

Table S1 **Primers used in supplementary experiments.**

Primer	Sequence (from 5' to 3')	Purpose
<i>QCecropin</i> F	GGCAAGAAAATTGAGCGGGT	qRT-PCR
<i>QCecropin</i> R	CCTTCAATGTTGCTGCCACA	qRT-PCR
<i>QAttacinA</i> F	GTGGCAACCTTAATTGGGCG	qRT-PCR
<i>QAttacinA</i> R	AGATTGGAAGTTGCGCCGTA	qRT-PCR
<i>QAttacinB</i> F	ACACGCTTGGACTTGACAGG	qRT-PCR
<i>QAttacinB</i> R	ATGAGTCAATCCCAAGCCGG	qRT-PCR
<i>QAttacinC</i> F	GAGTTGGCCGGTAGAGCAAA	qRT-PCR
<i>QAttacinC</i> R	GTAGTCGCGTTGTCCACTCA	qRT-PCR

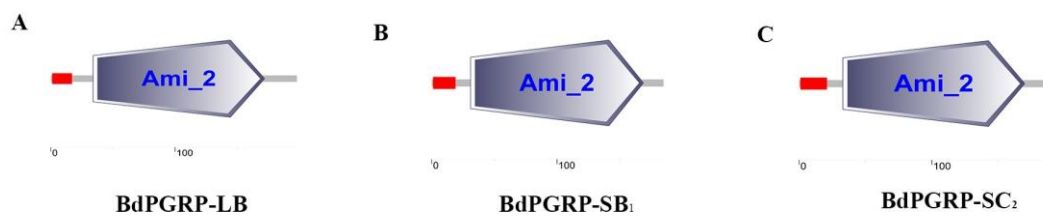


Figure S1. **Prediction of BdPGRPs' functional domains.** (A) PGRP-LB, (B) PGRP-SB₁, (C) PGRP-SC₂. Signal peptides are shown in red boxes. Ami₂ indicates amidase domain.

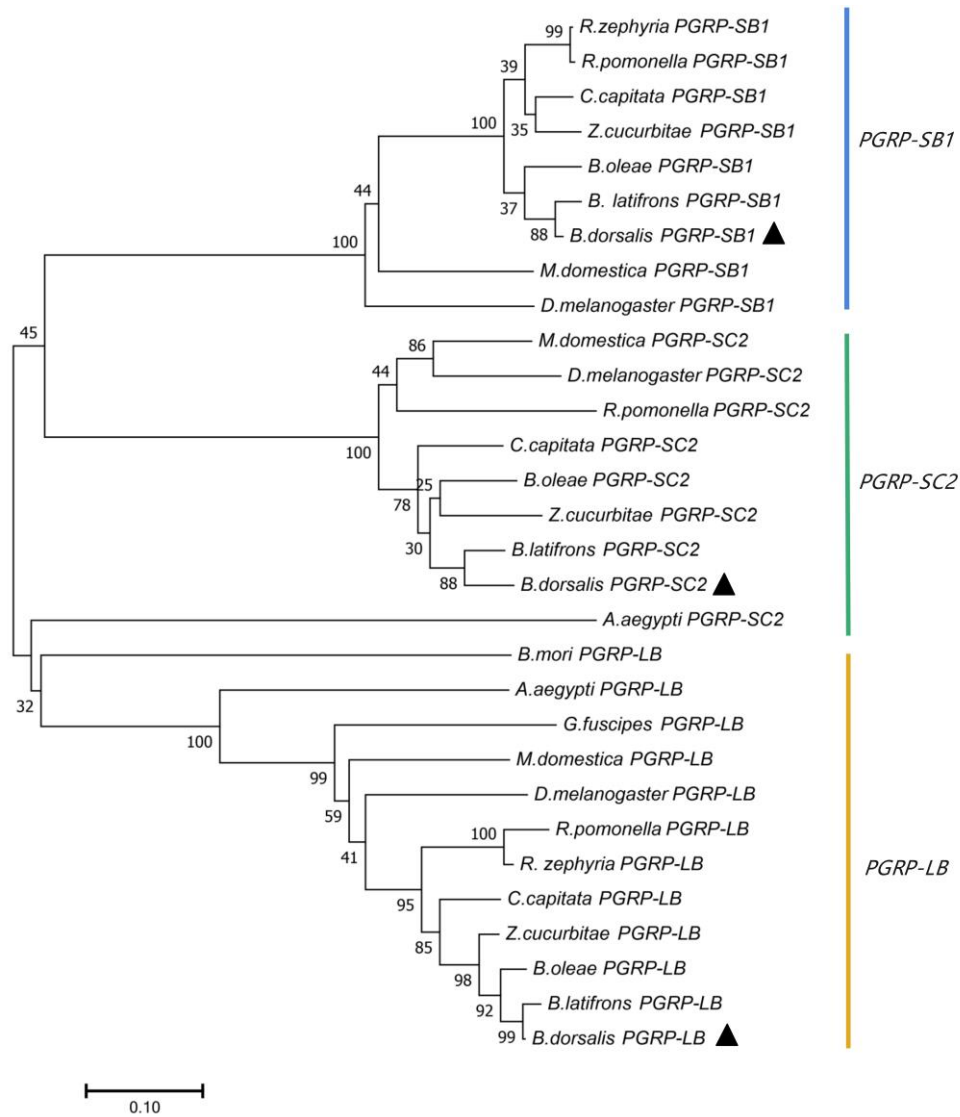


Figure S2. **Phylogenetic tree of peptidoglycan recognition proteins of *B. dorsalis* and other insects.** The genetic distance in phylogenetic neighbour-joining tree was calculated using the Kimura two parameter models. The result repeatability of NJ tree was validated through 1000 bootstraps. The numbers above the branches indicate the percentages of times that the species are grouped together in the bootstrap trees. The scale bar indicates the number of substitutions per site for a unit branch length. *BdPGRP-LB*, *BdPGRP-SB₁*, and *BdPGRP-SC₂* were aligned with *Bactrocera latifrons* PGRP-LB (XP_018789449.1), *Bactrocera oleae* PGRP-LB (XP_014091181.2), *Zeugodacus cucurbitae* PGRP-LB (XP_011197144.1), *Ceratitis capitata* PGRP-LB (XP_004518089.1), *Rhagoletis zephyria* PGRP-LB (XP_017470705.1), *Rhagoletis pomonella* PGRP-LB (XP_036322481.1), *Aedes aegypti* PGRP-LB (XP_021709443.1), *Drosophila melanogaster* PGRP-LB (NP_731575.1), *Bombyx mori* PGRP-LB (XP_012548100.1), *Musca domestica*

PGRP-LB (XP_005180889.1), *Glossina fuscipes PGRP-LB* (ACI22620.1), *B. latifrons PGRP-SB* (XP_018789286.1), *B. oleae PGRP-SB* (XP_014099773.1), *Z. cucurbitae PGRP-SB* (XP_011181375.1), *C. capitata PGRP-SB* (XP_004537949.1), *R. zephyria PGRP-SB* (XP_017486043.1), *R. pomonella PGRP-SB* (XP_036336342.1), *D. melanogaster PGRP-SB* (CAD89135.1), *M. domestica PGRP-SB* (NP_001295929.1), *B. mori PGRP-SB* (XP_004929843.1), *B. latifrons PGRP-SC₂* (XP_018798904.1), *B. oleae PGRP-SC₂* (XP_014085196.2), *C. capitata PGRP-SC₂* (XP_004520319.1), *Z. cucurbitae PGRP-SC₂* (XP_011180165.1), *R. pomonella PGRP-SC₂* (XP_036334551.1), *M. domestica PGRP-SC₂* (XP_005184140.3), *D. melanogaster PGRP-SC₂* (CAD89184.1), *A. aegypti PGRP-SC₂* (XP_011492940.1), and *B. mori PGRP-SC₂* (XP_004929814.1).

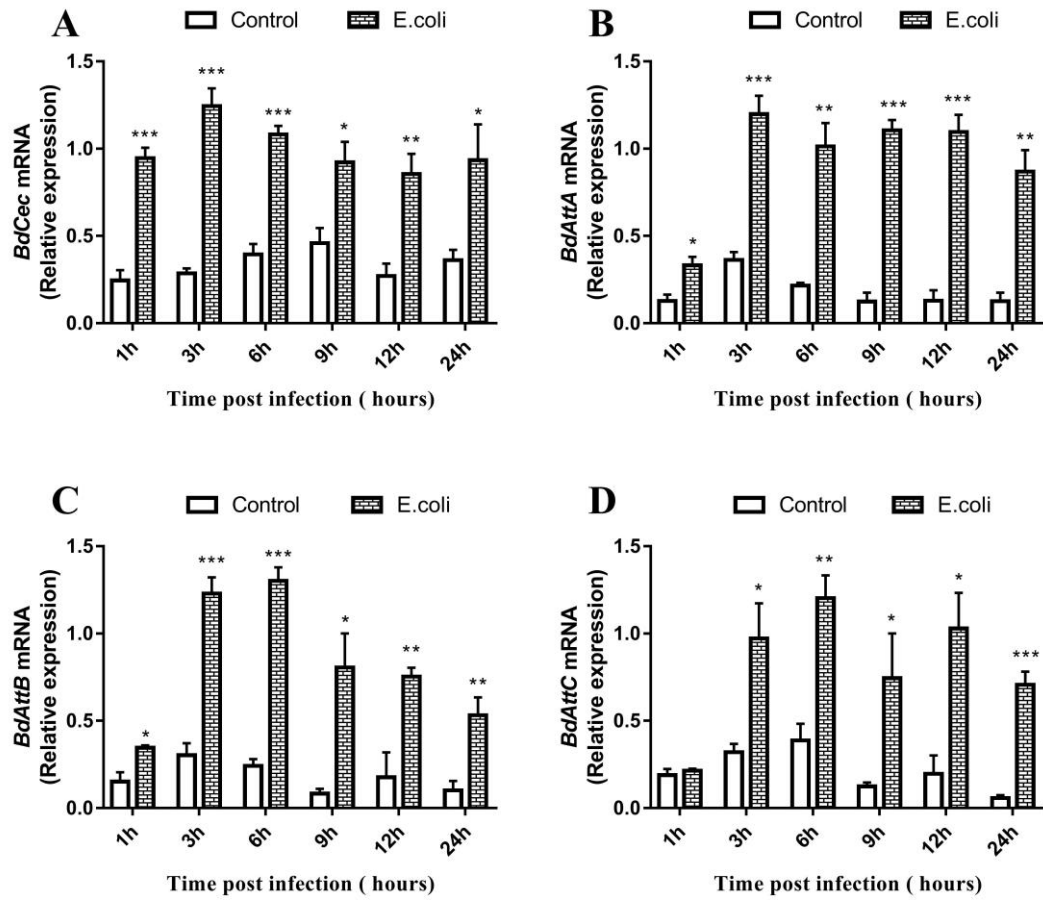


Figure S3. Expression levels of AMPs in Imd pathway after *E. coli* challenge. The expressions of (A) *Cecropin*, (B) *AttcinA*, (C) *AttcinB*, and (D) *AttcinC* in *B. dorsalis* were measured by qRT-PCR. The control was inoculated with LB medium. All error bars represent the SEM of the mean of three independent biological replicates. Statistical analysis was based on Student's t-test. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; NS, no significant difference ($P > 0.05$).