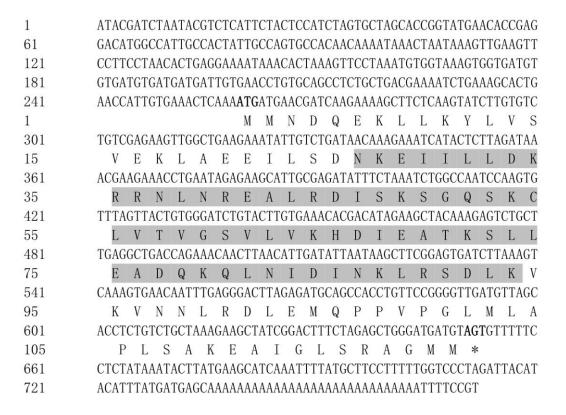
Cloning of *Px-pdrg* and *Px-aspp2* and mRNA expression under heat stress in insecticide-resistant and -susceptible diamondback moth, *Plutella xylostella* (Lepidoptera: Plutellidae)

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Supplemental Figure S1. The amino acid sequence and nucleotide sequence of *Px-pdrg* 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.

AGTCTCACGCAGAGTACATGGGGGAAACTGGATCACGGGCTTTCACTGCTCACAGCGGCC TCAAACTTAGTTTCGACTTAACTTCGATCGACTCGAGTGTTTTATACGAATAACCGTCGG TTTATTTCAAAAAATGCTGTGCTTAACTCGCCTTATGATGGATTGAGGTACTGAGTTTGT GTTTTAAGTGGTTTCAGTGTTCGATTCAGTGTTCAAGTTGACAGTTTATCTCATGGTGG ${\sf TCGTGGAGAGTGCTGGCTGAATCACGCTGGTCCTCATACCTCCGTGCTTTACAACATCCT}$ AAAGTGTAGGTACCTACTTGTGCAAAGTTTACATGTGAAGTGTTTGGTTTTGGAAAGTTA TACGTAGACGTCCATACCCAGTGAGTGTGTTAATTGTTGTGATTCAGGAACATACGCAAA GGATTGAGATTGACATAAAATTGGCTTCAAAACAACACAGGAGACCGGGAGCTCAGACAA GAGCAATGGT**ATG**AAGGAACCGGGATCTCCTGAGGAATTGCTGGGGGAAGGGGTGGAGCT M K E P G S P E E L L G E G V E L GACGCTGGGCGAGCTGCGCCATGGCGCTCCGGCAGCAGCAGCAGATCGACACGCAACA T L G E L R A M A L R Q Q Q I D T Q H Q L L C A K E Q R L R Y L K Q Q E A R Q H Q V A V E G E R L R R L R E R V E A Q AGAGTTGAAGTTGCGCCGCATGGAGGAGCGCAAAGATATTGAAAATTACAAGGAACACAT E L K L R R M E E R K D I E N Y K E H I CCCTTTTCTGTTGCCAGCCAGCGACCTCGAGTCGATCCGCGCGCTGTTCAATGAGAAGGA P F L L P A S D L E S I R A L F N E K E GAAGGAGCTGTCGGTGGCCGTGGCCAAGGTGGAGGAGCTGACGAGACAGCTGGAGGAGCT K E L S V A V A K V E E L T R Q L E E L GCGCCGCGGCCGGCCAGCAGCAGCGCGCCGCCGCACGAGCTTGACAAACTTAGGAG R R G R A S S A P P P A H E L D K L R R GGAACTTATGTACCGCAACAAACTGAACGAGCAGCAGAACGGGCGGCTGTCTGCGCAGCG E L M Y R N K L N E Q Q N G R L S A Q R CGCGGCGCTGGGCGACAAGAGAGAGATGCGGAATAAACAATATTTAAGCACTCATCT A A L G V R Q E E M R N K Q Y L S T H L CATCGCGCATAGACAACCGCAACAGGGACAAACAACCCAACGCCGATGCAACAGTT I A H R Q Q P Q Q R T N N P T P M Q Q L GCCTAACTATCCAACCAGTGGAAGCAATGGAATAAGCAGTCAACCAAAGAAGCAACAAAC PNYPTSGSNGISSQPKKQQT GCGGGGAAATATCGCCGCTGTCGAGCATTATAACCACGTGCGCCACGCTCAGAGCATCAG R G N I A A V E H Y N H V R H A Q S I S CCATAACCAGAATTTCCAGGCGTTAAAGCAGAACGTAATACAAAATAACGTGCCATTGAA H N Q N F Q A L K Q N V I Q N N V P L K ACAGCTAACACAACCGGACAATATTCAAAGCCATTTAACACAACAAGAAGCGCATTATCT Q L T Q P D N I Q S H L T Q Q E A H Y L ACAACAGAAACAAATGATAAACCCACTGTATAACGGTGGCTACAACAACTTACCTCCGGG Q Q K Q M I N P L Y N G G Y N N L P P G AATTCAGGACAGCCAGTATCAAGGGCAATATCCAAACAACATGCAGATATCAACTCCTT I Q D S Q Y Q G Q Y P N K H A D I N S F TAGTCACGTTCAACAGGGAATCAGCAATGCATACGACCAGAAAGCCATGTTTGAACATAT S H V Q Q G I S N A Y D Q K A M F E H I AAATAAGTATCCTGATTATCCGAAACAACCACAATACAGCCCTAACAGTACAAGTAGTTG

1

61

121

181

241

301

361 421

481

1 541

18

601

38

661

58 721

78

781

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841

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901

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961

1581021

178

1081 198

1141

218

1201

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1261

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1321 278

1381 298

1441

318

1501

338 1561

N K Y P D Y P K Q P Q Y S P N S T S S C TAACAGTAACCAAAATGGAAAGGAACTTAAAATAAATGAACAAGAGTTCTTACCTGAATT N S N Q N G K E L K I N E Q E F L P E F TGCGGCCAGCAAATCGGACCCGAAGTATCAGACGTTGCCATATAACACTAAGTTCCCACA A A S K S D P K Y Q T L P Y N T K F P Q AAATGCTACAGGTAAAATAAAACAAGATGATAATAGTAAAAACAGTAATGAGTTGAGTCA N A T G K I K Q D D N S K N S N E L S Q AGAGAGCAAAAACCAGAATCAGAATGCAGCCAACATAAATCACATGACGGTGCATTCTAC E S K N Q N Q N A A N I N H M T V H S T GCCCTGTCCGTGGTGAACAAGAGTCTAGCCACACCTCTAAGTCAAACAGAAGCAACATA P L S V V N K S L A T P L S Q T E A T Y TCAACAGGACCAGAACACATATCAATTGCAGAAATCTGACTCTTCAAGTAGATGTAACCA Q Q D Q N T Y Q L Q K S D S S S R C N Q AGAGGGTAAAGAGAATCAAGCATATCCACAAAACAATAGGCTAAGTCAGAGTAACAGTAC E G K E N Q A Y P Q N N R L S Q S N S T AGAAGGATCCAAGAGCAATGGCACAAAGAGCCAACAGGGTAGCACAATACTGAAAGGCAG E G S K S N G T K S Q Q G S T I L K G S TTCACCGAGTCTCGCTCAAACGGGCAGCAGTAGCTCTTTAAGATTTGGAAAGCCCGTGTC S P S L A Q T G S S S S L R F G K P V S GAGTGTGGCACCCACTACGGTGCAGGTGTCCAGCGGCCTCCGGTGCAGTTCCAGCGGTCG S V A P T T V Q V S S G L R C S S S G R ACCGTCACCCATTTACCAGACATCCTCCACCAAAATCCAACCTGTCCAACCACAAACTGT P S P I Y Q T S S T K I Q P V Q P Q T V TCAAACATCTGTACAAAACTCATCTAATATCATAAACCCAGTAGCGAGTAACCCGGTTGT Q T S V Q N S S N I I N P V A S N P V V $\tt CTCCCAACCCCAGATTGTTAGGAACACAGCCTCGGGACTGTCTTCGAGTGCTTCAGCTTT$ S Q P Q I V R N T A S G L S S A S A F ${\sf CGGTCAGAATGCGTCTCAGAGTATCTTGCTGTCTCCTCCGCAAAGTGCCAGTACCCC}$ G Q N A S S Q S I L L S P P Q S A S T P $\tt CTTGTCTACCTGTGCAACGCCTGATGTTAGTGGCACTGACAAGTCCCCCAAGCCCGCACT$ L S T C A T P D V S G T D K S P K P A L ACCTCCTAAGCCGACAATCAAGACGCCGCCGCGACAATCAGCCAACAATGACACCAATTT P P K P T I K T P P R Q S A N N D T N F Q A K D Q D T A L P T L P I P D N S S N CGACAGCGACAACCCATCCCGGGACACCAACAACGAAATGATCATCAAAGCGAGGCCGCT D S D N P S R D T N N E M I I K A R P L CACCATACGAAAACCCCCCCTAAGCGAACAGCCCAAACTAAGAAACATGAATACCACCAA T I R K P P L S E Q P K L R N M N T T K AAACGGTATCAGTGTAAGCATCAACAGACGCATCGAAATGCCTCCAGCGTTCTTATTCCC N G I S V S I N R R I E M P P A F L F P TGAAATGGACCACCTAACGAGGGAGGCGCCTAGCGAGAACGGCCTAATTCAGAAGAGGGA E M D H L T R E A P S E N G L I Q K R D CGAAGTAGATAAGGCTTTAAATAATAATGTAGATGTAATTTCTAATGAGAAGATGGAGGA E V D K A L N N N V D V I S N E K M E E

358

1621 378

1681

398

1741

418

1801 438

1861

458 1921

478

1981

498

2041 518

2101

538

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678 2581

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2641 718

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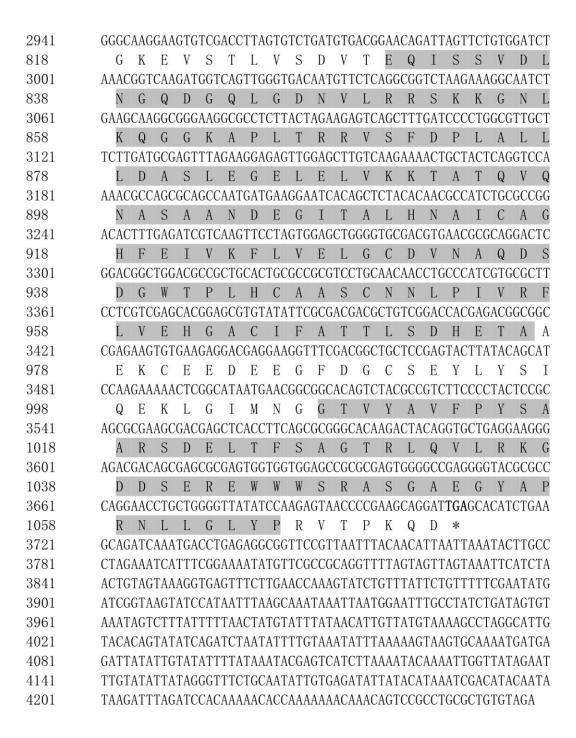
2761

758

2821

778 2881

798



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-bolded 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.