

A

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Dazao : ACTCAGACAGTCTTCAAATCACCTGAACATTACAAAAATGAAATTCCTGATTCTCCTCCCGCTCCCGCTCCCGTCCCG : 79
Dazao-stony : ACTCAGACAGTCTTCAAATCACCTGAACATTACAAAAATGAAATTCCTGATTCTCCTCCCGCTCCCGCTCCCGTCCCG : 79
ACTCAGACAGTCTTCAAATCACCTGAACATTACAAAAATGAAATTCCTGATTCTCCTCCCGCTCCCGCTCCCGTCCCG

0 * 100 * 120 * 140 * 1
Dazao : AAGCCCGGACCTCTCCACATCCCAAGTCTGACGAGTACGCCCGCCCAAGTGGTCAAATCCACCTACGACATCACCCCT : 158
Dazao-stony : AAGCCCGGACCTCTCCACATCCCAAGTCTGACGAGTACGCCCGCCCAAGTGGTCAAATCCACCTACGACATCACCCCT : 158
AAGCCCGGACCTCTCCACATCCCAAGTCTGACGAGTACGCCCGCCCAAGTGGTCAAATCCACCTACGACATCACCCCT

60 * 180 * 200 * 220 *
Dazao : GAAGCCCACTTCCAGTCAACTACGAGACCCGCAACCGAATTTACGCCACCGCTGAAGGTCCCGTCAAGCAACCTCAACT : 237
Dazao-stony : GAAGCCCA-----GTCCCGTCCAGCAAG----- : 181
GAAGCCCA GT CCGT AG A G

240 * 260 * 280 * 300 *
Dazao : CAGAAATACCCCGCCATCGAAGTTAAGCGTCCCTACAAGTACACTTCCCGTGACGGACAACCCATCGACCTCCCGTACCT : 316
Dazao-stony : --CAATACCCCGCCATCGAAGTTAAGCGTCCCTACAAGTACACTTCCCGTGACGGACAACCCATCGACCTCCCGTACCT : 258
CAATACCCCGCCATCGAAGTTAAGCGTCCCTACAAGTACACTTCCCGTGACGGACAACCCATCGACCTCCCGTACCT

320 * 340 * 360 * 380 *
Dazao : CCCTCACCAGAACCGTTACCAACCCGAGGGAACCCATCTCCCGACCCCTCACCCAATTCCCGAGCCGATCCCGCCCGCT : 395
Dazao-stony : CCCTCACCAGAACCGTTACCAACCCGAGGGAACCCATCTCCCGACCCCTCACCCAATTCCCGAGCCGATCCCGCCCGCT : 337
CCCTCACCAGAACCGTTACCAACCCGAGGGAACCCATCTCCCGACCCCTCACCCAATTCCCGAGCCGATCCCGCCCGCT

400 * 420 * 440 * 460 *
Dazao : CTTCCCTACATCGAGCCCAACCCCGGACCCCTCCCGTCTGGAAGAAAAGTCTCCGCAACTTGTAGGATAAGTCA : 474
Dazao-stony : CTTCCCTACATCGAGCCCAACCCCGGACCCCTCCCGTCTGGAAGAAAAGTCTCCGCAACTTGTAGGATAAGTCA : 416
CTTCCCTACATCGAGCCCAACCCCGGACCCCTCCCGTCTGGAAGAAAAGTCTCCGCAACTTGTAGGATAAGTCA

480 * 500 * 520 * 540
Dazao : AGACAACAACATACCCCACTACTACAAACGAAACTGACATAATGTACGAAATAAACTGTTGATTTAATTTT : 547
Dazao-stony : AGACAACAACATACCCCACTACTACAAACGAAACTGACATAATGTACGAAATAAACTGTTGATTTAATTTT : 489
AGACAACAACATACCCCACTACTACAAACGAAACTGACATAATGTACGAAATAAACTGTTGATTTAATTTT

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B

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P. xylostella : MKTI I MLALVAVAFAPCA- - - - PTEPI PL LRGESI SFDGS- YSWAYETGNGI SA'DEKGSLKNI CAEEPAL EVCCGF : 73
S. frugiperda : MKFLVVLTVAVACASADVSHVVK- DDFHAPI ESSSFDI EPGGD- FKYSFKTGNGI YAEESGVLKNANSDYPSLDVSCGF : 77
S. cynthia ricini : MKFLVVLAVAVACASADVSHVVRQDEYVAPI VKSSYDI TPEGN- FCYNFETGNGI YAAADGVKDFNSEYPSLEIKGAY : 78
B. mori : MKFLI VLAVAVACASADVSHI AKSDEYAAPVKSSYDI TPEGH- FCFNYETGNGI YACAECVAVKNVNSEYPAL EVKGAY : 78
M. sexta : MKFLVVLAVAVACASADVSHI VK- DEASAPVLKSSYDI SPEGN- FCYLYETGNGI VACADGSKVKNVNSEYPAVGI VCGY : 77
P. polytes : MKFLVLFVAV- VALASADVSHI VRTDEYCAPI I KSSYADFPVGN- FCYEYETGNGI AACAGGVVKNVNSEAATLEVKGSV : 77
P. xuthus : MKFLVLFVAV- VALASADVSHI VRSDESCAPI LKSA'ESSSPEGN- YCYVYETGNGI SACAEGVKNANSESATLEVKGSV : 77
D. plexippus : MKFLVVLAVWAYVSAEYKY- - - - DESAASI VKSS'DSSPEGNFSYGFESNNGI I SCAECVKNVNSGENPAL EVKGSV : 75
H. melpomene : MKFLVVLAVAVACAADVSHI VRSDESCAPI VKSA'EI SPEGHSFCYAYETANGI YSEADGVLKNVNSDYPAL EVKGSV : 79
MkF 666l a va a adv h de ap6 s P G 5 5 5e3gNGI a a G 6K1 nse p 6e6 G

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P. xylostella : AYPSEDGCGN CLTYI ANENGFPCQCAHLPTPPP I PEALCFALAYLATAPPQPE SRR : 129
S. frugiperda : KYTSPECCAL ELSYADENGYRPGGSHLPVGPPEI PAAL I RSL EYI AAHPSPA E V R : 133
S. cynthia ricini : KYTAPDGTPEVETTYI AXENGYCAGSGSHLPVGPPEI PEYI ARSLAYI AAHTFCQVAPEV : 134
B. mori : KYTSPDCCPI DLAYVADENGYCPCGSHLPVGPPEI PEALARALAYI EAHPSPSV E : 134
M. sexta : KYTAPDGCVM DVVYKADENGYCPCGSHLPVAPPTPEPI LRALAWI AAHPPAVEKVA : 133
P. polytes : RYTSPDGTPVETTYI VADENGYCAGGSHI PVPPPEI PELI LRSLQYI AEHPPAEYK : 133
P. xuthus : RYTAPDGTPEVETTYI ADENGYCAGGSHI PVPPPI PELI LRSLQYI ADHPPAEYK : 133
D. plexippus : KYNAPDGTPELVVYVADENGYCAGSGSHI PVPPPI PELI LRSLQYI AEHPAPVERV : 131
H. melpomene : KYNAPDGTPEVSLQVADENGYCAGSGSHI PCPPPI PELI LRSLQYI ESHPPAVERV : 135
Y pdG 6 5 A EN5q GsH6P p i Pe I R L 56a hpp e

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**Figure S3** Sequence characteristics of *BmorCPR2* between Dazao and Dazao-stony. A. Full-length cDNA sequences of *BmorCPR2* between Dazao and Dazao-stony. B. Alignment of *BmorCPR2* and orthologs among nine Lepidoptera species. The orthologs were identified using BLAST (blastp and tblastn), known genomes or EST databases of selected Lepidoptera insects, NCBI, CuticleDB (<http://bioinformatics.biol.uoa.gr/cuticleDB> and OrhtoDB (<http://cegg.unige.ch/orthodb6>). Sequence alignment using Muscle program (<http://www.ebi.ac.uk/Tools/msa/muscle/>), is listed as follows: *Bombyx mori* BmorCPR2, *Papilio polytes* CPR2, BAM18876.1, *Papilio xuthus* CPR2, BAG30800.1, *Danaus plexippus* EHJ77392.1, *Manduca sexta* Msex000162-RB, (Manduca base), *Heliconius melpomene* HMEL002550-PA, (Heliconius Genome Project), *Samia cynthia ricini* I10A02NGRL0007\_H08 (SilkBase), *Plutella xylostella* Px003256.1 (Diamondback moth Genome Database), *Spodoptera frugiperda* Sf1P23819-5-1, (SPODOBASE). The black line represents the RR1 motif.