

Cloning of *Px-pdrg* and *Px-aspp2* and mRNA expression under heat stress in insecticide-resistant and -susceptible diamondback moth, *Plutella xylostella* (Lepidoptera: Plutellidae)

Yu Wang¹, Jing Nan Wang¹, Xue Zhun Chen¹, Qi Xing Hu¹, Qi Qing Liu¹, Gang Wu^{1,*}

¹ Key Laboratory of Biopesticide and Chemical Biology (Ministry of Education), Fujian Agriculture and Forestry University, Fuzhou, China

* Corresponding authors

E-mail: newugang@163.com (GW)

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1      ATACGATCTAATACGTCTCATTCTACTCCATCTAGTGCTAGCACCGGTATGAACACCGAG
61     GACATGGCCATTGCCACTATTGCCAGTGCCACAACAAAATAAACTAATAAAAGTTGAAGTT
121    CCTTCCTAACACTGAGGAAAATAAACACTAAAGTTCCTAAATGTGGTAAAGTGGTGATGT
181    GTGATGTGATGATGATTGTGAACCTGTGCAGCCTCTGCTGACGAAAATCTGAAAGCACTG
241    AACCATTTGTGAAACTCAAAATGATGAACGATCAAGAAAAGCTTCTCAAGTATCTTGTGTC
1      M M N D Q E K L L K Y L V S
301    TGTCGAGAAGTTGGCTGAAGAAATATTGTCTGATAACAAAGAAATCATACTCTTAGATAA
15     V E K L A E E I L S D N K E I I L L D K
361    ACGAAGAAACCTGAATAGAGAAGCATTGCGAGATATTTCTAAATCTGGCCAATCCAAGTG
35     R R N L N R E A L R D I S K S G Q S K C
421    TTTAGTTACTGTGGGATCTGTACTTGTGAAACACGACATAGAAGCTACAAAGAGTCTGCT
55     L V T V G S V L V K H D I E A T K S L L
481    TGAGGCTGACCAGAAACAACTTAACATTGATATTAATAAGCTTCGGAGTGATCTTAAAGT
75     E A D Q K Q L N I D I N K L R S D L K V
541    CAAAGTGAACAATTTGAGGGACTTAGAGATGCAGCCACCTGTTCCGGGGTTGATGTTAGC
95     K V N N L R D L E M Q P P V P G L M L A
601    ACCTCTGTCTGCTAAAGAAGCTATCGGACTTTCTAGAGCTGGGATGATGTAGTGTTTTTC
105    P L S A K E A I G L S R A G M M *
661    CTCTATAAATACTTATGAAGCATCAAATTTTATGCTTCCTTTTTGGTCCCTAGATTACAT
721    ACATTTATGATGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTCCGT

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Supplemental Figure S1. The amino acid sequence and nucleotide sequence of *Px-pdr* in DBM. Numbers on the left of each row represent amino acid or nucleotide position. The black-bolded sequence represents the beginning codon (ATG) and the ending codon (AGT). The shaded area is a conservative structural domain.

1 AGTCTCACGCAGAGTACATGGGGAAACTGGATCACGGGCTTTCCTGCTCACAGCGGCC
61 TCAAACCTAGTTTCGACTTAACTTCGATCGACTCGAGTGTTTTATACGAATAACCGTCGG
121 TTTATTTCAAAAAATGCTGTGCTTAACTCGCCTTATGATGGATTGAGGTACTGAGTTTGT
181 GTTTTAAGTGGTTTTTCAGTGTTTCGATTCAGTGTTCAAGTTGACAGTTTATCTCATGGTGG
241 TCGTGGAGAGTGCTGGCTGAATCACGCTGGTCTCATACTCCGTGCTTTACAACATCCT
301 AAAGTGTAGGTACCTACTTGTGCAAAGTTTACATGTGAAGTGTGGTTTTGGAAAGTTA
361 TACGTAGACGTCCATAACCCAGTGAGTGTGTTAATTGTTGTGATTTCAGGAACATACGCAA
421 GGATTGAGATTGACATAAAAATTGGCTTCAAAAACAACACAGGAGACCGGGAGCTCAGACAA
481 GAGCAATGGTATGAAGGAACCGGGATCTCTGAGGAATTGCTGGGGGAAGGGGTGGAGCT
1 M K E P G S P E E L L G E G V E L
541 GACGCTGGGCGAGCTGCGGCCATGGCGCTCCGGCAGCAGCAGATCGACACGCAACA
18 T L G E L R A M A L R Q Q Q Q I D T Q H
601 CCAGTCTGTGCGCTAAGGAACAGAGGCTACGGTACCTGAAGCAGCAGGAGGCACGGCA
38 Q L L C A K E Q R L R Y L K Q Q E A R Q
661 ACATCAGGTGGCGGTAGAGGGCGAGCGGCTGCGGCGGCTGCGCGAGCGGTGGAGGCGCA
58 H Q V A V E G E R L R R L R E R V E A Q
721 AGAGTTGAAGTTGCGCCGCATGGAGGAGCGAAAGATATTGAAAATTACAAGGAACACAT
78 E L K L R R M E E R K D I E N Y K E H I
781 CCCTTTTCTGTTGCCAGCCAGCGACCTCGAGTCGATCCGCGCGCTGTTCAATGAGAAGGA
98 P F L L P A S D L E S I R A L F N E K E
841 GAAGGAGCTGTGGTGGCGGTGGCCAAGGTGGAGGAGCTGACGAGACAGCTGGAGGAGCT
118 K E L S V A V A K V E E L T R Q L E E L
901 GCGCCGCGGCCGGCCAGCAGCGCGCCGCCCGCGCACGAGCTTGACAACTTAGGAG
138 R R G R A S S A P P P A H E L D K L R R
961 GGAACCTATGTACCGCAACAACTGAACGAGCAGCAGAACGGGCGGCTGTCTGCGCAGCG
158 E L M Y R N K L N E Q Q N G R L S A Q R
1021 CGCGGCGCTGGGCGTGCACAAGAGGAGATGCGGAATAACAATATTTAAGCACTCATCT
178 A A L G V R Q E E M R N K Q Y L S T H L
1081 CATCGGCATAGACAACAACCGCAACAGAGGACAAAACAACCAACGCCGATGCAACAGTT
198 I A H R Q Q P Q Q R T N N P T P M Q Q L
1141 GCCTAATCAACAGTGAAGCAATGGAATAAGCAGTCAACCAAGAAGCAACAAAC
218 P N Y P T S G S N G I S S Q P K K Q Q T
1201 GCGGGGAAATATCGCCGCTGTCGAGCATTATAACCACGTGCGCCACGCTCAGAGCATCAG
238 R G N I A A V E H Y N H V R H A Q S I S
1261 CCATAACCAGAATTTCCAGGCGTTAAAGCAGAACGTAATACAAAATAACGTGCCATTGAA
258 H N Q N F Q A L K Q N V I Q N N V P L K
1321 ACAGCTAACACAACCGGACAATATCAAAGCCATTTAACACAACAAGAAGCGCATTATCT
278 Q L T Q P D N I Q S H L T Q Q E A H Y L
1381 ACAACAGAAACAAATGATAAACCCACTGTATAACGGTGGCTACAACAACTTACCTCCGGG
298 Q Q K Q M I N P L Y N G G Y N N L P P G
1441 AATTCAGGACAGCCAGTATCAAGGGCAATATCCAAACAAACATGCAGATATCAACTCCTT
318 I Q D S Q Y Q G Q Y P N K H A D I N S F
1501 TAGTCACGTTCAACAGGGAATCAGCAATGCATACGACCAGAAAGCCATGTTTGAACATAT
338 S H V Q Q G I S N A Y D Q K A M F E H I
1561 AAATAAGTATCCTGATTATCCGAAACAACCACAATACAGCCCTAACAGTACAAGTAGTTG

358 N K Y P D Y P K Q P Q Y S P N S T S S C
1621 TAACAGTAACCAAAATGGAAAGGAACTAAAATAAATGAACAAGAGTTCTTACCTGAATT
378 N S N Q N G K E L K I N E Q E F L P E F
1681 TGCGGCCAGCAAATCGGACCCGAAGTATCAGACGTTGCCATATAACACTAAGTTCCCACA
398 A A S K S D P K Y Q T L P Y N T K F P Q
1741 AAATGCTACAGGTAATAAAAACAAGATGATAATAGTAAAAACAGTAATGAGTTGAGTCA
418 N A T G K I K Q D D N S K N S N E L S Q
1801 AGAGAGCAAAAACCAGAATCAGAATGCAGCCAACATAAATCACATGACGGTGCATTCTAC
438 E S K N Q N Q N A A N I N H M T V H S T
1861 GCCCCTGTCCGTGGTGAACAAGAGTCTAGCCACACCTCTAAGTCAAACAGAAGCAACATA
458 P L S V V N K S L A T P L S Q T E A T Y
1921 TCAACAGGACCAGAACACATATCAATTGCAGAAATCTGACTCTTCAAGTAGATGTAACCA
478 Q Q D Q N T Y Q L Q K S D S S S R C N Q
1981 AGAGGGTAAAGAGAATCAAGCATATCCACAAAACAATAGGCTAAGTCAGAGTAACAGTAC
498 E G K E N Q A Y P Q N N R L S Q S N S T
2041 AGAAGGATCCAAGAGCAATGGCACAAAGAGCCAACAGGGTAGCACAATACTGAAAGGCAG
518 E G S K S N G T K S Q Q G S T I L K G S
2101 TTCACCGAGTCTCGCTCAAACGGGCAGCAGTAGCTCTTTAAGATTGGAAAGCCCGTGT
538 S P S L A Q T G S S S S L R F G K P V S
2161 GAGTGTGGCACCCTACTACGGTGCAGGTGTCCAGCGGCCTCCGGTGCAGTTCCAGCGGTG
558 S V A P T T V Q V S S G L R C S S S G R
2221 ACCGTCACCCATTTACCAGACATCCTCCACAAAATCCAACCTGTCCAACCACAACTGT
578 P S P I Y Q T S S T K I Q P V Q P Q T V
2281 TCAAACATCTGTACAAAACCTCATCTAATATCATAAACCCAGTAGCGAGTAACCCGGTTGT
598 Q T S V Q N S S N I I N P V A S N P V V
2341 CTCCCAACCCAGATTGTTAGGAACACAGCCTCGGGACTGTCTTCGAGTGCTTCAGCTTT
618 S Q P Q I V R N T A S G L S S S A S A F
2401 CGGTCAGAAATGCGTCGTCTCAGAGTATCTTGCTGTCTCCTCCGAAAAGTGCCAGTACCC
638 G Q N A S S Q S I L L S P P Q S A S T P
2461 CTTGTCTACCTGTGCAACGCCTGATGTTAGTGGCACTGACAAGTCCCCAAGCCCGCACT
658 L S T C A T P D V S G T D K S P K P A L
2521 ACCTCCTAAGCCGACAATCAAGACGCCGCCGACAATCAGCCAACAATGACACCAATTT
678 P P K P T I K T P P R Q S A N N D T N F
2581 CCAGGCTAAGGACCAGGACACAGCGCTACCCACGCTTCCATACCAGACAACCTCATCCAA
698 Q A K D Q D T A L P T L P I P D N S S N
2641 CGACAGCGACAACCCATCCCGGGACCAACAACGAAATGATCATCAAAGCGAGGCCGCT
718 D S D N P S R D T N N E M I I K A R P L
2701 CACCATACGAAAACCCCCCTAAGCGAACAGCCCAAACTAAGAAACATGAATACCACCAA
738 T I R K P P L S E Q P K L R N M N T T K
2761 AAACGGTATCAGTGTAAGCATCAACAGACGCATCGAAATGCCTCCAGCGTTCTTATCCC
758 N G I S V S I N R R I E M P P A F L F P
2821 TGAATGGACCACCTAACGAGGGAGCGCCTAGCGAGAACGGCCTAATTCAGAAGAGGGA
778 E M D H L T R E A P S E N G L I Q K R D
2881 CGAAGTAGATAAGGCTTTAAATAATAATGTAGATGTAATTTCTAATGAGAAGATGGAGGA
798 E V D K A L N N N V D V I S N E K M E E

2941 GGGCAAGGAAGTGTGACCTTAGTGTCTGATGTGACGGAACAGATTAGTTCTGTGGATCT
 818 G K E V S T L V S D V T **E Q I S S V D L**
 3001 AAACGGTCAAGATGGTCAGTTGGGTGACAATGTTCTCAGGCGGTCTAAGAAAGGCAATCT
 838 **N G Q D G Q L G D N V L R R S K K G N L**
 3061 GAAGCAAGGCGGAAGGCGCCTCTTACTAGAAGAGTCAGCTTTGATCCCTGGCGTTGCT
 858 **K Q G G K A P L T R R V S F D P L A L L**
 3121 TCTTGATGCGAGTTTAGAAGGAGAGTTGGAGCTTGTCAAGAAAAGTCTACTCAGGTCCA
 878 **L D A S L E G E L E L V K K T A T Q V Q**
 3181 AAACGCCAGCGCAGCCAATGATGAAGGAATCACAGCTCTACACAACGCCATCTGCGCCGG
 898 **N A S A A N D E G I T A L H N A I C A G**
 3241 ACACCTTTGAGATCGTCAAGTTCCTAGTGGAGCTGGGGTGGCAGCTGAACGCGCAGGACTC
 918 **H F E I V K F L V E L G C D V N A Q D S**
 3301 GGACGGCTGGACGCCGCTGCACTGCGCCGCTCCTGCAACAACCTGCCATCGTGGCGTT
 938 **D G W T P L H C A A S C N N L P I V R F**
 3361 CCTCGTGCAGCACGGAGCGTGTATATTCGCGACGAGCTGTCCGACCACGAGACGGCGGC
 958 **L V E H G A C I F A T T L S D H E T A A**
 3421 CGAGAAGTGTGAAGAGGACGAGGAAGTTTCGACGGCTGCTCCGAGTACTTATACAGCAT
 978 **E K C E E D E E G F D G C S E Y L Y S I**
 3481 CCAAGAAAAGTCTGGCATAATGAACGGCGGCACAGTCTACGCCGCTCTCCCTACTCCGC
 998 **Q E K L G I M N G G T V Y A V F P Y S A**
 3541 AGCGCGAAGCGACGAGCTCACCTTCAGCGCGGGCACAAGACTACAGGTGCTGAGGAAGGG
 1018 **A R S D E L T F S A G T R L Q V L R K G**
 3601 AGACGACAGCGAGCGAGTGGTGGTGGAGCCGCGAGTGGGGCCGAGGGGTACGCGCC
 1038 **D D S E R E W W W S R A S G A E G Y A P**
 3661 CAGGAACCTGCTGGGGTTATATCCAAGAGTAACCCGAAGCAGGATTGAGCACATCTGAA
 1058 **R N L L G L Y P R V T P K Q D ***
 3721 GCAGATCAAATGACCTGAGAGGCGGTTCCGTTAATTTACAACATTAATTAATACTTGCC
 3781 CTAGAAATCATTTCGGAATAATGTTTCGCCGAGGTTTTAGTAGTTAGTAAATTCATCTA
 3841 ACTGTAGTAAAGGTGAGTTTCTTGAACCAAAGTATCTGTTTATTCTGTTTTTCGAATATG
 3901 ATCGGTAAGTATCCATAATTTAAGCAAATAAATTAATGGAATTTGCCTATCTGATAGTGT
 3961 AAATAGTCTTTATTTTAACTATGTATTTATAACATTGTTATGTAAGCCTAGGCATTG
 4021 TACACAGTATATCAGATCTAATATTTTGTAAATATTTAAAAAGTAAGTGCAAAATGATGA
 4081 GATTATATTGTATATTTTATAAATACGAGTCATCTTAAAATACAAAATGGTTATAGAAT
 4141 TTGTATATTATAGGGTTTCTGCAATATTGTGAGATATTATACATAAATCGACATAAATA
 4201 TAAGATTTAGATCCACAAAAACACCAAAAAACAAACAGTCCGCTGCGCTGTGTAGA

Supplemental Figure S2. Deduced amino acid and sequences of *Px-aspp2* in DBM, collected from Fuzhou. Numbers on the left of each row represent nucleotide position or amino acid. The black-boldded sequence represents the beginning codon (ATG) and the ending codon (TGA). In order, respectively, three separate grey areas were represented: a coiled coli region, a ARD(ankyrin repeat domain)domain , a SH3 domain.

