



Supplementary materials

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1   M G V P A G N A E N G K K I F V Q R C A T C A
61  CAGGCCACACTGTTGAAGCTGGCAACACAAAGTAGGACAGAACATCTACATGGATTC
21  Q C H T V E A G G K H K V G Q N L H G F
121 TTTGGCCGAAAAACTGGCCAGGCTGCAGGATTCTCATACTCGATGCCAATAAGCTAAG
41  F G R K T G Q A A G F S Y S D A N K A K
181 GGCATTACATGGAATGACGACACTCTCTTTGAATATCTTGAGAATCCCAAGAAATACATC
61  G I T W N D D T L F E Y L E N P K K Y I
241 CCTGGAACCAAGATGGTGTGACTCAAGAAGGAAATGAGCGTGCTGACCTTATT
81  P G T K M V F A G L K K A N E R A D L I
301 GCCTATCTCAAATCTGCTACCAAGTAAttttaaagtaatagaaaattccataagaagcat
101 A Y L K S A T K *
tttccataacatttctggaaatttacttcttatttagccaaatcagtatgatcagttatgt
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acaatc

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Figure S1. The full-length nucleotide sequence and deduced amino acid sequence of *Bmcytc*. The start and termination codons are denoted in the black frame. The functional domain of the *Bmcytc* protein is underlined.

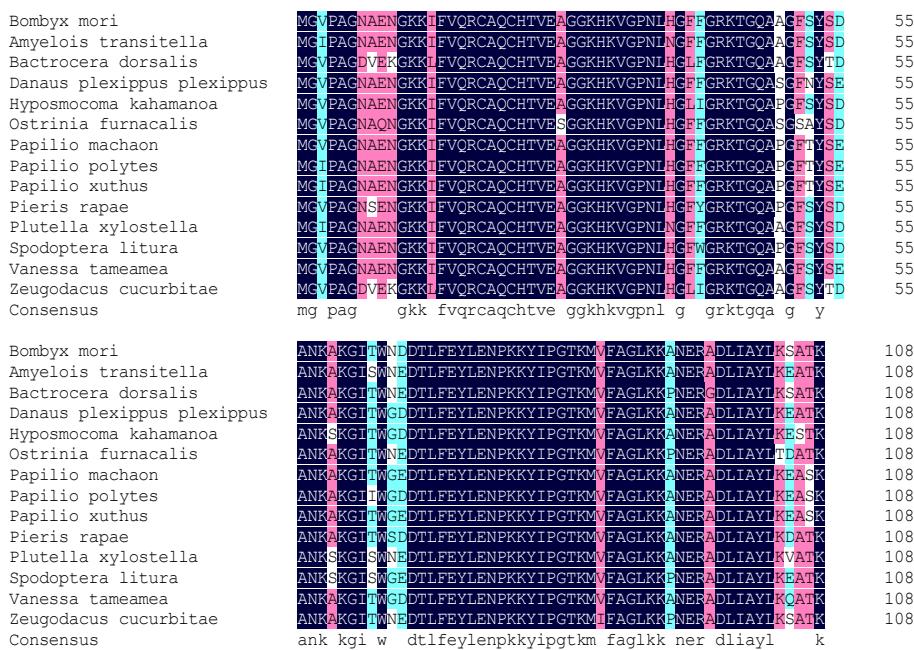


Figure S2. Multiple sequence alignment of *Bmcytc* amino acids with its homologous proteins of other species. The deduced amino acid sequence of *Bmcytc* and its homologs in other species were retrieved from the NCBI database. Identical amino acids are highlighted in dark blue, and the positive amino acids are highlighted in pink and aqua.

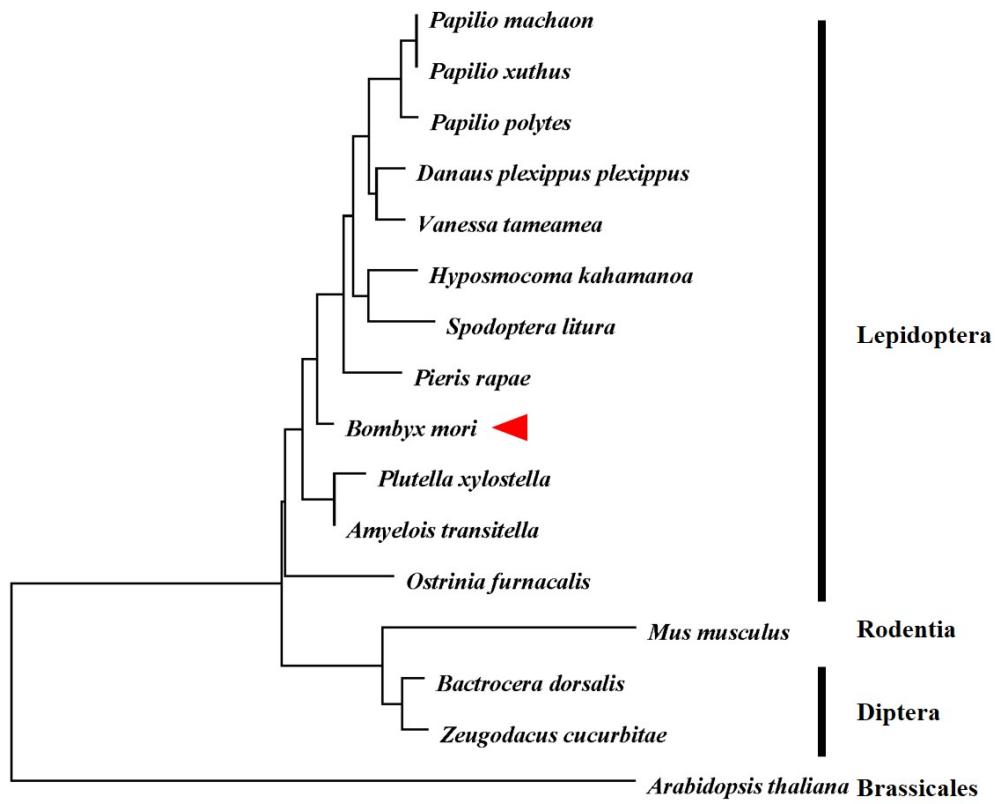


Figure S3. Phylogenetic analysis of *Bmcytc* using the maximum-likelihood method. The tree was constructed with pairwise deletion of gaps in MEGA 7. The percentages on the branches indicate bootstrap values from 1000 replicates. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the *p*-distance method. The analysis involved 16 amino acid sequences. All positions containing gaps and missing data were eliminated. Taxonomic names are shown on the right of the branches.

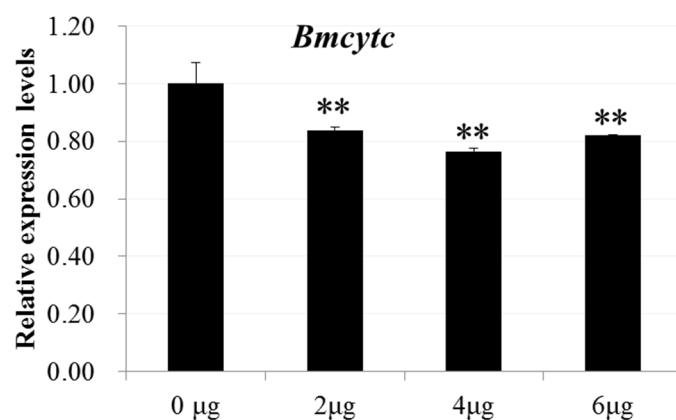


Figure S4. Expression level analysis of *Bmcytc* at different concentrations of siRNA. The data were normalized using *BmGAPDH* and are represented as the mean \pm standard error of the mean, from three independent experiments. Relative expression levels were calculated using the $2^{-\Delta\Delta Ct}$ method. Statistical analysis was performed using GraphPad Prism 5 software.