

## Supplementary Tables and Figures

**Table S1.** Primers used in RT-PCR, RACE or qRT-PCR.

<b>Primer name</b>	<b>Primers nucleotide sequence (5' to 3')</b>
<i>Actin</i> -F	CATCTACGAGGGTTACGC
<i>Actin</i> -R	CATCTGTTGGAAGGTGGA
<i>PmHsc70</i> 3'F1	TAACACGACCATCCCCACCAAGCA
<i>PmHsc70</i> 3'F2	CCCAGACTTTTACGACCTATTCCGACA
<i>PmHsc70</i> 5'R1	CGGGTTGGTTGTTCGGAATAGGTCG
<i>PmHsc70</i> 5'R2	GCCTCGTCAGGGTTGATGGACTTGTT
<i>PmHsc70</i> 5'R3	ACCTCCCAAGTGAGTGTCTCCAGCAGT
<i>PmHsp70a</i> 3'F1	GCTGAGGCGTATTTGGGTAGTTCGGTC
<i>PmHsp70a</i> 3'F2	TCTACACCAGGGTTTCTCGGGCACG
<i>PmHsp70a</i> 5'R1	AGCGTCTATTTCAATGGTGGCTTCCGT
<i>PmHsp70a</i> 5'R2	CAGCGTCTCTGACCGAACTACCCAAAT
<i>PmHsp70b</i> 3'F1	CGCCGCTGTCACTTGGCATAGAACTG
<i>PmHsp70b</i> 3'F2	GAATGCTGGCAGAGGCTGAACGATACA
<i>PmHsp70b</i> 5'R1	ATTCCAGCAATAACCCCAGCATCCTT
<i>PmHsp70b</i> 5'R2	TGAAATAGGCGGGCACTGTGACGAC
<i>PmHsp70b</i> 5'R3	GATGGTGTGTTGTTTCGGTTGCCCTGGT
<i>PmHsc70</i> ORF F	GTGATAGAAACAACTATACGC
<i>PmHsc70</i> ORF R	TAATTGAGAGGATTACATCGAG
<i>PmHsp70a</i> ORF F	AGCGAATACTAAACAAGTGG
<i>PmHsp70a</i> ORF R	AGTACATGATCATGGATTGC
<i>PmHsp70b</i> ORF F	CAGTGATATTGTTTATCAGAAG
<i>PmHsp70b</i> ORF R	CATATGTTTTTAACACTGCAGTC
<i>PmActin</i> F	CAGGGAAAAGATGACCCAGA
<i>PmActin</i> R	GCAGAGCGTAACCCTCGTAG
<i>Pm18S</i> F	AATGCCGCTTGAATATTTTCG
<i>Pm18S</i> R	TTTCGCTGATGTTCGTCTTG
<i>PmHsp70a</i> F	TCCGCGAGGAGTACCTAAGA
<i>PmHsp70a</i> R	GGCTTCAGCCAACATACGAT
<i>PmHsp70b</i> F	CGCTGTCACTTGGCATAGAA
<i>PmHsp70b</i> R	TACAGCAGGCTGGTTGTCAG
<i>PmHsc70</i> F	TGCTGGAGACACTCACTTGG
<i>PmHsc70</i> R	TTCAATGCTAGCCTGTGTCTG

Table S2. ANOVA results for the differential relative mRNA levels of *PmHsc70*, *PmHsp70a*, and *PmHsp70b* in response to 0°C cryogenic chilling for different duration in non-diapause (ND), summer diapause (SD), and winter diapause (WD) pupae of *P. melete*.

Gene	Source	df	MS	F	Sig.
<i>PmHsc70</i>	Type of Diapause/nondiapause	2	89.221	61.06	0.0000
	Duration of chilling	3	2.463	1.69	0.1967
	Type of diapause * Duration	6	3.364	2.30	0.0675
<i>PmHsp70a</i>	Type of Diapause/nondiapause	2	1.179	173.31	0.0000
	Duration of chilling	3	1.940	285.09	0.0000
	Type of diapause * Duration	6	0.581	85.320	0.0000
<i>PmHsp70b</i>	Type of Diapause/nondiapause	2	0.554	51.72	0.0000
	Duration of chilling	3	1.208	112.74	0.0000
	Type of diapause * Duration	6	0.219	20.42	0.0000

Table S3. ANOVA results for the differential relative mRNA levels of *PmHsc70*, *PmHsp70a*, and *PmHsp70b* in response to different heat stress temperatures in non-diapause (ND), summer diapause (SD), and winter diapause (WD) pupae of *P. melete*.

Gene	Source	df	MS	F	Sig.
<i>PmHsc70</i>	Type of Diapause/nondiapause	2	115701.732	427.04	0.0000
	Temperature	4	27773.736	102.51	0.0000
	Type of diapause * Temperature	8	24349.575	89.87	0.0000
<i>PmHsp70a</i>	Type of Diapause/nondiapause	2	465025.497	147.22	0.0000
	Temperature	4	91058.6437	28.83	0.0000
	Type of diapause * Temperature	8	110894.094	35.11	0.0000
<i>PmHsp70b</i>	Type of Diapause/nondiapause	2	71344.563	100.69	0.0000
	Temperature	4	25683.945	36.25	0.0000
	Type of diapause * Temperature	8	24889.397	35.13	0.0000

Table S4. ANOVA results for the differential relative mRNA levels of *PmHsc70*, *PmHsp70a*, and *PmHsp70b* in response to 39°C heat stress at different time procedures in non-diapause (ND), summer diapause (SD), and winter diapause (WD) pupae of *P. melete*.

Gene	Source	df	MS	F	Sig.
<i>PmHsc70</i>	Type of Diapause/nondiapause	2	11621.189	145.18	0.0000
	Hours at 39 °C	4	30762.762	384.32	0.0000
	Type of diapause * Hours at 39 °C	8	11545.736	144.24	0.0000
<i>PmHsp70a</i>	Type of Diapause/nondiapause	2	109542.901	41.39	0.0000
	Hours at 39 °C	4	110593.749	41.79	0.0000
	Type of diapause * Hours at 39 °C	8	118227.429	44.67	0.0000
<i>PmHsp70b</i>	Type of Diapause/nondiapause	2	31874.158	46.78	0.0000
	Hours at 39 °C	4	28642.747	42.04	0.0000
	Type of diapause * Hours at 39 °C	8	29046.4764	42.63	0.0000

1 TGATAATTCTTTTGAAGTGATAGAAAACAACTATACGCAATGACTACTAAAAACCAGCGGTAGGTATTGACTTGGGTACCACATACTCG

1 M T T K T P A V G I D L G T T Y S

91 TCGGTGGCGGTGTTCAGTACGGTAAGGTGGAGATCATCGCCAACGATCAGGGCAACAGGACTACACCTTCATATGTTGCCCTTCACAGAC

31 C V G V F Q Y G K V E I I A N D Q G N R T T P S Y V A F T D

181 ACCGAACGTCTCATCGGAGATGCCGCCAAGAACCAGGTGGCCCTGAACCCAAACACCATCTTTGATGCCAAACGTCTCATCGGGCGT

61 T E R L I G D A A K N Q V A L N P N N T I F D A K R L I G R

271 AAGTTCGAAGATGCCACAGTTCAGGCTGACATGAAACACTGGCCTTTTGAGGTAAATCAGTGATGGTGGAAAACCAAGATCAAGGTTGCA

91 K F E D A T V Q A D M K H W P F E V I S D G G K P K I K V A

361 TACAAGGGTGAAGACAAAACATTCTTCCAGAGGAAGTCAGTTCAATGGTATTAAACAAAATGAAAGAAACAGCTGAAGTTTACCTTGGC

121 Y K G E D K T F F P E E V S S M V L T K M K E T A E V Y L G

451 AAAACGGTGCAGATGCAGTAATTACAGTCCAGCATACTTTAATGACTCCCAAGACAGGCCACAAAAGATTCTGGTACAATCTCTGGT

151 K T V Q N A V I T V P A Y F N D S Q R Q A T K D S G T I S G

541 CTGAACGTTCTCCGAATCATCAATGAACCACTGCTGCTGCGATTGCATATGGTCTTGACAAGAAAGAGGTGGAGAACGTAACGCTCT

181 L N V L R I I N E P T A A A I A Y G L D K K G G G E R N V L

631 ATTTTCGATCTTGGCGGTGGTACTTTTGATGTATCCATCCTGACCATCGAGGATGATCTTTGAAGTGAAGTCCACTGCTGGAGACACT

211 I F D L G G G T F D V S I L T I E D G I F E V K S T A G D T

721 CACTTGGGAGGTGAGGACTTTGACAACCGCATGGTCAACCACTTTGTACAGGAGTTCAAGCGGAAGTACAAAAGGACATTTCTCCAC

241 H L G G E D F D N R M V N H F V Q E F K R K Y K K D I S S H

811 AAGAGGGCCCTGCGTAGGTGAGGACAGCTTGTGAGCGCCGAAGAGGACTCTTTCCTCGTCGACACAGGCTAGCATTTGAATCGACTCT

271 K R A L R R L R T A C E R A K R T L S S S T Q A S I E I D S

901 CTGTTTGAGGGTATCGATTACTACACATCCATCACCAGGGCGCGTTTCGAAGAACTGAACGCCGACTTATTAGATCTACCATGGAGCCT

301 L F E G I D Y Y T S I T R A R F E E L N A D L F R S T M E P

391 GTAGAGAAGTCCCTCCGTGACGCCAAGATGGACAAGCGCAAGTGCACGACATTGTCTCGTCGGAGGTTCACATCGTATCCCAAGAGTG

331 V E K S L R D A K M D K A Q V H D I V L V G G S T R I P R V

1081 CAGAAGCTCCTTCAAGACTTCTTCAATGGCAAGGAGTTGAACAAGTCCATCAACCCTGACGAGGCCGTAGCCTACGAGCGCGCTTCAG

361 Q K L L Q D F F N G K E L N K S I N P D E A V A Y G A A V Q

1171 GCCCGCATCTTGACGGTGATAAGTCTGAAGAAGTACAGGATCTGCTCTGTGGATGTGACCCCGCTGTCCCTCGGTATCGAGATGCA

391 A A I L H G D K S E E V Q D L L L L D V T P L S L G I E T A

1261 GCGGTGTCTATGACCACCTTGATTAAGCGTAACACGACCATCCCAAGCAACCCAGACTTTACGACCTATTCCGACAACCAACCC

421 G G V M T T L I K R N T T I P T K Q T Q T F T T Y S D N Q P

1351 GGTGTGCTTATTCAAGTATTGAGGGTGAGCGTGCCATGACCCGAGACAACAACCTTCTCGGTAATTTGAGCTCACTGGTATTCCTCCCA

451 G V L I Q V F E G E R A M T R D N N L L G K F E L T G I P P

1441 GCGCCCCGTGGTGTCCCAAAATCGAAGTTACTTTTCGACATTGACGCCAACGGTATCCTTAACGTATCGGCTGTGCAAAAATCTACCAAC

481 A P R G V P Q I E V T F D I D A N G I L N V S A V E K S T N

1531 AAGGAGAACAGATCAGGATCACCATGACAAGGGTCTGCTGTCCAAGAAGAGATCGAGCGTATGGTCAACGACGCTGAGAAATACAGG

511 K E N K I T I T N D K G R L S K E E I E R M V N D A E K Y R

1621 AACGAAGATGAGAAACAGAAGGAACCATTCAGGCTAAGAACCGCTCGAATCTTACTGCTTCAACATGAAGTCTACCATGGAGGATGAG

541 N E D E K Q K E T I Q A K N A L E S Y C F N M K S T M E D E

1711 AAGCTTAAGGACAAAATCACAGACTCCGACAAGCAAAATCATTTTGGACAAATGCAACGACACCATCAAAATGGTTGGACGCTAACCACTG

571 K L K D K I T D S D K Q I I L D K C N D T I K W L D A N Q L

1801 GCTGACAAGGAAGAATATGAGCACAAAGCAAGGAACGGAGGGTGTGTGCAACCCGATTATAACCAAGCTTTACCAGGGTGACGGTGA

601 A D K E E Y E H K Q K E L E G V C N P I I T K L Y Q G A G G

1891 GCCCCGAGGCGATGCCCGGTGGTATGCCAGGCTTCCCTGGCGGAGCGCTGGAGCCGGTGGAGCAGCCCTGGTGGCGGATCCCGACCC

631 A P G G M P G G M P G F P G G A P G A G A A P G G G S G P

1981 ACCATCGAAGAGGTTGATTAACTATTGAAATATACATTCCACTTTTCACATTGTAAGATCTTCTGATGTAATCTCTCAATTAATAA

661 T I E E V D

2071 ATGAATGCAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**Figure S1.** Nucleotide and deduced amino acid sequences of *PmHsc70*.



1 AGACTAATTCGAAATACGAGAGAGTGAACAAGTGATATTCAGTGAGAATCGAGGCATATTATACTATCTTGCGAATATTTCTGTGAAG  
 91 TTTGTTGAAGATTATATATTCAGTGATATTGTTTATCAGAAGACACAATGCCAGCTATTGGAATTGATCTTGGTACAACCTACTCTTGC  
 1 M P A I G I D L G T T Y S C  
 181 GTTGGTGTTTGGCAACATGGAATGTGGAGATCATCGCAAATGACCAGGGCAACCGAACACACCATCGTACGTTCGATTACGGACACG  
 31 V G V W Q H G N V E I I A N D Q G N R T T P S Y V A F T D T  
 271 GAGCGTCTGATCGGCGATGCTGCTAAGAACCAAGTAGCTTTAAACCCCTAGCAACACAGTGTTCGATGCGAAAAGGCTGATCGGCCGTAAA  
 61 E R L I G D A A K N Q V A L N P S N T V F D A K R L I G R K  
 361 TTCGACGATCCCAAAATTCACAGGACATGAAACATTGGCCTTTTAAAGTTATCAATGACTGCGGTAAGCCTAAGATCCAGGTTGAATTC  
 91 F D D P K I Q Q D M K H W P F K V I N D C G K P K I Q V E F  
 451 AAAGGCGAAACAAACGATTGCCCCAGAAGAAGTCAGCAGCATGGTTTGGTGAAAATGAAGGAGACAGCTGAGGCCTACCTTGGATCA  
 121 K G E T T K R F A P E E V S S M V L V K M K E T A E A Y L G S  
 541 TCAGTCGAGATGCGCTCGTCAGTGCCTGCTTTCATGATTTCACAGCGTCAGGCGACCAAGGATGCTGGGGTTATTGCTGGAATA  
 151 S V R D A V V T V P A Y F N D S Q R Q A T K D A G V I A G I  
 631 AATGTTTTACGTATCATAAACGAGCCACTGCCGTCTCTGGCATATGGCTAGACAAAAATCTAAAGGGCGAACGCAATGTCCTTAT  
 181 N V L R I I N E P T A A A L A Y G L D K N L K G E R N V L I  
 721 TTCGATCTTGGTGGCGGCACATTGACGTTTCCATTTTGACGATCGACGAGGGTTTCGCTTTTGAAGTGAAGGCCACGGCCGGAGACACA  
 211 F D L G G G T F D V S I L T I D E G S L F E V K A T A G D T  
 811 CACCTTGAGGTGAAGCTTTGACAACAGGCTCGTTAACCTAGCGGAGGAGTTCCAACGAAAATACAAGAAAGATTGGCCACGAAAC  
 241 H L G G E D F D N R L V N H L A E E F Q R K Y K K D L R T N  
 901 CCACGCGCATGGCGACCTCCGACCGCCGAGAGCGGCCAAGCGCACTTTATCATCTAGCACCGAGGCCACGGTTGAAATCGACGCG  
 271 P R A L R R L R T A A E R A K R T L S S S T E A T V E I D A  
 991 CTATACGAGGTATTGATTCTACACTCGCGTATCTCGGGCTCGGTTCAAGAATTAAACGCTGATCTATTCCGGGGCACCCCTCGAACCA  
 301 L Y E G I D F Y T R V S R A R F E E L N A D L F R G T L E P  
 1081 GTGGAAGAACGATGAAGATGCTAAGATGGATAAGAGCCAAATACATGACGTGGTTCTCGTCGGAGGGTCCACTCGTATTCCCTAAGGTA  
 331 V E K A L K D A K M D K S Q I H D V V L V G G S T R I P K V  
 1171 CAATCCCTGCTCAAAAACCTTCTCTGTGGTAAGAACTTAACTTTCCATCAACCCCGACGAGGCTGTAGCATATGGAGCGGGCGTCCAG  
 361 Q S L L Q N F F C G K K L N L S I N P D E A V A Y G A A V Q  
 1261 GCAGTATTTTGAAGCGGAACTCACTCTAAGATCCAGGATGTGTTATTGGTAGATGTAGCGCGCTGTCACTTGGCATAGAAATGCT  
 391 A A I L S G E T H S K I Q D V L L V D V A P L S L G I E T A  
 1351 GGAGGAGTCATGACCAAGATAATTGAACGTAACGTGCAAAATCCCGTGAAGCAATCGCAGACATTACCACTATTCTGACAACCGCCT  
 421 G G V M T K I I E R N C K I P C K Q S Q T F T T Y S D N Q P  
 1441 GCTGTAACTATCCAAGTGTATGAAGGTGAACGAGCAATGACAAAAGATAACAATCTCCTTGGTACTTTCGATCTGACAGGCATACCCT  
 451 A V T I Q V Y E G E R A M T K D N N L L G T F D L T G I P P  
 1531 GCACCGCGGGCGTGCCATAAATCGACGTCACATTCGACATGGACGCCAACGGTATTCTTAATGTCTCGGCAAGGAAAAACAGTACTGGT  
 481 A P R G V P K I D V T F D M D A N G I L N V S A K E N S T G  
 1621 CGTAGTAAAAATATCGTGATAAAGATGATAAGGACGTTTGTACAGGCTGAGATTGACAGAATGCTGGCAGAGGCTGAACGATACAAG  
 511 R S K N I V I K N D K G R L S Q A E I D R M L A E A E R Y K  
 1711 GAAGAGGATGATAAGCAGAGGGAGAGGGTGGCCGCTCGTAACCAACTGGAGACATATGTCTTCAGCGTGGACAGGCGCTAGATGATGCC  
 541 E E D D K Q R E R V A A R N Q L E T Y V F S V R Q A L D D A  
 1801 GGAGCGAAGTTACCAGACCAAGACAAAGATTCTGCACGATCACAATGCGACGAAGCGATAAAGTGGTTAGAGAACAACTTTGGCCGAG  
 571 G A K L P D Q D K D S A R S Q C D E A I K W L E N N T L A E  
 1891 AAGGAGGAATACGAGCATAAGTTGAAGGAGCTCCAGAGAGTTTGTCTACCCATTATGAGTAAGCTGCATGGTGTGGTGGTGGCCGCCCT  
 601 K E E Y E H K L K E L Q R V C S P I M S K L H G A G G A A P  
 1981 GGAGGCCAATCAATGGACCCACCGTAGAGGAAGTGGATTAAACCTAGTATTAAGAATAATAGTTATAATTATTTTAAAGACTGATTA  
 631 G G Q S N G P T V E E V D  
 2071 ATTTATTTGACTGCAGTGTTAAACATATGTTTAATAAACATTATTTAATTTAAAAA

**Figure S3.** Nucleotide and deduced amino acid sequences of *PmHsp70b*.

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PmHSC70      : MTTKT PAVGIDLGTYSYCVGVFQY GKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALN
XP_022130638.1 : MTTKT PAVGIDLGTYSYCVGVFQY GKVDIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALN
XP_041970467.1 : -MAKA PAVGIDLGTYSYCVGVFQH GKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMN
XP_026489199.1 : -MAKA PAVGIDLGTYSYCVGVFQH GKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMN
XP_028170304.1 : MATKA PAVGIDLGTYSYCVGVFQH GKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMN
               K PAVGIDLGTYSYCVGVFQ GKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVA6N

PmHSC70      : TAEVYLGKTVQNAVITVPAYFNDSQRQATKDS GTISGLNVLRIINEPTAAAIAYGLDKKGGGE
XP_022130638.1 : TAEVYLGKTVQNAVITVPAYFNDSQRQATKDS GTISGLNVLRIINEPTAAAIAYGLDKKGGGE
XP_041970467.1 : TAEVYLGKTVQNAVITVPAYFNDSQRQATKDS GTISGLNVLRIINEPTAAAIAYGLDKKGGGE
XP_026489199.1 : TAEVYLGKTVQNAVITVPAYFNDSQRQATKDA GTISGLNVLRIINEPTAAAIAYGLDKKGGTGE
XP_028170304.1 : TAEVYLGKTVQNAVITVPAYFNDSQRQATKDA GTISGLNVLRIINEPTAAAIAYGLDKKGGGE
               TAE YLGKTVQNAVITVPAYFNDSQRQATKD GTISGLN6LRIINEPTAAAIAYGLDKKGGGE

PmHSC70      : LRRRLTACERAKRTLSSSTQASIEIDSLFEGIDYYTSITRARFEELNADLFRSTMEPVEKSLR
XP_022130638.1 : LRRRLTACERAKRTLSSSTQASIEIDSLFEGIDYYTSITRARFEELNADLFRSTMEPVEKSLR
XP_041970467.1 : LRRRLTACERAKRTLSSSTQASIEIDSLFEGIDFYTSITRARFEELNADLFRSTMEPVEKSLR
XP_026489199.1 : LRRRLTACERAKRTLSSSTQASIEIDSLFEGIDFYTSITRARFEELNADLFRSTMEPVEKSLR
XP_028170304.1 : LRRRLTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRSTMEPVEKSLR
               LRRRLTACERAKRTLSSSTQASIEIDSL5EGID5YTSITRARFEELNADLFRSTMEPVEKSLR

PmHSC70      : DLLLLDVTPSLSLGIETAGGVMTTLIKRNTTIPKQTQTFTTYSNQPVGVLIOVFEGERAMTRD
XP_022130638.1 : DLLLLDVTPSLSLGIETAGGVMTTLIKRNTTIPKQTQTFTTYSNQPVGVLIOVFEGERAMTRD
XP_041970467.1 : DLLLLDVTPSLSLGIETAGGVMTTLIKRNTTIPKQTQTFTTYSNQPVGVLIOVFEGERAMTKD
XP_026489199.1 : DLLLLDVTPSLSLGIETAGGVMTTLIKRNTTIPKQTQTFTTYSNQPVGVLIOVFEGERAMTKD
XP_028170304.1 : DLLLLDVTPSLSLGIETAGGVMTTLIKRNTTIPKQTQTFTTYSNQPVGVLIOVFEGERAMTKD
               DLLLLDVTPSLSLGIETAGGVMTTLIKRNTTIPKQTQTFTTYSNQPVGVLIOVFEGERAMT4D

PmHSC70      : NDAEKYRNEDKQKETIQAKNALESYCFNMKSTMEDEKLKDKITDSDKQIILDKCNDTIKWLE
XP_022130638.1 : NDAEKYRNEDKQKETIQAKNALESYCFNMKSTMEDEKLKDKITDSDKQIILDKCNDTIKWLE
XP_041970467.1 : NEAEKYRNEDKQKETIQAKNLESYCFNMKSTMEDEKLKDKITDSDKQIILDKCNDTIKWLE
XP_026489199.1 : NEAEKYRNEDKQKETIQAKNALESYCFNMKSTMEDEKLKDKITDSDKQIILDKCNDTIKWLE
XP_028170304.1 : NEAEKYRNEDKQKETIQAKNALESYCFNMKSTMEDEANLKDKITADKQIILDKCNDTIKWLE
               N AEKYRNEDKQKETIQAKNALESYCFNMKSTMEDEKLKDKIT3DSDKQ IILDKCNDTIKWLE

PmHSC70      : EVDD
XP_022130638.1 : EVD-
XP_041970467.1 : EVD-
XP_026489199.1 : EVD-
XP_028170304.1 : EVD-
               EVD

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**Figure S4.** Sequence alignment of PmHSC70 with HSP70 proteins of *Pieris rapae* (XP\_022130638.1), *Aricia agestis* (XP\_041970467.1), *Vanessa tameamea* (XP\_026489199.1) and *Ostrinia furnacalis* (XP\_028170304.1).

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PmHSP70a      : MPAIGIDLGTITYSCVGWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNQVALNPNT
QWV59544.1    : MPAIGIDLGTITYSCVGWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNQVALNPNT
XP_038210277.1 : MPAVGIDLGTITYSCVGWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNQVALNPNT
KAG8115787.1  : MPAIGIDLGTITYSCVGWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNQVALNPNT
XP_045456590.1 : MPAIGIDLGTITYSCVGWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNQVALNPNT
                MPA6GIDLGTITYSCVGWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNQVALNPNT

PmHSP70a      : YLGSSVRDAVITVPAYFNDSQRQATKDAGAIAGINVLRIINEPTAAALAYGLDKSLKGERNVL
QWV59544.1    : YLGSSVRDAVITVPAYFNDSQRQATKDAGAIAGINVLRIINEPTAAALAYGLDKSLKGERNVL
XP_038210277.1 : YLGSAVKDAVITVPAYFNDSQRQATKDAGAIAGINVLRIINEPTAAALAYGLDKDLKGERNVL
KAG8115787.1  : YLGTSVRDAVITVPAYFNDSQRQATKDAGAIAGINVLRIINEPTAAALAYGLDKNLKGERNVL
XP_045456590.1 : YLGTSVRDAVITVPAYFNDSQRQATKDAGAIAGINVLRIINEPTAAALAYGLDKNLKGERNVL
                YLG3sV4DAVITVPAYFNDSQRQATKDAGAIAG6NVLRIINEPTAAALAYGLDK LKGERNVL

PmHSP70a      : LRTAERAKRTLSSSTEATIEIDALYEGMDFYTRVSRARFEELNSDLFRGTLEPVEKALKDAK
QWV59544.1    : LRTAERAKRTLSSSTEATIEIDALYEGIDYTRVSRARFEELNSDLFRGTLEPVEKALKDAK
XP_038210277.1 : LRTAERAKRTLSSSTEATIEIDALYEGIDFYTRVSRARFEELNADLFRGTLEPVEKALKDAK
KAG8115787.1  : LRTAERAKRTLSSSTEATIEIDALYEGIDFYTRVSRARFEELNADLFRGTLEPVEKALKDAK
XP_045456590.1 : LRTAERAKRTLSSSTEATIEIDALYEGIDFYTRVSRARFEELNSDLFRGTLEPVEKALKDAK
                LRTAERAKRTLSSSTEATIEIDALYEG6D5YTRVSRARFEELN DLFRGTLEPVEKALKDAK

PmHSP70a      : LVDVAPLSLGIETAGGVMTKIIERNAKIPCRQSQTFTTYSNQPAVTIQVYEGERAMTKDNNL
QWV59544.1    : LVDVAPLSLGIETAGGVMTKIIERNAKIPCRQSQTFTTYSNQPAVTIQVYEGERAMTKDNNL
XP_038210277.1 : LVDVAPLSLGIETAGGVMTKIIERNAKIPCKQSQTFTTYSNQPAVTIQVYEGERAMTKDNNL
KAG8115787.1  : LVDVAPLSLGIETAGGVMTKIIERNAKIPCRQSQTFTTYSNQPAVTIQVYEGERAMTKDNNL
XP_045456590.1 : LVDVAPLSLGIETAGGVMTKIIERNCKIPCKQSQTFTTYSNQPAVTIQVYEGERAMTKDNNL
                LVDVAPLSLGIETAGGVMTKIIERNaKIPC4QSQTFTTYSNQPAVTIQVYEGERAMTKDNNL

PmHSP70a      : ERYKEEDNRQRERVASRNQLESYIFSVKQALDDAGEKLSQEEKNSARNA CDEALKWFENNTLA
QWV59544.1    : ERYKEEDNRQRERVATRQLESYIFSVKQALDDAGEKLGQEDKNTALNA CDEALKWFENNTLA
XP_038210277.1 : ERYKEEDSRQRERVAARNQLESYVFSVKQALDEAGEKIGQDDKDTARKACDDALKWLDNNTLA
KAG8115787.1  : ERYKEEDERQRQVARSARNQLESYIFSVKQALDDAGDKLSEQDKQTARNBCDEALKWLDNNTLA
XP_045456590.1 : ERYKEEDEKQRQRVAAARNQLESYVFSVRQALDDAGSKLSDEDKNTARNVCDEALQWLDNNTLA
                ERYKEED 4QR2RVa RNQLESY6FSV4QALDdAG K6 2dK 3Arn CDeAlkW NNTLA

PmHSP70a      : PTVEEVDD
QWV59544.1    : PTVEEVD-
XP_038210277.1 : PTVEEVD-
KAG8115787.1  : PTVEEVD-
XP_045456590.1 : PTVEEVD-
                PTVEEVDD

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**Figure S5.** Sequence alignment of PmHSP70a with HSP70 proteins of *Pieris rapae* (QWV59544.1), *Zerene cesonia* (XP\_038210277.1), *Spodoptera frugiperda* (KAG8115787.1), and *Melitaea cinxia* (XP\_045456590.1) .



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PmHSP70b      : MPAIGIDLGTTYSCVGVWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNOVALNESNT
QWV59542.1    : MPAIGIDLGTTYSCVGVWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNOVALNESNT
XP_045456597.1 : MPAIGIDLGTTYSCVGVWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNOVALNESNT
XP_045456601.1 : MPAIGIDLGTTYSCVGVWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNOVALNESNT
XP_039760955.1 : MPAIGIDLGTTYSCVGVWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNOVALNESNT
                MPAIGIDLGTTYSCVGVWQHGNVEIIANDQGNRTTPSYVAFDTERLIGDAAKNOVALNP NT

PmHSP70b      : YLGSSVRDAVVTPPAYFNDSQRQATKDAGVIAGINVLRIINEPTAAALAYGLDKNLKGERNVL
QWV59542.1    : YLGSSVRDAVVTPPAYFNDSQRQATKDAGVIAGINVLRIINEPTAAALAYGLDKNLKGERNVL
XP_045456597.1 : YLGTSVRDAVITVPAYFNDSQRQATKDAGAIAGLNVLRINEPTAAALAYGLDKNLKGERNVL
XP_045456601.1 : YLGTSVRDAVITVPAYFNDSQRQATKDAGAIAGLNVLRINEPTAAALAYGLDKNLKGERNVL
XP_039760955.1 : YLGTSVVDVAVITVPAYFNDSQRQATKDAGAIAGLNVLRINEPTAAALAYGLDKNLKGERNVL
                YLG3SV4DAV6TVPAYFNDSQRQATKDAG IAG6NVLRINEPTAAALAYGLDKNLKGERNVL

PmHSP70b      : LRTAAERAKRTLSSSTEATVEIDALYEGIDFYTRVSRARFEELNADLFRGTLEPVEKALKDAK
QWV59542.1    : LRTAAERAKRTLSSSTEATVEIDALYEGIDFYTRVSRARFEELNADLFRGTLEPVEKALKDAK
XP_045456597.1 : LRTAAERAKRTLSSSTEATVEIDALYEGIDFYTRVSRARFEELNSDLFRGTLEPVEKALKDAK
XP_045456601.1 : LRTAAERAKRTLSSSTEATVEIDALYEGIDFYTRVSRARFEELNSDLFRGTLEPVEKALKDAK
XP_039760955.1 : LRTAAERAKRTLSSSTEATVEIDALYEGIDFYTRVSRARFEELNSDLFRGTLEPVEKALKDAK
                LRTAAERAKRTLSSSTEAT6EIDALYEGIDFYTRVSRARFEELN DLFRGTLEPVEKALKDAK

PmHSP70b      : LVDVAPLSLGIETAGGVMTKIIERNCKIPCKQSQTFTTYSNDQPAVTIQVYEGERAMTKDNNL
QWV59542.1    : LVDVAPLSLGIETAGGVMTKIIERNCKIPCKQSQTFTTYSNDQPAVTIQVYEGERAMTKDNNL
XP_045456597.1 : LVDVAPLSLGIETAGGVMTKIIERNCKIPCKQSQTFTTYSNDQPAVTIQVYEGERAMTKDNNL
XP_045456601.1 : LVDVAPLSLGIETAGGVMTKIIERNCKIPCKQSQTFTTYSNDQPAVTIQVYEGERAMTKDNNL
XP_039760955.1 : LVDVAPLSLGIETAGGVMTKIIERNCKIPCKQSQTFTTYSNDQPAVTIQVYEGERAMTKDNNL
                LVDVAPLSLGIETAGGVMTKIIERNCKIPCKQSQTFTTYSNDQPAVTIQVYEGERAMTKDNNL

PmHSP70b      : ERYKEEDDKQREHVAARNQLETYVFSVRQALDDAGAKLPDQDKDSARSHCDEAIKWLDNNTLA
QWV59542.1    : ERYKEEDDKQREHVAARNQLETYVFSVRQALDDAGAKLPDQDKDSARSHCDEAIKWLDNNTLA
XP_045456597.1 : ERYKEEDDKQRRQVVAARNQLESYVFSVRQALDDAGSKLSEEDKNTAFNVCEALQWLDNNTLA
XP_045456601.1 : ERYKEEDDKQRRQVVAARNQLESYVFSVRQALDDAGSKLSEEDKNTAFNVCEALQWLDNNTLA
XP_039760955.1 : ERYKEEDDKQRRQVVAARNQLESYVFSVRQALDDAGSKLSEEDKNTAFNVCEALQWLDNNTLA
                E4YKEED 4Qr 4VaARNQLE3Y6FSVRQALDDAG KL d DK13A4 CdEA6 WLdNNTLA

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**Figure S6.** Sequence alignment of PmHSP70b with HSP70 proteins of *Pieris rapae* (QWV59542.1), *Melitaea cinxias* (XP\_045456597.1), *Melitaea cinxia* (XP\_045456601.1), and *Pararge aegeria* (XP\_039760955.1).