

## Supplementary Tables and Figures

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

Primer name	Primers nucleotide sequence (5' to 3')
<i>Actin</i> -F	CATCTACGAGGGTTACGC
<i>Actin</i> -R	CATCTGTTGGAAGGTGGA
<i>PmHsc70</i> 3'F1	TAACACGACCATCCCCACCAAGCA
<i>PmHsc70</i> 3'F2	CCCAGACTTCACGACCTATTCCGACA
<i>PmHsc70</i> 5'R1	CGGGTTGGTTGTCGGAATAGGTCTG
<i>PmHsc70</i> 5'R2	GCCTCGTCAGGGTTGATGGACTTGT
<i>PmHsc70</i> 5'R3	ACCTCCCAAGTGAGTGTCTCCAGCAGT
<i>PmHsp70a</i> 3'F1	GCTGAGGCGTATTGGGTAGTCGGTC
<i>PmHsp70a</i> 3'F2	TCTACACCAGGGTTCTCGGGCACG
<i>PmHsp70a</i> 5'R1	AGCGTCTATTCAATGGTGGCTTCCGT
<i>PmHsp70a</i> 5'R2	CAGCGTCTTGACCGAACTACCCAAAT
<i>PmHsp70b</i> 3'F1	CGCCGCTGTCACTTGGCATAGAAACTG
<i>PmHsp70b</i> 3'F2	GAATGCTGGCAGAGGCTGAACGATA
<i>PmHsp70b</i> 5'R1	ATTCCAGCAATAACCCCAGCATCCTT
<i>PmHsp70b</i> 5'R2	TGAAATAGGCAGGGCACTGTGACGAC
<i>PmHsp70b</i> 5'R3	GATGGTGTGTTGGTTGCCCTGGT
<i>PmHsc70</i> ORF F	GTGATAGAAACAAACTATACGC
<i>PmHsc70</i> ORF R	TAATTGAGAGGATTACATCGAG
<i>PmHsp70a</i> ORF F	AGCGAATACTAAACAAGTGG
<i>PmHsp70a</i> ORF R	AGTACATGATCATGGATTGC
<i>PmHsp70b</i> ORF F	CAGTGATATTGTTATCAGAAG
<i>PmHsp70b</i> ORF R	CATATGTTAACACTGCAGTC
<i>PmActin</i> F	CAGGGAAAAGATGACCCAGA
<i>PmActin</i> R	GCAGAGCGTAACCCCTCGTAG
<i>Pm18S</i> F	AATGCCGCTGAAATATTTCG
<i>Pm18S</i> R	TTTCGCTGATGTTCGTCTTG
<i>PmHsp70a</i> F	TCCCGAGGAGTACCTAAGA
<i>PmHsp70a</i> R	GGCTTCAGCCAACATACGAT
<i>PmHsp70b</i> F	CGCTGTCACTTGGCATAGAA
<i>PmHsp70b</i> R	TACAGCAGGCTGGTTGTCA
<i>PmHsc70</i> F	TGCTGGAGACACTCACTTGG
<i>PmHsc70</i> R	TTCAATGCTAGCCTGTGTCG

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*.

<b>Gene</b>	<b>Source</b>	<b>df</b>	<b>MS</b>	<b>F</b>	<b>Sig.</b>
<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*.

<b>Gene</b>	<b>Source</b>	<b>df</b>	<b>MS</b>	<b>F</b>	<b>Sig.</b>
<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*.

<b>Gene</b>	<b>Source</b>	<b>df</b>	<b>MS</b>	<b>F</b>	<b>Sig.</b>
	Type of Diapause/nondiapause	2	11621.189	145.18	0.0000
<i>PmHsc70</i>	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
	Type of Diapause/nondiapause	2	109542.901	41.39	0.0000
<i>PmHsp70a</i>	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
	Type of Diapause/nondiapause	2	31874.158	46.78	0.0000
<i>PmHsp70b</i>	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 TGATAATTCTTTGAAGTGATAGAACAAACTATACCGAATGACTACTAAAACCAGCCGTAGGTATTGACTTGGTACCATACTCG  
 1 M T T K T P A V G I D L G T T Y S  
 91 TGCGTGGCGTGTCCAGTACGTAAGGTGGAGATCATCGCAACGATCAGGGCAACAGGACTACACCTTCATATGTTGCCCTCACAGAC  
 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 ACCGAACGTCATCGGAGATGCCCAAGAACCGAGTGGCCCTGAACCCAAACAACACCATCTTGTATGCCAAACGTCATGGGGT  
 61 T E R L I G D A K N Q V A L N P N T I F D A K R L I G R  
 271 ACTCGAAGATGCCACAGTCAGGCTGACATGAAACACTGGCCCTTGAGGTAATCAGTGATGGAAAACCAAAGATCAAGGTTGCA  
 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 TACAAGGGTAAGAACAAACATTCTCCAGAGGAAGTCAGTTCAATGGTATTAACAAAATGAAAGAACAGCTGAAGTTACCTGGC  
 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 AAACCGTGCAGAATGCACTTAACAGTGCAGCATACTTAATGACTCCAAAGACAGGCCACAAAGGATTCTGGTACAATCTCTGGT  
 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 CTGAACGTTCTCCGAATCATCAATGAAACCAACTGCTGCGATTGATATGGCTTGACAAAGAAAGGGTGGAGAACGTAACGTCCTT  
 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 ATTTTCGATCTGGCGGTGGTACTTTGATGTTATCCATCCCTGACCATCGAGGATGGTATCTTGAGGTAAGTGAAGTCCACTGCTGGAGACACT  
 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 CACTGGGAGGTGGAGACTTGACAACCGCATGGTCAACCCACTTGTACAGGAGTTCAAGCGGAAGTACAAAAGGACATTCTCCAC  
 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 AGAGGGCCCTGCGTAGGGTGAGGACAGCTGTGAGGCCGAAGGGACTTCTCTGACACAGGCTAGCATTGAAATCGACTCT  
 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 CTGTTGAGGGTATCGATTACTACACATCCATCACCCTGGCGCTTCTGAGAACACTGAACGCCACTTATTAGATCTACCATGGAGCCT  
 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  
 991 GTAGAGAAGTCCCCTCGTGACGCCAAGATGGACAAGGCAGTGCACGACATGTCCTGCGAGGTCCACTCGTATCCAAGAGTG  
 331 V E K S L R D A K M D K A Q V H D I L V L V G G S T R I P R V  
 1081 CAGAAGCTCTTCAAGACTTCAATGGCAAGGAGTTGAACAAGTCCATCAACCCCTGACGGCCGTAGCCTACGGAGCGCCGTTCA  
 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 GCCCCCATCTGCAACGGTATAACTCTGAAGAACTACAGGATCTGCTCTGTTGATGTCACCCCGCTGCTCCCTGGTATCGAGACTGCA  
 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 GCGGGTGTATGACCCACTTGATAAGCTGAAACGACCCATCCCCACCAAGAACCCAGACTTCAAGGACTATTCCGACAACCAACCC  
 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 GGTGTGCTTATTCAAGTATTGAGGGTGACCGTGCATGACCCGAGACAAACCTCTCGGTAATTGAGCTACTGGTATTCCCCCA  
 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 GCGCCCGTGTGGTCCCACAAATCGAAGTACTTCGACATTGACGCCAACGGTATCCTTAACGATCGCTGCGAAAGATCTACCAAC  
 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 AAGGAGAACAGATCACGATACCAATGACAAGGGTGTCTGTCAGGAAAGAGATCGAGGCTATGGTCAACGACGCTGAGAAATACAGG  
 511 K E N K I T T N D K G R L S K E E I E R M V N D A E K Y R  
 1621 AACGAAGATGAGAACAGAACGAGAACATTCAAGGCTAAGAACGCCGCTGAATCTACTGCTAACATGAAGTCTACCATGGAGGATGAG  
 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 AAGCTTAAGGACAAATCACAGACTCCGACAAGCAATCTTGGACAAATGCAACGACACCATCAAATGGTGGAGCCTAACAGCTG  
 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 GCTGACAAGGAAGAATATGAGCACAGAACAGAGGACTGGAGGGTGTGCAACCCGATTATAACCAAGCTTACCAAGGTGAGGTGAG  
 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 GCCCCCGAGGTGCGCTGCTGAGGCTCCCTGGCGAGGCCCTGGAGGCCGTTGGAGGCCGTTGGAGCAGGCCCTGGTGGAGCCTGGACCC  
 631 A P G G M P G G M P G F P G G A P G A G G A A P G G G S G P  
 1981 ACCATCGAAGAGGTGATTAACATTGAAATTACATTCCACTTTCACATTGTAAGATCTCTCGATGTAATCCTCTCAATTAAATAA  
 661 T I E E V D  
 2071 ATGAATGCAACTGAAAAAAAAAAAAAAA

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

1 ATCACTATTGAAAAGACAACAAAGCGAACAGTAAAAGTGAAGTCGGTGTCAATACCAAGTTATAACAAGCAACTAAACAAGTGGAGC  
 91 GAATACTAAACAAGTGGATCTATTATTGAACGAGTGATAAAATAATTAAAAAATCATCAAAATGCCAGCTATTGAAATTGATCTTGA  
 1 M P A I G I D L G  
 181 ACCACATACATGTGTGGAGTGTGGCAACATGGAAACAGTGGAAATCATCGCAACCGACCAAGGCACCGAACACACCATCATACGTT  
 31 T T Y S C 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  
 271 GCATTACAGACACAGAGAGACTTATTGGAGATGCGCTAAGAACCCAGGTCGCTTGAACCGAATAACACAGTGTTCGACGCAAAGCGA  
 61 A F T D T E R L I G D A A K N Q V A L N P N N T V F D A K R  
 361 CTGATCGGCAGAAAATTCCGACGCCAACATTAGCAAGATATGAAACACTGGCCTTCAGGTATCAACGACTACGGTAATGTAAA  
 91 L I G R K F D D P K I Q Q D M K H W P F K V I N D Y G K C K  
 451 ATTCAAGGTGAAATTCAAGGGCAGAACAAAACGATTTCTCCGGAAGAAATCAGCAGCATGGTGTCAAGAAGATGAAGGAAACTGCTGAG  
 121 I Q V E F K G E T K R F S P E E I S S M V L T K M K E T A E  
 541 GCGTATTGGTAGTTCGCTCAGAGACGCTGTATAACGGTACCGACTTCAACGACTCCAACGCCAGGCAACCGATGCGGT  
 151 A Y L G S S V R D A V I T V P A Y F N D S Q R Q A T K D A G  
 631 GCGATCGCCGATCAACGCTTAAAGATAATAATGAAACCCACCGCTGCCCTTGGCATATGGCTGGACAAAAGTCTCAAAGGAGAA  
 181 A I A G I N V L R I I N E P T A A A A L A Y G L D K S L K G E  
 721 CGTAAACGCTTGTATTTGATCTGGAGGCGGTACCTTGATGTATCCATCTAACTATCGACGAGGGATCATTGTTGAAGTAAAGCT  
 211 R N V L I 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  
 811 ACTGCGCGATACGCTATCGGTGGTGGAGACTTGACAACAGACTAGTCACACCACCTGGCTGATGAATTCTCCGAAAGTACAAGAAG  
 241 T A G D T H L G G E D F D N R L V N H L A D E F F R K Y K K  
 901 GACATAAGGAATAATGCTCGCCTCTCGTCAACTACGACGACGCTTATCATCGACGACGGACC  
 271 D I R R N N A R A L R R L R T A A E R A K R T L S S S T E A T  
 991 ATTGAAAATAGACGCTCTACGAAGGAATGGACTTCTACACCGGGTCTCGGGCACGGTTGAGGAATTAAACTGGATTGTCGCG  
 301 I E I D A L Y E G M D F Y T R V S R A R F E E L N S D L F R  
 1081 GGTACTCTGGAACCAAGCTCGAGAAGGCCCTAAAGGTGCTAAGCTTACGTTGACAAGAGTTCTATTACGATGTAGTTGGCTGGCTACT  
 331 G T L E P V E K A L K D A K L D K S S I H D V V L V G G S T  
 1171 CGTATTCAAAATTCAGAGCATGCTGCACAAACTCTCTGTTGTAAGAAATTAACCTCTCCATCAACCCGATGAAGCAGTTGCCAT  
 361 R I P K I Q S M L Q N F F C G K K L N L S I N P D E A V A Y  
 1261 GGCGCTGGGTCAAGCAGCTATCTTAAGTGGGAACAGCACAGTAAATCCAGGATGTACTGCTAGTAGACGTTGCTCCATTGTCATTG  
 391 G A A V Q A A I L S G E Q H S K I Q D V L L V D V A P L S L  
 1351 GGTATTGAGACTCGAGGAGACTAATGACGAAGATCATTGAGCGGAATGCCAGATTCATGCCAGACAGTCACAAACCTCACACATAC  
 421 G I E T A G G V M T K I I E R N A K I P C R Q S Q T F T T Y  
 1441 TCCGACAACCAACCGCCCTAACGATCCAGGTGATGAGGGTGAACGAGCAACTAAAGACAACACCTGCTGGCGATTGATCTT  
 451 S D N Q P A V T I Q V Y E G E R A M T K D N N L L G R F D L  
 1531 ACTGGAATACCAACCCAGCTCCCGAGGACTACCTAACAGATAGACCTCACCTTCGATTAGATGCCAATGGAATCTAAACGTATCCC  
 481 A A E R Y K E E D N R Q R E R V A S R N Q L E S Y I F S V K Q  
 1621 GAAAACAGTACTGCCCTAACGAAAGAACATCGTGTACAGAAGATGATAAGGGCGCTTTCGCAAGCTGAGATCGATGTTGGCTGAA  
 511 E N S T G L S K N I V I K N D K G R L S Q A E I D R M L A E  
 1711 GCCGAAAGGTACAAAGAAGACAACCGCAAAGAGAAAGAGTAGCATCTCGCAATCAACTAGAATCTTACATCTTGTGAAACAG  
 541 A E R Y K E E D N R Q R E R V A S R N Q L E S Y I F S V K Q  
 1801 GCTTGGAGCTGCTGGTAAAGAAAATCTCAGTCAGAAGAGAAACAGTGTGCTGAAATGCCAGTGTGATGAAAGCTCTCAAATGTTGAAAC  
 571 A L D D A G E K L S Q E E K N S A R N A C D E A L K W F E N  
 1891 AATACCTAGCGGAAAAGAAGAATATGAACACCGCTTAAGGAATTACAAAGGACTTGCTCTCCAATAATTAGCAAGATGCACGGAGCT  
 601 N T L A E K E E Y E H Q L K E L Q R T C S P I I I S K M H G A  
 1981 GGTCCAGTAACCCAGGTGGCTTCCAGCCCGACAAGGATCACAACAAAGGGCAAGGATTCAGCAAGGCCAGTGTGATGAACTGCTGAA  
 631 G S S N P G G F Q P G Q G F Q Q G Q G F Q Q G P S F Q P G Q  
 2071 GGCTACCAACAATACAGCAACCAAGGTCCCACAGTAGAGGAAGTAGATTAAATGACATAAAATCCAATTAAATCTAGTACAACCTTGT  
 661 G Y Q Q Y S N Q G P T V E E V D  
 2161 AATAGTATTGTTAAGTTCTGACTGATTAGTTCTAAATATTATTAGCAATCCATGATCATGTACTGCAATCCATGATCATGTACT  
 2251 GCTTAATCTAGAATAATTAGTAAAAAAAAAAAAAAAAAAAAAA

**Figure S2.** Nucleotide and deduced amino acid sequences of *PmHsp70a*.

1           AGACTAATTGCAAATCGAGAGAGTGAAACAAGTGTATTCACTGGAGATTTTACGATCTTCGCAATTATACATCTTGCATAATTCTGTGAAG  
 91         TTTGTGAAATTATATTCAGTGTATTGGTACAAACAGCAGCTATTGGAATTGATCTTGTACAAACCTACTCTTGC  
 1           M P A I G I D L G T T Y S C  
 181         GTTGGTGTGGCAACATGGAATGTGGAGATCATCGAAATGACCAGGGCAACCAACCATCGTACGTCGATTCAGCAG  
 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         GAGCGTCTGATCGGCATGCTGCTAAAGAACCAAGTAGCTTAAACCCCTAGCAACACAGTGTTCGATCGCAAAGGCTATCGGCCGAA  
 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         TTCGACGATCCAAAATTCAACAGGACATGAAACATTGGCCTTTAAAGTTACATGACTGGTAAGGCTAACATCCAGGTTGAATT  
 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         AAAGGCAGAACAAAACGATTGCCCCAGAAGAACAGTCAGCAGATGGTTGGTAAAGGAGACAGCTGAGGCCTACCTGGATCA  
 121           K G E 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         TCAGTGCAGATGCCGTCGTACAGTGCCTCCATTCAATGATTCAACAGCGTCAAGGCCAGGATGCTGGGTATTGCTGGATA  
 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         ATATGTTTACGTATCAAACGAGCCCAGTCGGCTGCTGGCATATGGCTAGACAAAAATCTAAAGGGCAACGCAATGCTTATT  
 181           N V L R I I N E P T A A A A L A Y G L D K N L K G E R N V L I  
 721         TCGATCTGGTGGCGCACATTGACGTTCCATTGACGATCGACGAGGGTCGCTTTGAAGTGAAGGCCAGGCCGAGACACA  
 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         CACCTGGAGGTGAAGACTTGAACACAGGCTCGTAAACCCATTAGCGGAGGTCCAACGAAAATACAAGAAAGATTGCGCACGAA  
 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         CCACCGCATTGCGACGCCCTCCGACCGCCAGAGCGCACTTATCATCTAGCACCAGGCCAGGTTGAATCGACGCCG  
 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         CTATACGAAGGTATTGATTTCTACACTCGCTATCTGGCTCGTGAAGAATTAAACGCTGATCTATTCCGGGCAACCTGAAACCA  
 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         GTGGAAAAGCATTGAAAGATGCTAAGATGGATAAGAGCCAATACATGACGTTCTGGCTGGAGGTTCAACTCGTATTCTAAAGGTA  
 331           V E K A L K D A K M D K S Q I H D V V V L V G G S T R I P K V  
 1171         CAATCCCCTGCTACAAAATCTCTGTGTAAGAACTTAACCTTCCATCAACCCCGACGAGGGCTGTCAGCATATGGAGCGCGCTCAG  
 361           Q S L L Q N F F C G K K L N L S I N N P D E A V A Y G A A V Q  
 1261         GCAGCTATTGAGCGCGAACACTCACTCTAAAGATCCAGGTGTTATTGGTAGATGTAGCCTGGCTGCACTGGCATAGAACTGCT  
 391           A A T 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         GGAGGAGTCATGACCAAGATAATTGAACTGAACTGCAAATCCGTCAAGCAATCGCAGACATTACCCCTATTGACAACCGCCT  
 421           G G V M T K I T E R N C K I P C K Q S Q T F T T Y S D N Q P  
 1441         GCTGTAACTATCCAAGTGTAGAGGTGAACGAGCAATGACAACAAAGATAACATCCCTGGTACTTCGATCTGACAGGCATACCACCT  
 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         GCACCCGGGGGTGTCCAAATCGACGTCACATTGACATGGACGCCAAGCTATTCTTAATGTCGCGCAAAGGAAAAGACTACTGGT  
 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         CGTAGAAAATATCGTATAAGAATGATAAGGGGACGCTTGTCACAGGTGAGATTGACAGAAATGCTGGCAGAGGTGAACGATAAG  
 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         GAAGAGGATGATAAGCAGAGGGAGAGGGTGGCCGCTCGTAACCAACTGGAGACATATGTCAGCGTGTGAGCAGGGCTAGATGCCC  
 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         GGAGCGAACGGTACCGACACAAAGATTCTGCACGATCACATGCGACGAGCGATAAGGGTTAGAGAACAACACTTGGCCGAG  
 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         AAGGAGGAATACGAGCATAAGTTGAAGGAGCTCCAGAGAGTTGCTCACCAATTGAGTAAGCTGATGGTGTGGTGCCTCCT  
 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         GGAGGCCAATCAAATGGACCCACCGTAGAGGAAGTGATTAAACCTAGTATTAAGAACTAATAGTTAATTAAAAA  
 631           G G Q S N G P T V E E V D  
 2071         ATTATTTGACTGCACTGTTAAACATATGTTAATAACATTATTAAATTAAAAAAAAAAAAAAAAAAAAAAA

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

PmHSC70	:	MTT <b>K</b> T PAVGIDLGTTYSCGVVFQY <b>GKVE</b> II AND QGNRTTPSYVAFTDTERLIGDAAKNQVALN
XP_022130638.1	:	MTT <b>T</b> PAVGIDLGTTYSCGVVFQY <b>GKVD</b> II AND QGNRTTPSYVAFTDTERLIGDAAKNQVALN
XP_041970467.1	:	-MA <b>K</b> PAVGIDLGTTYSCGVVFQ <b>HGKV</b> EII AND QGNRTTPSYVAFTDTERLIGDAAKNQVAMN
XP_026489199.1	:	-MA <b>K</b> PAVGIDLGTTYSCGVVFQ <b>HGKV</b> EII AND QGNRTTPSYVAFTDTERLIGDAAKNQVAMN
XP_028170304.1	:	<b>MAT</b> <b>K</b> PAVGIDLGTTYSCGVVFQ <b>HGKV</b> EII AND QGNRTTPSYVAFTDTERLIGDAAKNQVAMN K PAVGIDLGTTYSCGVVFQ <b>GKVe</b> II AND QGNRTTPSYVAFTDTERLIGDAAKNQVA6N
PmHSC70	:	TAE <b>V</b> YLGKTVQNAVITVPAYFND <b>SQRQATKD</b> S GTISGLNVLR <sub>I</sub> INEPTAAAIAYG <b>LDDKKGGGE</b>
XP_022130638.1	:	TAE <b>V</b> YLGKTVQNAVITVPAYFND <b>SQRQATKD</b> S GTISGLNVLR <sub>I</sub> INEPTAAAIAYG <b>LDDKKGGGE</b>
XP_041970467.1	:	TAE <b>A</b> YLGKTVQNAVITVPAYFND <b>SQRQATKD</b> S GTISGLNVLR <sub>I</sub> INEPTAAAIAYG <b>LDDKKGGGE</b>
XP_026489199.1	:	TAE <b>A</b> YLGKTVQNAVITVPAYFND <b>SQRQATKD</b> A GTISGLNLRI <sub>I</sub> INEPTAAAIAYG <b>LDDKKGTGE</b>
XP_028170304.1	:	TAE <b>A</b> YLGKTVQNAVITVPAYFND <b>SQRQATKD</b> A GTISGLNLRI <sub>I</sub> INEPTAAAIAYG <b>LDDKKGGGE</b> TAE YLGKTVQNAVITVPAYFND <b>SQRQATKD</b> GTISGLN6LRI <sub>I</sub> INEPTAAAIAYG <b>LDDKKGgGE</b>
PmHSC70	:	LRRRLTACERAKR <b>T</b> LSSSTQASIEIDS <b>L</b> FEGIDYYTSITRARFEELNADLF <b>R</b> STMEP <b>V</b> E <b>K</b> SLR
XP_022130638.1	:	LRRRLTACERAKR <b>T</b> LSSSTQASIEIDS <b>L</b> FEGIDYYTSITRARFEELNADLF <b>R</b> STMEP <b>V</b> E <b>K</b> SLR
XP_041970467.1	:	LRRRLTACERAKR <b>T</b> LSSSTQASIEIDS <b>L</b> FEGIDFYTSITRARFEELNADLF <b>R</b> STMEP <b>V</b> E <b>K</b> SLR
XP_026489199.1	:	LRRRLTACERAKR <b>T</b> LSSSTQASIEIDS <b>L</b> FEGIDFYTSITRARFEELNADLF <b>R</b> STMEP <b>V</b> E <b>K</b> SLR
XP_028170304.1	:	LRRRLTACERAKR <b>T</b> LSSSTQASIEIDS <b>L</b> 5EG1D5YTTSITRARFEELNADLF <b>R</b> STMEP <b>V</b> E <b>K</b> SLR LRRRLTACERAKR <b>T</b> LSSSTQASIEIDS <b>L</b> 5EG1D5YTTSITRARFEELNADLF <b>R</b> STMEP <b>V</b> E <b>K</b> SLR
PmHSC70	:	DLLLDVTPLS <b>LGIETAGGVMTTLIKRNNTI</b> PTKQTQTFTTYS <b>DNQPGVLIQVF</b> EGERAMTRD
XP_022130638.1	:	DLLLDVTPLS <b>LGIETAGGVMTTLIKRNNTI</b> PTKQTQTFTTYS <b>DNQPGVLIQVF</b> EGERAMTRD
XP_041970467.1	:	DLLLDVTPLS <b>LGIETAGGVMTTLIKRNNTI</b> PTKQTQTFTTYS <b>DNQPGVLIQVF</b> EGERAMTKD
XP_026489199.1	:	DLLLDVTPLS <b>LGIETAGGVMTTLIKRNNTI</b> PTKQTQTFTTYS <b>DNQPGVLIQVF</b> EGERAMTKD
XP_028170304.1	:	DLLLDVTPLS <b>LGIETAGGVMTTLIKRNNTI</b> PTKQTQTFTTYS <b>DNQPGVLIQVF</b> EGERAMTKD DLLLDVTPLS <b>LGIETAGGVMTTLIKRNNTI</b> PTKQTQTFTTYS <b>DNQPGVLIQVF</b> EGERAMT4D
PmHSC70	:	NDAE <b>KYRNEDEK</b> QKETI <b>QAKNALESYCFNMKSTMED</b> EKL <b>KITDSDKQ</b> I I LD <b>KCNDTIKWLD</b>
XP_022130638.1	:	NDAE <b>KYRNEDEK</b> QKETI <b>QAKNALESYCFNMKSTMED</b> EKL <b>KITDSDKQ</b> I I LD <b>KCNDTIKWLD</b>
XP_041970467.1	:	NDAE <b>KYRNEDEK</b> QKETI <b>QAKNALESYCFNMKSTMED</b> EKL <b>KITDSDKQ</b> T I LD <b>KCNDTIKWLD</b>
XP_026489199.1	:	NDAE <b>KYRNEDEK</b> QKETI <b>QAKNALESYCFNMKSTMED</b> EKL <b>KITDSDKQ</b> T I LD <b>KCNDTIKWLD</b>
XP_028170304.1	:	NDAE <b>KYRNEDEK</b> QKETI <b>QAKNALESYCFNMKSTMED</b> AN <b>LKDKitDADKQ</b> T I LD <b>KCNDTIKWLD</b> N AE <b>KYRNEDeK</b> QKETI <b>QAKNALESYCFNMKSTMED</b> E <b>kLKDKitDADKQ</b> I LD <b>KCNDTIKWLD</b>
PmHSC70	:	EVD
XP_022130638.1	:	EVD-
XP_041970467.1	:	EVD-
XP_026489199.1	:	EVD-
XP_028170304.1	:	EVD- EVD

**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).

PmHSP70a	:	MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPNN
QWV59544.1	:	MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPNN
XP_038210277.1	:	MPAVGIDLGTTYSCGVWQHGNVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPNN
KAG8115787.1	:	MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPNN
XP_045456590.1	:	MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPNN MPA6GIDLGTTYSCGVWQHGNVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPNN
PmHSP70a	:	YLGS <sub>5</sub> VRDAVITVPAYFNDSQRQATKDAGAIAGINVLR <sub>11</sub> INEPTAAALAYGLDK <sub>16</sub> SLKGERNVL
QWV59544.1	:	YLGS <sub>5</sub> VRDAVITVPAYFNDSQRQATKDAGAIAGINVLR <sub>11</sub> INEPTAAALAYGLDK <sub>16</sub> SLKGERNVL
XP_038210277.1	:	YLGS <sub>5</sub> AVKDAVITVPAYFNDSQRQATKDAGAIAGINVLR <sub>11</sub> INEPTAAALAYGLDK <sub>16</sub> SLKGERNVL
KAG8115787.1	:	YLGT <sub>5</sub> SVRDAVITVPAYFNDSQRQATKDAGAIAGLNVL <sub>11</sub> R <sub>16</sub> INEPTAAALAYGLDK <sub>21</sub> SLKGERNVL
XP_045456590.1	:	YLGT <sub>5</sub> SVRDAVITVPAYFNDSQRQATKDAGAIAGLNVL <sub>11</sub> R <sub>16</sub> INEPTAAALAYGLDK <sub>21</sub> SLKGERNVL YLG3sV4DAVITVPAYFNDSQRQATKDAGAIAG6NVLR <sub>11</sub> INEPTAAALAYGLDK <sub>21</sub> SLKGERNVL
PmHSP70a	:	LRTAAERAKRTLSSSTEATIEIDAL <sub>11</sub> YEGMDFYTRVSRARFEELNSDLFRGTLPEVKALKDAK
QWV59544.1	:	LRTAAERAKRTLSSSTEATIEIDAL <sub>11</sub> YEGIDFYTRVSRARFEELNSDLFRGTLPEVKALKDAK
XP_038210277.1	:	LRTAAERAKRTLSSSTEATIEIDAL <sub>11</sub> YEGIDFYTRVSRARFEELNADLFRGTLPEVKALKDAK
KAG8115787.1	:	LRTAAERAKRTLSSSTEATIEIDAL <sub>11</sub> HEGIDFYTRVSRARFEELNADLFRGTLPEVKALKDAK
XP_045456590.1	:	LRTAAERAKRTLSSSTEATIEIDAL <sub>11</sub> YEGIDFYTRVSRARFEELNSDLFRGTLPEVKALKDAK LRTAAERAKRTLSSSTEATIEIDAL <sub>11</sub> yEG6D5YTRVSRARFEELN DLFRGTLPEVKALKDAK
PmHSP70a	:	LVDVAPLSLGIETAGGVMTK <sub>11</sub> IERN <sub>16</sub> AKIPCRQSQTFTTYSNDNQPAVTI <sub>21</sub> IQVYEGERAMTKDN <sub>26</sub> N
QWV59544.1	:	LVDVAPLSLGIETAGGVMTK <sub>11</sub> IERN <sub>16</sub> AKIPCRQSQTFTTYSNDNQPAVTI <sub>21</sub> IQVYEGERAMTKDN <sub>26</sub> N
XP_038210277.1	:	LVDVAPLSLGIETAGGVMTK <sub>11</sub> IERN <sub>16</sub> AKIPCRQSQTFTTYSNDNQPAVTI <sub>21</sub> IQVYEGERAMTKDN <sub>26</sub> N
KAG8115787.1	:	LVDVAPLSLGIETAGGVMTK <sub>11</sub> IERN <sub>16</sub> AKIPCKQSQTFTTYSNDNQPAVTI <sub>21</sub> IQVYEGERAMTKDN <sub>26</sub> N
XP_045456590.1	:	LVDVAPLSLGIETAGGVMTK <sub>11</sub> IERN <sub>16</sub> CKIPCKQSQTFTTYSNDNQPAVTI <sub>21</sub> IQVYEGERAMTKDN <sub>26</sub> N LVDVAPLSLGIETAGGVMTK <sub>11</sub> IERN <sub>16</sub> aKIPC4QSQTFTTYSNDNQPAVTI <sub>21</sub> IQVYEGERAMTKDN <sub>26</sub> N
PmHSP70a	:	ERYKEEDNRQRERVA <sub>11</sub> SRNQLESYIFSVKQALDDAG <sub>16</sub> EK1 <sub>17</sub> SQEE <sub>18</sub> KNSARN <sub>19</sub> CDEALKW <sub>20</sub> FENNTLA
QWV59544.1	:	ERYKEEDNRQRERVA <sub>11</sub> TRNQLESYIFSVKQALDDAG <sub>16</sub> EK1 <sub>17</sub> GQEDKNTA <sub>18</sub> LNACDEALKW <sub>20</sub> FENNTLA
XP_038210277.1	:	ERYKEEDSRQRERVA <sub>11</sub> ARNQLESYVF <sub>16</sub> FSVKQALDDAGE <sub>17</sub> EK1 <sub>18</sub> GQDKDTAE <sub>19</sub> KACDDALKWLDNNNTLA
KAG8115787.1	:	ERYKEEDEQRQRQRV <sub>11</sub> SARNQLESYIFSVKQALDDAG <sub>16</sub> K1 <sub>17</sub> SEQDKQTARNE <sub>18</sub> CDEALKWLDNNNTLA
XP_045456590.1	:	ERYKEEDEKQRQRV <sub>11</sub> A <sub>12</sub> RNQLESYVF <sub>16</sub> FSVRQALDDAGSK1 <sub>17</sub> SDEDKNTARNVCDEALQ <sub>18</sub> WLDNNNTLA ERYKEED 4QR2RVa RNQLESY6FSV4QALDdAG K6 2dK 3Arn CDeALKW NNTLA
PmHSP70a	:	PTV <sub>5</sub> EVD <sub>10</sub> D
QWV59544.1	:	PTV <sub>5</sub> EVD <sub>10</sub> -
XP_038210277.1	:	PTV <sub>5</sub> EVD <sub>10</sub> -
KAG8115787.1	:	PTV <sub>5</sub> EVD <sub>10</sub> -
XP_045456590.1	:	PTV <sub>5</sub> EVD <sub>10</sub> - PTV <sub>5</sub> EVD

**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).

PmHSP70b	:	MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTFSYVAFDTERLIGDAAKNQVALNHSNT
QWV59542.1	:	MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTFSYVAFDTERLIGDAAKNQVALNFSNT
XP_045456597.1	:	MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTFSYVAFDTERLIGDAAKNQVALNNT
XP_045456601.1	:	MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTFSYVAFDTERLIGDAAKNQVALNNT
XP_039760955.1	:	MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTFSYVAFDTERLIGDAAKNQVALNNT MPAIGIDLGTTYSCGVWQHGNVEIIANDQGNRTTFSYVAFDTERLIGDAAKNQVALNPT
PmHSP70b	:	YLGSSVRDAVTVPAYFNDSQRQATKDAGVIAGINVRLIINEPTAAALAYGLDKNLKGERNVL
QWV59542.1	:	YLGSSVRDAVTVPAYFNDSQRQATKDAGVIAGINVRLIINEPTAAALAYGLDKNLKGERNVL
XP_045456597.1	:	YLGTTSVRDAVITVPAYFNDSQRQATKDAGAIAGLNVLRIINEPTAAALAYGLDKNLKGERNVL
XP_045456601.1	:	YLGTTSVRDAVITVPAYFNDSQRQATKDAGAIAGLNVLRIINEPTAAALAYGLDKNLKGERNVL
XP_039760955.1	:	YLGTTSVRDAVITVPAYFNDSQRQATKDAGAIAGLNVLRIINEPTAAALAYGLDKSLKGERNVL YLG3SV4DAV6TVPAYFNDSQRQATKDAG IAG6NVLRINEPTAAALAYGLDKnLKGERNVL
PmHSP70b	:	LRTAAERAKRTLSSSTEATVEIDALYEGIDFYTRVSRARFEELNADLFRTGLEPVEKALKDAK
QWV59542.1	:	LRTAAERAKRTLSSSTEATVEIDALYEGIDFYTRVSARFEELNADLFRTGLEPVEKALKDAK
XP_045456597.1	:	LRTAAERAKRTLSSSTEATIEIDALYEGIDFYTRVSARFEELNSDLFRGTLLEPVEKALKDAK
XP_045456601.1	:	LRTAAERAKRTLSSSTEATIEIDALYEGIDFYTRVSARFEELNSDLFRGTLLEPVEKALKDAK
XP_039760955.1	:	LRTAAERAKRTLSSSTEAT6IDALYEGIDFYTRVSARFEELNSDLFRGTLLEPVEKALKDAK LRTAAERAKRTLSSSTEAT6IDALYEGIDFYTRVSARFEELN DLFRTGLEPVEKALKDAK
PmHSP70b	:	LVDVAPLSLGIELTAGGVMTKIIERNCKIPCKQSQTFTTYSDNQPAVTIQVYEGERAMTKDNNL
QWV59542.1	:	LVDVAPLSLGIELTAGGVMTKIIERNCKIPCKQSQTFTTYSDNQPAVTIQVYEGERAMTKDNNL
XP_045456597.1	:	LVDVAPLSLGIELTAGGVMTKIIERNCKIPCKQSQTFTTYSDNQPAVTIQVYEGERAMTKDNNL
XP_045456601.1	:	LVDVAPLSLGIELTAGGVMTKIIERNCKIPCKQSQTFTTYADNQPAVTIQVYEGERAMTKDNNL
XP_039760955.1	:	LVDVAPLSLGIELTAGGVMTKIIERNCKIPCKQSQTFTTYSDNQPAVTIQVYEGERAMTKDNNL LVDVAPLSLGIELTAGGVMTKIIERNCKIPCKQSQTFTTYSDNQPAVTIQVYEGERAMTKDNNL
PmHSP70b	:	ERYKEEDDKORERVAARNQLETYVFVSRQALDDAGAKLPDKDKDSARSQCDDEAIKWLENNNTLA
QWV59542.1	:	ERYKEEDDKORERVAARNQLETYVFVSRQALDDAGAKLPDKDKDSARSQCDDEAIKWLDNNNTLA
XP_045456597.1	:	ERYKEEDEKORORVAARNQLESYVFVSRQALDDAGSKLSEDKNTARNVCDEALQWLDDNNNTLA
XP_045456601.1	:	ERYKEEDEKOROKVAARNQLESYIFVSRQALDDAGQKLSADKNSAKSEEAIRWLDDNNNTLA
XP_039760955.1	:	EKYKEEDEKOROKVAARNQLESYIFVSRQALDDAGQKLSADKNSAKSEEAIRWLDDNNNTLA E4YKEED 4Qr 4VaARNQLE3Y6FSVRQALDDAG KL d DK13A4 CdEA6 WLdNNNTLA

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