitin synthase I	Choristoneura fumiferana	4.00E-38	73
Unigene4562_mk	3480	ABX46067.1	chitin synthase	Ostrinia furnacalis	0	1165
Unigene12371_mk	609	AAX20091.1	chitin synthase 2	Manduca sexta	1.00E-34	187

Table S17 Putative Chitin deacetylase genes in *Plutella xylostella* larval midgut transcriptome.

Sequence name	Sequence length (bp)	Hit accession number	Hit sequence description	Species	E-value	Alignment length
Unigene10923_mk	894	ADB43610.1	chitin deacetylase 1	Helicoverpa armigera	1.00E-128	217
Unigene53741_mk	245	NP_001107799.1	chitin deacetylase 5B	Tribolium castaneum	1.00E-44	80
Unigene1326_mk	1161	NP_001103903.1	chitin deacetylase 4	Tribolium castaneum	0	383
Unigene21083_mk	561	NP_001103796.1	chitin deacetylase 2	Bombyx mori	1.00E-109	186
Unigene21269_mk	366	NP_001103795.1	chitin deacetylase 1	Bombyx mori	4.00E-37	102
Unigene2459_mk	187	ADB43612.1	chitin deacetylase 5b	Helicoverpa armigera	2.00E-16	62
Unigene34327_mk	515	ADB43611.1	chitin deacetylase 5a	Helicoverpa armigera	1.00E-24	101
Unigene59063_mk	695	ADB43610.1	chitin deacetylase 1	Helicoverpa armigera	1.00E-134	231
Unigene35229_mk	774	ACD37362.1	chitin deacetylase 1	Mamestra configurata	1.00E-101	258