

Figure S1. Sequence alignment of CLK amino acid sequences. bHLH (basic helix-loop-helix), PAS-A (Per-Arnt-Sim-A), PAS-B (Per-Arnt-Sim-B) and PAC (PAS associated C terminal) domains are shown based on the reference [1]. Pv_CLK: CLK from *Pachycrepoideus vindemmiae* (OQ145164), Gb_CLK: CLK from *Gryllus bimaculatus* (GenBank: AB738083), Dm_CLK: CLK from *Drosophila melanogaster* (GenBank: AF067207).

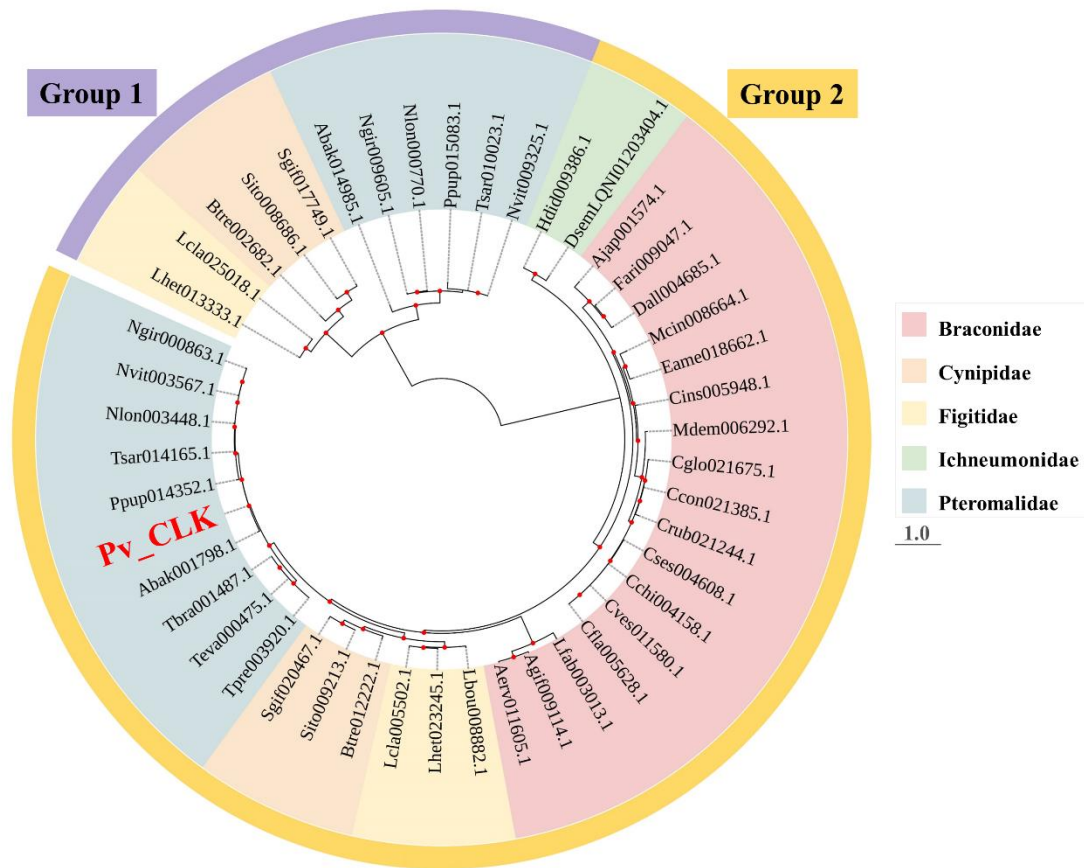


Figure S2. Phylogenetic relationships of CLKs from parasitoid wasps. The phylogenetic tree of amino acid sequences is constructed using the maximum likelihood method. The best model is JTT+G4. Red dots at the nodes denote bootstrap values greater than 500 from 1000 trials. Tip labels show the protein names in InsectBase 2.0. The species information is listed in Table S1.

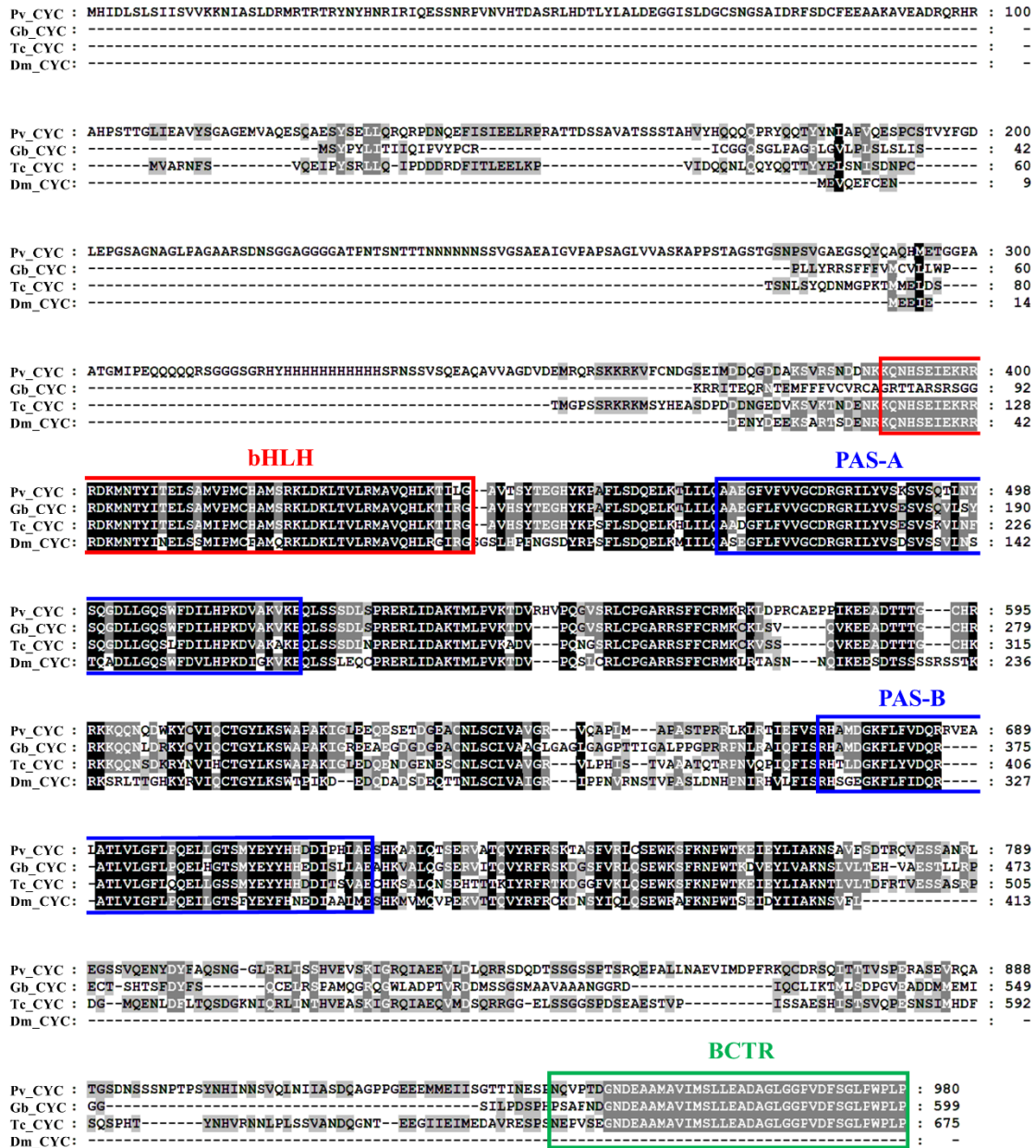


Figure S3. Sequence alignment of alignment of of CYC amino acid sequences. bHLH (basic helix-loop-helix), PAS-A (Per-arnt-Sim-A), PAS-B (Per-arnt-Sim-B) and brain and muscle aryl hydrocarbon receptor nuclear translocator- like C-terminal region (BCTR) domains based on the reference [2]. Pv_CYC: CYC from *Pachycrepoideus vindemmiæ* (OQ145166), Gb_CYC: CYC from *Gryllus bimaculatus* (GenBank: BAN28450.1), Tc_CYC: CYC from *Tribolium castaneum* (GenBank: NP_001107795.1), Dm_CYC: CYC from *Drosophila melanogaster* (GenBank: AAF49107.1).

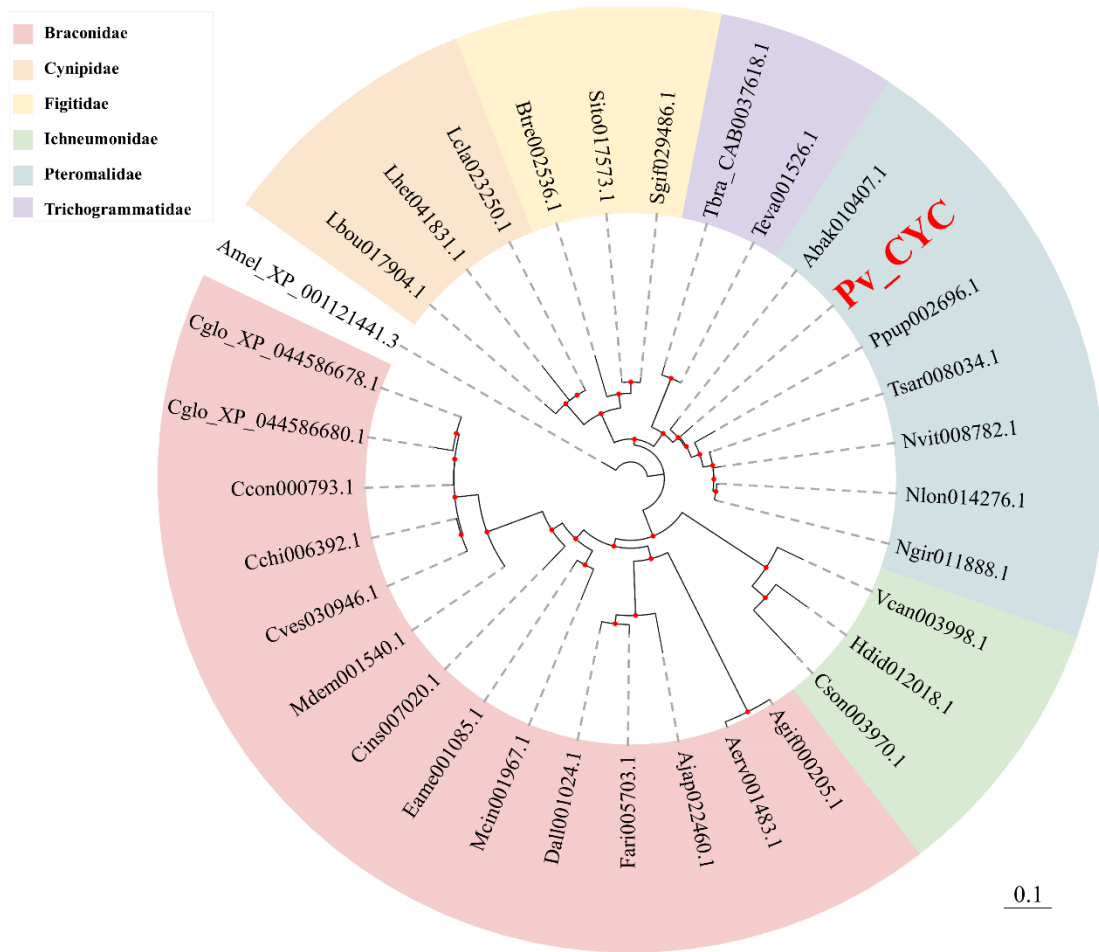


Figure S4. Phylogenetic relationships of CYCs from parasitoid wasps. The phylogenetic tree of amino acid sequences is constructed using the maximum likelihood method. The best model is JTT+G4. Red dots at the nodes denote bootstrap values greater than 500 from 1000 trials. This phylogenetic tree is rooted by ARNT-like protein 1 isoform X1 (Amel_XP_001121441.3) from *Apis mellifera*. Tip labels show the protein names in InsectBase 2.0. The species information is listed in Table S1.

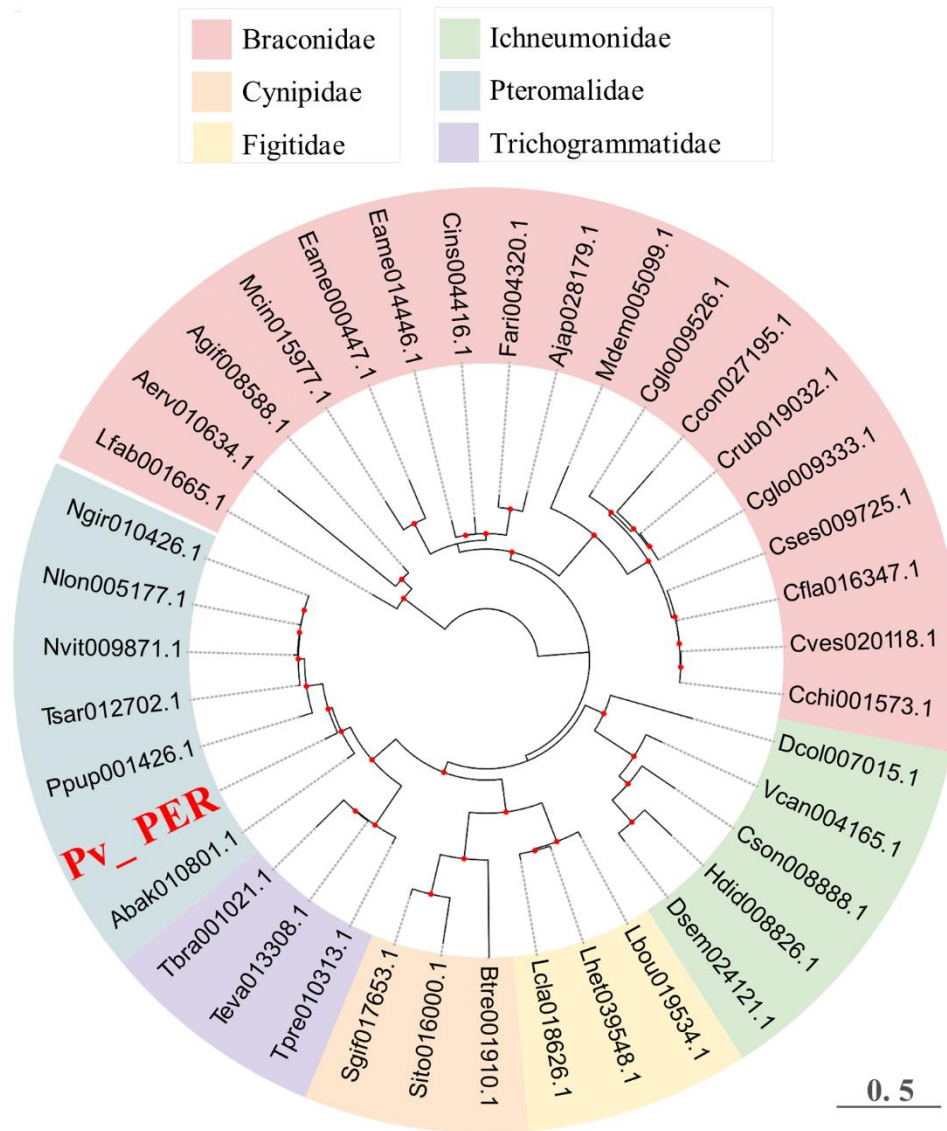


Figure S6. Phylogenetic relationships of PERs from parasitoid wasps. The phylogenetic tree is constructed using the maximum likelihood method. The best model is JTT+G4. Red dots at the nodes denote bootstrap values greater than 500 from 1000 trials. Tip labels show the protein names in InsectBase 2.0. The species information is listed in Table S1.

TIMELESS domain		
Pv_TIMEOUT	MTASATCMSDATVAETATCATGYNDE--NKENIDRNATEVLKDLIRYLRRDDTHSVRRYLGQNNILCRDLIRFVQYSEKVELNVLRLRLNLTSF	98
Tc_TIMEOUT	-----MSSLISAETATCATGYNVDATSNKYVADSNTEIEVVKDLIRYLRRDESDDRRGLGTHVLQNDIVPLIKSYWEDDLEFDVLLRLIVNLTF	93
Dm_TIMEOUT	-----MSLLIADATCATGYSDE--CKYQNEEDPTEGLKELWILRRDLNIEVRRRLGRSEVLQDQDLVYMPDVVVEHELSOLLIRILVILNTE	90
Pv_TIMEOUT	ALLVYNEELPERITRSFYQLIAHLCQYRSFMANDAWGVHMERKMNITLSESEERGEENELIMERITLIRNVIRVPS--QDTRADNDTSHDEVLE	197
Tc_TIMEOUT	ALMLWNEELPTDKITIRNRYLQDDHDKSYKQTALETWAVSTRLSKILLETSAERGDENSLIIERILLIRNILYVPPDPATEKREDNDASIHDCQVW	193
Dm_TIMEOUT	LLLYREGAEKQNHGRVEMELIDILQCYAAFAKQKWSAFERKLCALETAFAITSEQNLLIERILLVVRNVLCVFANPEACFRADNDASLHDQVW	190
Pv_TIMEOUT	AINTSGVSDLLVVIASSNKEQCYHVQILEITAMTQGCNFRALAVGAORTFEKCAEPORLLIRKKEQTEKLAKMKVAGSRHSRFGCIYVV--NMKA	297
Tc_TIMEOUT	ALHSGMDIILFIPSTTEKAYYMTLEILSMLRQKAPLARAALQSETEKMSDPAILLIIPRETNKQCKILLNCAHRSRFGCTVVLKSMKSI	293
Dm_TIMEOUT	ALHGTGMDLVLFVSSPDEQFLLGLEIVCLIFRQCS--ESLADSLQRSISEKQDQDELLARRRERARRQARP---PPCRHSRFGCIYVIRNMKSV	287
Pv_TIMEOUT	GDNEMICHKEVQKIEQLDESVTQKTKRRKNNEIMLGDERVSALSVRLFKEFCVEEINGAYNVMEYVRSCING--TGAVSASHYLWALRFFMNF	396
Tc_TIMEOUT	SDNELTYHKKFNKLEANNFADRRKFKTPKRNEMVQSTFERSSAFSIRLFLKEFCVEEINGAYNTIMYVKDNTVR--ARAQHEPSYILWALRFFMEFN	392
Dm_TIMEOUT	SDRVLIEHCALEVSSIDFLREKQCK--RSHRHCPEACVTRRSATVTRCLREYCYEIVRSAYNTIVEQVRRLVPEAGSSSHDSYLLWALRFFMEFN	386
Pv_TIMEOUT	RHNFRVRYVSETISIEVEYIVROTEHNVEMITDDKKVAVWSERLHICINACELLITLTEMGSDTS--GVRRSSRVINGNIEYVSEYRDIISQLIN	495
Tc_TIMEOUT	RLGKEEVKIVSEINAVQDERVYQLBKYEIMICSDKRNVIWSERLHIALPAYREELTHCAMDKSPDE--TVRDEARVRSNIEYVSEYREVIITLMT	491
Dm_TIMEOUT	RLSGLQIQVSESLVQCHVILTRIQHDMIMIVSDKKQRIWAKRLHVALKTFRELLCSLALQ--LRDNNARALFIMLNNVQYVREYRETVIHLIM	486
Pv_TIMEOUT	YNEITNSDYVLDVLTTHIFLRMRNFCC--KERNVVQVVRKKSKKKSKPKNSST--CHAAPLSLEPRWDICGEVAVVQCE--IPDWT--PFDG	589
Tc_TIMEOUT	YDELRMSNAYLQDLMETQVFIKLLSFPCSGNSGVVQKILKKCRKKIASQDGV---ED--YNLEPRWDEAAQQLSTVLEGADFSTDV--PFDG	584
Dm_TIMEOUT	YNEAHSYVFLRDLVVETANVFIRMMERFCCDSSVVQDRKCGGASRRKKCAATKSKFAAQPTTEESLSTKFAIATEVCSLSTELEMPDEEQIPFDA	586
Pv_TIMEOUT	ASDIPIDQK-----	599
Tc_TIMEOUT	ASDVFIDEQAEAKNVQKRNADYENASLLRAAREVWPENNCFSNNMAPESFATEDIFFADTGDDPTP-----TIECPYIDENDEE	674
Dm_TIMEOUT	ASEKSIDQREDOIRINLLRSEKLDCAALLRAAREVWPENVEFCAISAPDEDLPLREITMSNTTVSEDKENEKQKQDEYDQDDDLNDEYE	686
Pv_TIMEOUT	-----	-
Tc_TIMEOUT	DCEAGYGVNKFIDSSKRIAHPRIVRACGTATROESNSVNIHCHIKLHRIADCKLYVMIFGVSEFFTFCKLVANKDFPQYREIVFFTYIITQFI	774
Dm_TIMEOUT	ECDNGLTEKTEKEDDARRILNPKIVRACTIVSDWADIPTSLKAAVILHRIANGCCAGMLFCAKLFRIEQVSEVERDVHGEELRLATEVVRKEV	786
Pv_TIMEOUT	-----	-
Tc_TIMEOUT	KTEINKVYMESLEFFNINPAYEIEHGYGTTRKPSR--GWTEEEEDELRREMEHCT--QLQDVVDVWVNNLIINTRFAVLKKEKQCMQVNFAM	872
Dm_TIMEOUT	EVAPTINKIYAELEFYKIGIRANLESYCYDAYEGTNGATEEQESLELFEDEENRPEPTDQVIDWILDNLVKTNRREVLKKEKRGITFKAPK	886
Pv_TIMEOUT	-----	-
Tc_TIMEOUT	R-----KSTRCEVGDSEVMQRAIEHFRDAAPPLGCTVPRLEVRRSRMTKRLIDGVRDFAVRRKKGCAKPTATRRSDSESNSEDDYGGGA	967
Dm_TIMEOUT	STRKSAQSGNVQPEDEDELRSMDCHRIEPCIERVNEFAERRSKQCHIKRMCHHIADESRILEFAKRG--DKPKKIVEMEGEED--FDFAEPP	984
TIMELESS-C domain		
Pv_TIMEOUT	-----	-
Tc_TIMEOUT	SRGNSAAQRNITKTTSRKPKHTRCVNNSADARWAFIKIVESGMSEALEWIKDSFSDVEFENDD--GCEGIPIVPIINDYAVNANENADHETIKAI	1066
Dm_TIMEOUT	MFEQGYKKPKSKPKVQKRCMRTFLDVG---TIRILIGQDSEKYQSAIEWIQECLQDSSETAEAVEDDDGVPLLPIMENQRNAMEDGEQRVIVAI	1081
Pv_TIMEOUT	-----	-
Tc_TIMEOUT	GVAEHFDEQEMWRIEGNI--SVDVHRYIDILQCAVN-----TLWPESQCTGTAKNIAPF	1122
Dm_TIMEOUT	GVQPEISGMFAWRIEYINSADLITRSKIAGSEVVAEPEDEAAADDEDGEEAESEDEEDFLEKHSRQRKENIATQQQRKLDSEMFNSDDETEQRAPF	1181
Pv_TIMEOUT	-----	-
Tc_TIMEOUT	TS-----LKKKKRIENIVSDELTASNDGAR-----ETDGDGKSKCRKQKQGRNVSSDDEBTN	1177
Dm_TIMEOUT	KAKDKPRASERKARKRVKAKAKESKCNDDGTDKAELEKNTDDLFNQLRAKRATRIKISDMAINESTNAAQADDAFNESEDYARLIELEDEEENS	1281
Pv_TIMEOUT	-----	-
Tc_TIMEOUT	DCAN-----NQTSVSRQVPSDEEDNSTVSQVSKSVRIIPF-----PEENDIKRNIESDSEAEKAPKTRTSSSEF	1255
Dm_TIMEOUT	KDAPENGQKENITKSLQPARVNVDSNDNDGALADTNKPRSDGDSGHMDANAEPSDEEAFLEAKKFARVDBGELKRIATIDDDDE	1381
Pv_TIMEOUT	---	-
Tc_TIMEOUT	---	-
Dm_TIMEOUT	DDF : 1384	

Figure S7. Sequence alignment of TIMEOUT amino acid sequences. TIMELESS and TIMELESS-C domains are shown according to CDD search [5]. Pv_TIMEOUT: TIMEOUT from *Pachycrepoideus vindemniae* (OQ145168), Dm_TIMEOUT: TIMEOUT from *Drosophila melanogaster* (GenBank: AAF73481.1), Tc_TIMEOUT: TIMEOUT from *Tribolium castaneum* (GenBank: EEZ99220.1).

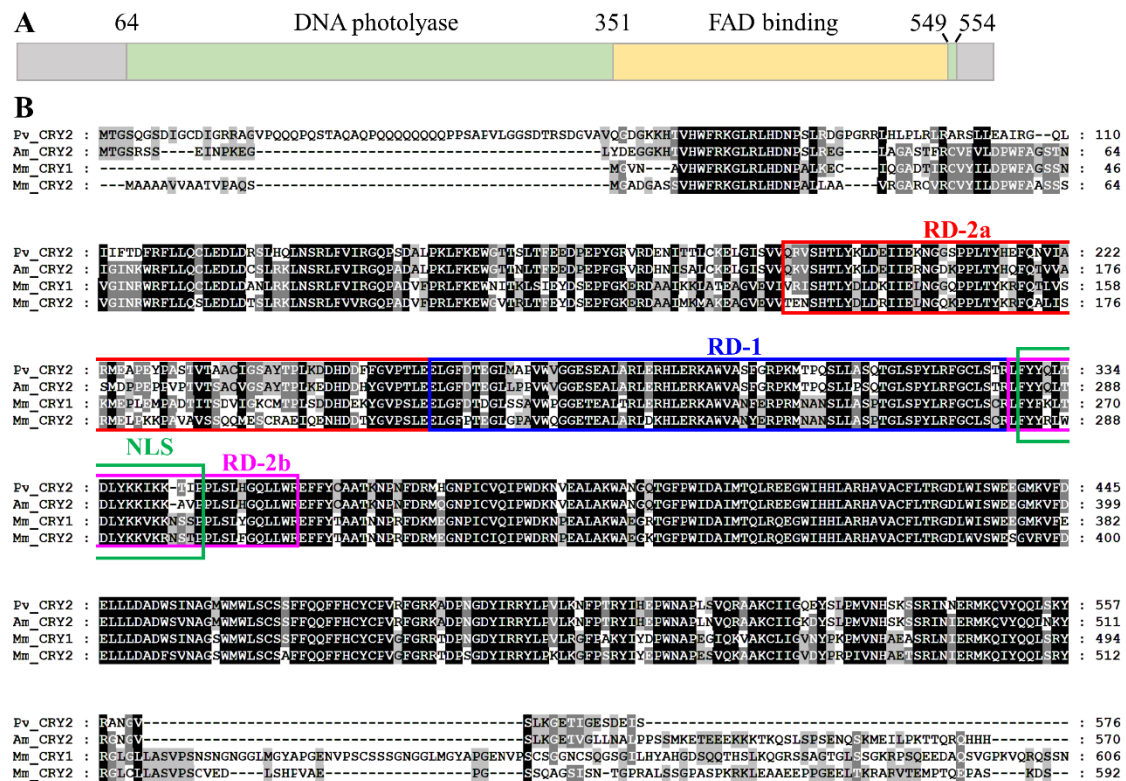


Figure S8. (A) Structure and organization of Pv_CRY2. DNA photolyase and flavin adenine dinucleotide (FAD) domains are indicated by green and yellow rectangles, respectively, according to CDD search [5]. **(B)** Sequence alignment of CRY amino acid sequences. RD-1, RD-2a, RD-2b, NLS (nuclear localization signal) and coiled-coil domains are shown based on the reference [6]. Pv_CRY2: CRY2 from *Pachycrepoideus vindemniae* (OQ145169), Am_CRY2: CRY2 from *Apis mellifera* (GenBank: NP_001077099.1), Mm_CRY1: CRY1 from *Mus musculus* (GenBank: P97784.1), Mm_CRY2: CRY2 from *M. musculus* (GenBank: Q9R194.1).

Pv VRILLE : **MGAVFFRP**DNADYGDGRQKCAL-----VQRSSK-----PLRGAFER-----ILG : 41
 Am VRILLE : MVAEIVARQSGSPINGETACLNENMPATHHTIAHTSHGGHGGHDAHGPLEPI^{THFV}EHGGPELTILQ : 65
 Gb_VRILLE : MVAEIVARQSGSPINGETPSLNSTMPGSHSASNSTSGGG-----GGGGAGAGGP^{LA}VIN : 56

Pv VRILLE : SWIVN-----EWSWTTASDEIVCQSDRCKWIARFR-----RLELPGNLS-- : 80
 Am VRILLE : QQQQQQQHQHQHPQHPPPEQQQPEQQHHHHHQPPQQTQQQQQQQSHHHHDAQV^{THPE}NFPN : 130
 Gb_VRILLE : GGGAGGPGG-----AEGFCPE^{DAM}LVDVARPPSPDGA^KSAGENG^{GGG}QGN^{GAY}PH^{SF}DT^{HLK} : 113

basic leucine zipper domain

Pv VRILLE : ---QELFSQ^{RKQ}REFIPDNKKDDSYWDRRRRNNEAAKRSREKRRFNDMVLEQ^{RV}MELSKENHIL : 142
 Am VRILLE : FDIRKELFSQ^{RKQ}REFIPDNKKDDSYWDRRRRNNEAAKRSREKRRFNDMVLEQ^{RV}MELSKENHIL : 195
 Gb_VRILLE : ---RKELFSQ^{RKQ}REFIPDNKKDDSYWDRRRRNNEAAKRSREKRRFNDMILE^{TRV}VELTKENHVI : 175

Pv VRILLE : KAQLDAIREKFGICGESVISTEFVLAALPAEPTL---VKRAKIQS---SAALLYARTPSFVHTSV : 201
 Am VRILLE : KAQLDAIRDKFGICGESVISTEFVLAALPTEPPIG---VKRAKIPP---SAALLYARTPSFVHTSV : 255
 Gb_VRILLE : KAQLAAEKDKYGVCGESLISVECVMATLPTTECVLSFTKRPKLTSGGAQHSLLYPENPSPIETEV : 240

Pv VRILLE : IHQEPFA-----SSIP-----FPHPMHSEDTSS----- : 225
 Am VRILLE : IHQPVSG-----ARSPRSPACLYVAETPSY^{ETES}FCY^{TY}PHPMH-LDTS----- : 301
 Gb_VRILLE : IHQPVSA^{GLAAS}PPPALHYPAQL^{CH}PHASHQH^{PA}PH^{PQ}L^{LP}HP^{HP}I^{PH}PHAAAGPEFVPFADA : 305

Pv VRILLE : -----ALNLSR--GR--RAQSPFELSSGSGDES----- : 249
 Am VRILLE : -----ALNLSR--GR--RAQSPFELSSGSGDEG----- : 325
 Gb_VRILLE : DSYPTTFPLQPHQAQPFESGAGSVLNLSRSAGRTRSRAQSPYELSSGSGDESSVPGLPLTVAPN : 370

Pv VRILLE : -----VQMTSSPTLIAQGVGACNSLPHKLRHKSEIGDKDAASALLALQGIKQEPGPRASPPWD : 307
 Am VRILLE : -----PQIVVS-----SCNPAANNSLPHKLRHKSEIGDKDAASALLALQGIKQEPGPRASPPWD : 379
 Gb_VRILLE : GASAAAAAAAAAAAAAAAAAANNSLPHKLRHKSELGDKDAATLLSLCN^{IKQ}EPGPRASPPWD : 435

Pv VRILLE : NEGSSDERDSGISLGAETG-----PSVSNMPESE^R-----EVKSRLD : 345
 Am VRILLE : NEGSSDERDSGISLGAETG-----STVSTVPEN^ER-----EVKSRLD : 417
 Gb_VRILLE : AEGSSDERDSGISLGV^{EW}SGNGIGSSSGAASAGAA^{SS}GPLPQQQPPQQH^{HL}SLSLSHAH^{HPL}LS : 500

Pv VRILLE : RLASEVASLQSI^{LR}LK^{AGE}GI^{NG}ST^{VI}SSAATNCVAAAP----- : 387
 Am VRILLE : RLASEVASLQSI^{LR}IGK^{PA}ESS^{IV}TGH^{SL}PPNA^VNGP----- : 455
 Gb_VRILLE : HHAHHEALAHPT^{PA}ASPCHAG^{VP}AAATAASVAAAAAAAAAADLECGPD^{DA}ALKNELARLASEV : 565

Pv VRILLE : ----- : -
 Am VRILLE : ----- : -
 Gb_VRILLE : ATIKSFLNSKGAAAAA^{VA}QH^Q : 587

Figure S9. Sequence alignment of VRILLE amino acid sequences. bZIP (basic leucine zipper) domain is identified by CDD [5]. Pv_VRILLE: VRILLE from *Pachycrepoides vindemmiae* (OQ145170), Am_VRILLE: VRILLE from *Apis mellifera* (GenBank: XP_393735.3), Gb_VRILLE: VRILLE from *Gryllus bimaculatus* (GenBank: BBQ05060.1).

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Pv_PDP1 : ----- : -
Am_PDP1 : MSCAMEYQQQLAPPFVPGVLHQAHHQQHQQQFVQPPHPHIVVAPAHQQQPQ : 50
Gb_PDP1 : ----- : -

Pv_PDP1 : -----MARKQ : 5
Am_PDP1 : QPPPPPLPPTSHGHQVHAPLPPIHEDSTSSRWSQYQHLWRQHVVYVNGKQ : 100
Gb_PDP1 : -----MLTLSTWTWTS : 11

Pv_PDP1 : GKDGPEKKDADGELWGNVEAQAFLGPNLWDKTLPYDADLK YVDLDEFL : 55
Am_PDP1 : GKDGPEKKDADGELWGNVEAQAFLGPNLWDKTLPYDADLK YVDLDEFL : 150
Gb_PDP1 : SCRRTASRWTAAWRRRPTRRPRTTRTPHPRTPT-PTRTTSRRPPSSSS : 60

Pv_PDP1 : SENGIFVDGVAGGGGGGAGAMQASQLHKLGANGNNNTAGPGGNGLVQA : 105
Am_PDP1 : SENGIFVDGVAG---GGQGTMQSGQLHKM-----NNTETPG----- : 183
Gb_PDP1 : STRRPRRPRCRSPAPPSLNGHVKVARLGALTTPPPAPAPAPAAAFLAAA : 110

Pv_PDP1 : TGHQGPAGLHLEFVTKRERSPSPSDCCSE-DTLNPPSPADS----- : 145
Am_PDP1 : --HQGPAGLHLEFVTKRERSPSPSECCSE-DTMNPPSPADSNSEDSSRIQ : 230
Gb_PDP1 : VAAAAAASVLEIVAKRERSPSPSEPLSEGLALNPPSPAES----- : 151

Pv_PDP1 : -----TLSMASSGRDFDPRTAFSDDEELKPQPMIKKSRKQFVPDDLKDD : 189
Am_PDP1 : YGLSIVALSMASGRDFDPRTAFSDDEELKPQPMIKKSRKQFVPDDLKDD : 280
Gb_PDP1 : -----TSLASSGRDFDPRTAFSDDEELKPQPMIKKSKKQFVPESMKDE : 195

basic leucine zipper domain

Pv_PDP1 : KYWARRRKNNMAAKRSRDARRMKENQIALRAGFLEKENMGLRQEMDRLKN : 239
Am_PDP1 : KYWARRRKNNMAAKRSRDARRMKENQIALRAGFLEKENMGLRQELDRLKN : 330
Gb_PDP1 : KYWARRRKNNMAAKRSRDARFVKENQIALRAGFLEKENMGLRQELDRLKK : 245

Pv_PDP1 : ENMLLRDKLSKYTDV : 254
Am_PDP1 : ENMLLRDKLSKYTDV : 345
Gb_PDP1 : ENLLLRDKLAKFTDV : 260

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Figure S10. Sequence alignment of PDP1 amino acid sequences. bZIP (basic leucine zipper) domain is identified by CDD [5]. Pv_PDP1: PDP1 from *Pachycrepoideus vindemniae* (OQ145171), Am_PDP1: PDP1 from *A. mellifera* (GenBank: XP_391997.3), Gb_PDP1: PDP1 from *G. bimaculatus* (GenBank: BBQ05061.2).

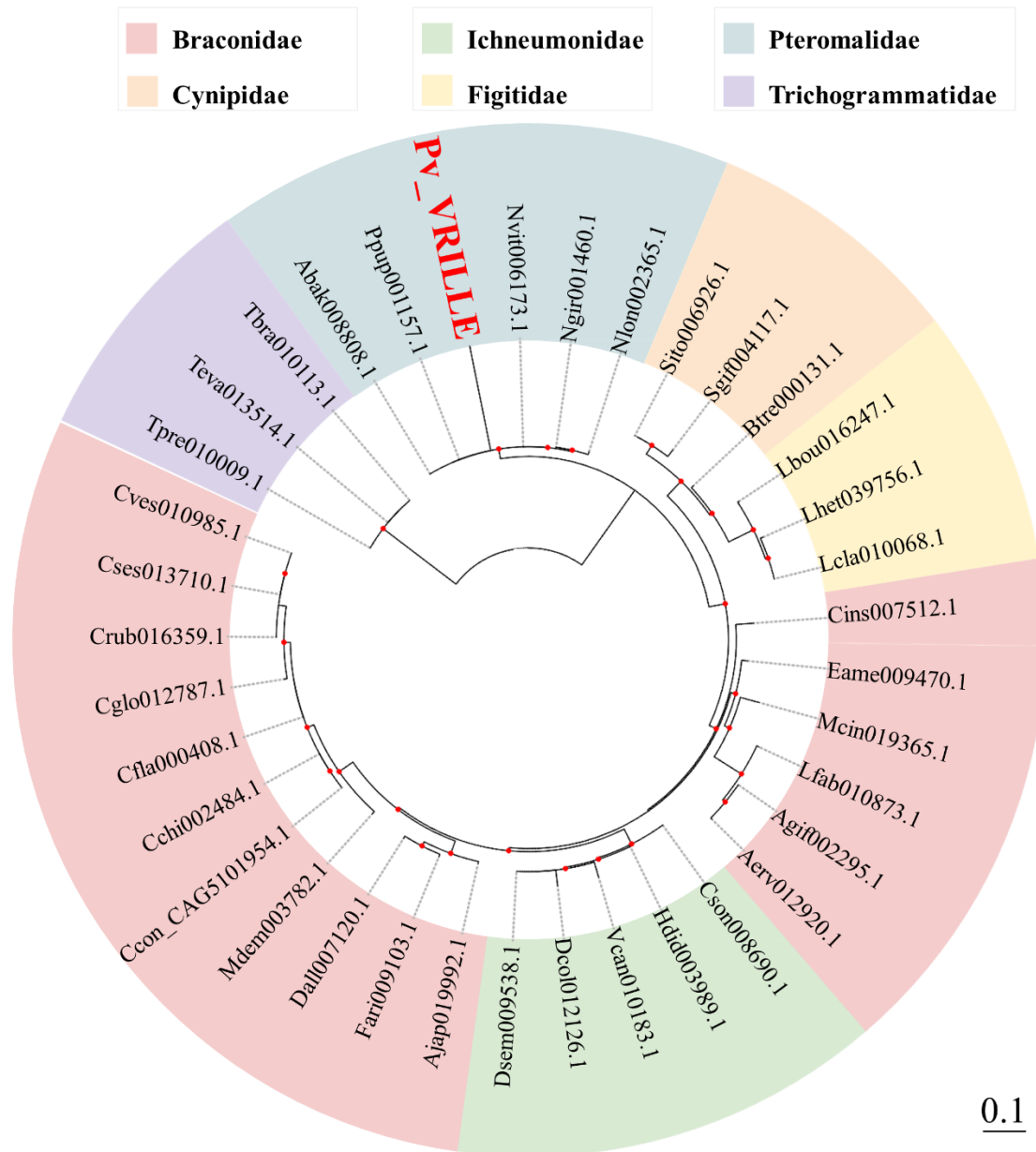


Figure S11. Phylogenetic relationships of VRILLE from parasitoid wasps. The phylogenetic tree is constructed using the maximum likelihood method. The best model is JTT+G4. Red dots at the nodes denote bootstrap values greater than 500 from 1000 trials. Tip labels show the protein names in InsectBase 2.0. The species information is listed in Table S1.

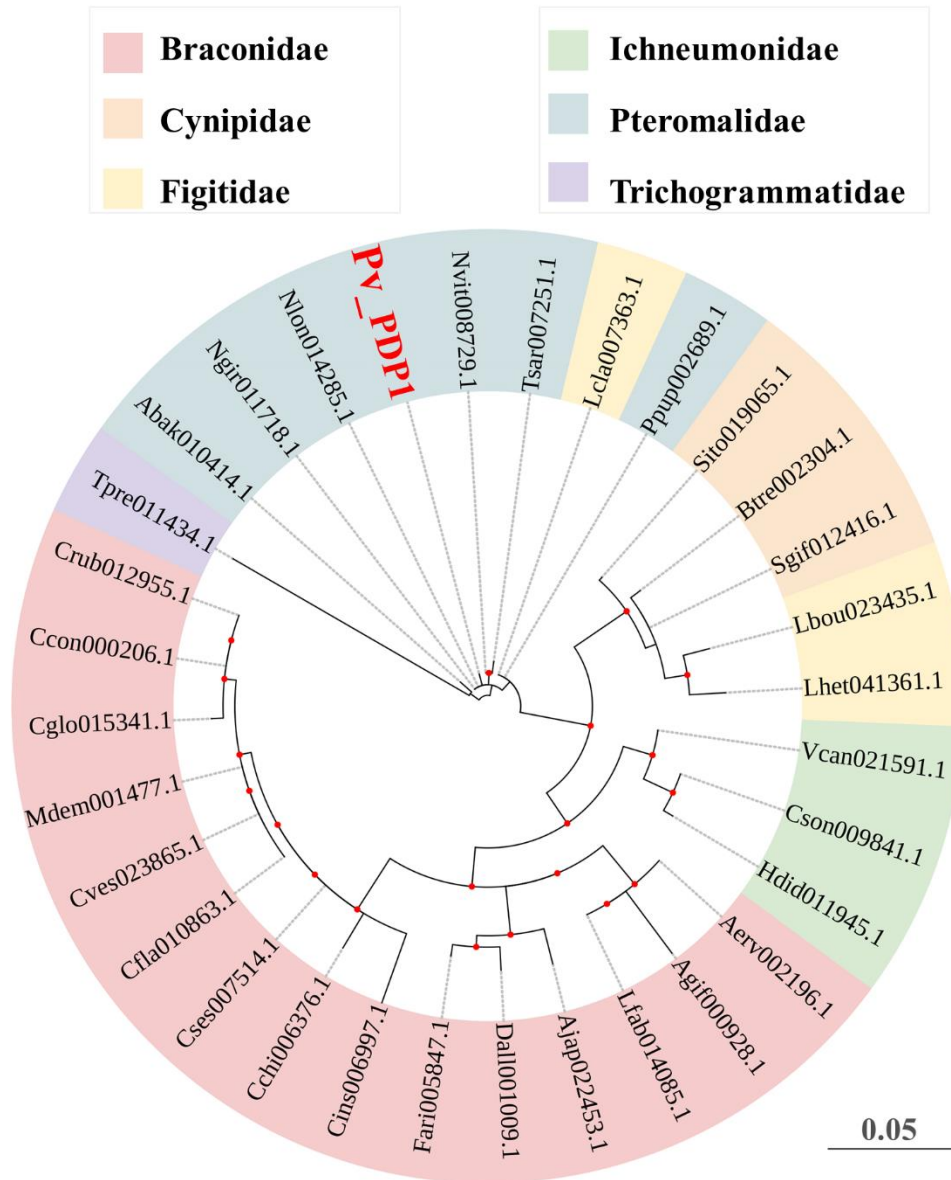


Figure S12. Phylogenetic relationships of PDP1 from parasitoid wasps. The phylogenetic tree is constructed using the maximum likelihood method. The best model is JTT+I+G4. Red dots at the nodes denote bootstrap values greater than 500 from 1000 trials. Tip labels show the protein names in InsectBase 2.0. The species information is listed in Table S1.

Pv_CWO : MV-----THSMENILN-----MQYYAFVSDEALHI----- : 25
 Nv_CWO : MV-----THSMDNILN-----MQYYAFVSDEALHS----- : 25
 Am_CWO : MVRRIASIIKRTHTIDRKFKRVCNIIIGPGASSRPFVNHVKEVQCMYMHKKGDRCNERS : 60

Pv_CWO : -----PPSRKK-----RCLAKEVNSTIYL----- : 43
 Nv_CWO : -----PPSRKK-----RCLAKE----- : 37
 Am_CWO : IYDRRFQKKKSGSRKKDGEEKKRAEVQIYRLDARSCKDEIYRMGIIGGGYCEGNLNFATAS : 120

basic helix-loop-helix domain

Pv_CWO : -----QDPMSHRIIEKRRRDRMNNCLADLSRLIPAAYLKKGRGRVEKTEIIE : 91
 Nv_CWO : -----QDPMSHRIIEKRRRDRMNNCLADLSRLIPAAYLKKGRGRVEKTEIIE : 84
 Am_CWO : EDDEVYTKKKVSFQDPMSHRIIEKRRRDRMNNCLADLSRLIPAAYLKKGRGRVEKTEIIE : 180

Pv_CWO : MAIRHMKHLQGLRQDSKHHTFVSSVHAMHTEDSVDSVSHPSAGGSSAAEFYRLGYQECLS : 151
 Nv_CWO : MAIRHMKHLQGLRQDSKHHTFVSSVHAMHTEDSVDSVSHPSITGSSAAEFYRLGYQECLS : 144
 Am_CWO : MAIRHMKHLQGLRQESK-HPAVTSVHSMHPEDSVDSVSH-STVASTAAEFYRLGFQECLS : 238

Hairy Orange domain

Pv_CWO : ETMHFIVEVEGYFARDALCVQLISHLQQHCDKILATSDRLGFPHPVDLPSSNGTACN--- : 208
 Nv_CWO : ETMHFIVEVEGYFARDALCVQLISHLQQHCDKILATSDRLGFPHPVDLPPTNGSACNGVS : 204
 Am_CWO : ETMHFIVEVEGFFARDSLCVQLINHLQQHCEKILATSDRLGFPHP-EMPTTNGVANGNS- : 296

Pv_CWO : -----GHQSR----- : 213
 Nv_CWO : SFAHNGGGLPSMCPNGANGSSPTNGIGLLTNNNNVNGNGHLSHNNNNSINNNNNNNNNNP : 264
 Am_CWO : --GYPHTSIPTICQP-----NGHSDHG----- : 316

Pv_CWO : -----GG--LIPPPNIVSDDSNHS : 230
 Nv_CWO : TSNQHHTLLHNNSSNSDRCSSSGCVSSFDSSSSSRASHHCGGRVLIIPPPNIVSDDSNHS : 324
 Am_CWO : -----SSGCVSSFGDPERP-----LRPTIATIPPPATVSDDSNHS : 350

Pv_CWO : SHSHGSSSLLLSHHHHHHHHHHHHHESORPPANYKFKNSIKQRFSAQRIKSSGSPPPS : 290
 Nv_CWO : SHSHGSSSLLLTFASSS-----EQORPPANYKFKNSIKQRFSAQRIKSSSPPPT : 375
 Am_CWO : THSHS-----TEPTTT-----CKPSNYKFKSSIKQRFSAER-IKS--SPPPT : 389

Pv_CWO : SSSAETSPKHHLQLQSGEGVPIFALHDNGGFYVPLTLEASLLRPHLGYAPADV-GPDVVL : 349
 Nv_CWO : SS-SEASPKHQQCSGPAQGVPIFALHDNGGFYVPLTLEASLLRPHMCCTAGDISGPDVVL : 434
 Am_CWO : TSTEKPSSSH-----GVPIFALHDAGSYVPLTVEASLLRPHINEMWDTG--PDTVL : 439

Pv_CWO : HEVTISVNFNHTPPGGD----- : 366
 Nv_CWO : HEVTISVNFNHSPTGWSHQQSEPHQIQ- : 463
 Am_CWO : HEVTISVNFNHSNP-PAWSHHSETHQPQT : 468

Figure S13. Sequence alignment of CWO amino acid sequences. basic helix-loop-helix (bHLH) and Hairy Orange domains are identified by CDD [5]. Pv_CWO: CWO from *Pachycrepoideus vindemmiae* (OQ145172), Nv_CWO: CWO from *Nasonia vitripennis* (GenBank: XP_003426877.1), Am_CWO: CWO from *Apis mellifera* (GenBank: GB52039).

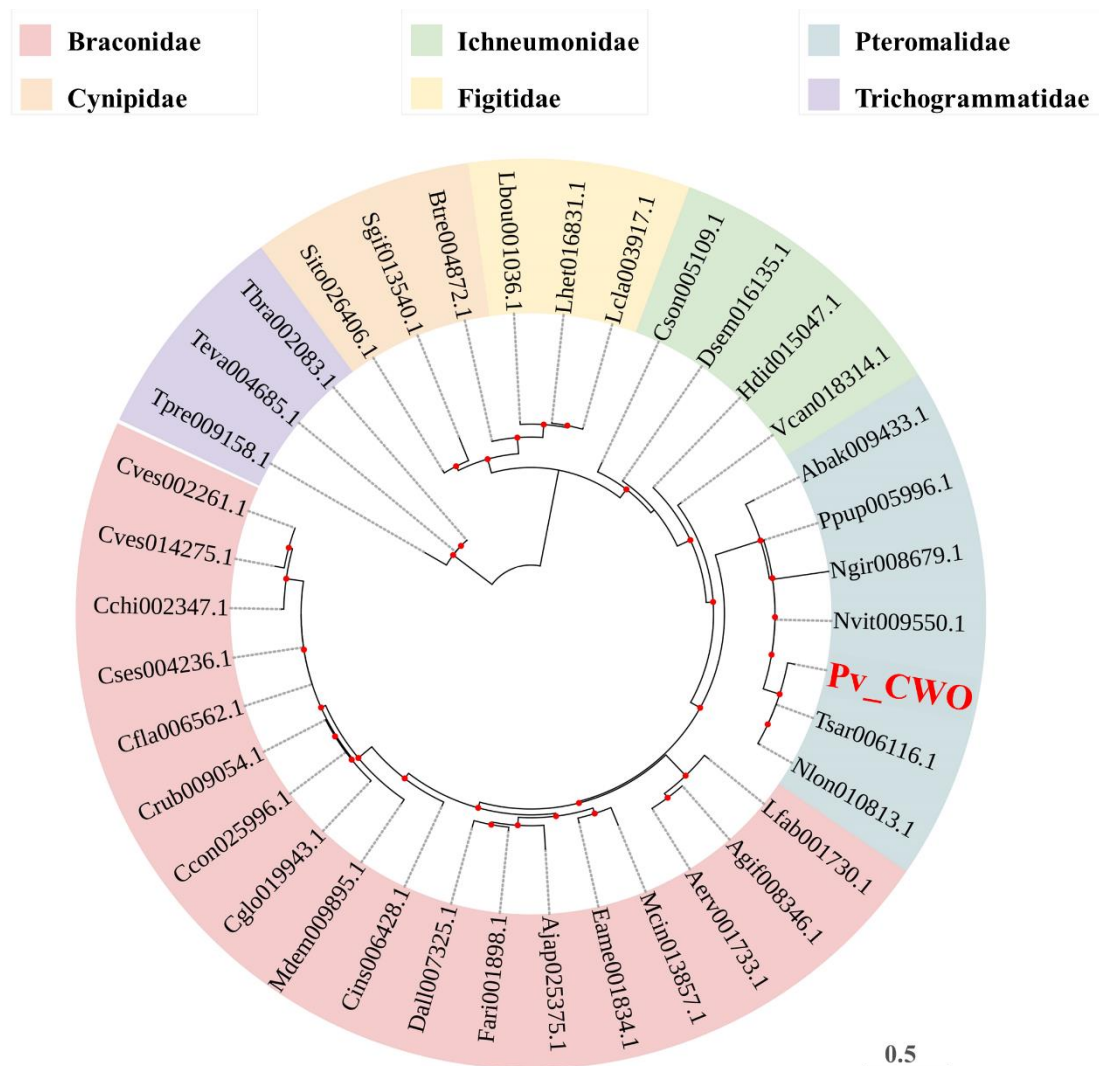


Figure S14. Phylogenetic relationships of CWO proteins from parasitoid wasps. The phylogenetic tree is constructed using the maximum likelihood method. The best model is JTT+G4. Red dots at the nodes denote bootstrap values greater than 500 from 1000 trials. Tip labels show the protein names in InsectBase 2.0. The species information is listed in Table S1.

References

1. Takekata, H.; Numata, H.; Shiga, S.; Goto, S.G. Silencing the circadian clock gene *Clock* using RNAi reveals dissociation of the circatidal clock from the circadian clock in the mangrove cricket. *J. Insect Physiol.* **2014**, *68*, 16-22.
2. Uryu, O.; Karpova, S.G.; Tomioka, K. The clock gene cycle plays an important role in the circadian clock of the cricket *Gryllus bimaculatus*. *J. Insect Physiol.* **2013**, *59*, 697-704.
3. Fergus, D.J.; Shaw, K.L. Circadian rhythms and *period* expression in the Hawaiian cricket genus *Laupala*. *Behav. Genet.* **2013**, *43*, 241-253.
4. Moriyama, Y.; Sakamoto, T.; Karpova, S.G.; Matsumoto, A.; Noji, S.; Tomioka, K. RNA interference of the clock gene *period* disrupts circadian rhythms in the cricket *Gryllus bimaculatus*. *J. Biol. Rhythm* **2008**, *23*, 308-318.
5. Marchler-Bauer, A.; Bo, Y.; Han, L.; He, J.; Lanczycki, C.J.; Lu, S.; Chitsaz, F.; Derbyshire, M.K.; Geer, R.C.; Gonzales, N.R.; Gwadz, M.; Hurwitz, D.I.; Lu, F.; Marchler, G.H.; Song, J.S.; Thanki, N.; Wang, Z.; Yamashita, R.A.; Zhang, D.; Zheng, C.; Geer, L.Y.; Bryant, S.H. CDD/SPARCLE:

functional classification of proteins via subfamily domain architectures. *Nucleic Acids Res.* **2017**, *45*, D200-D203.

6. Hirayama, J.; Nakamura, H.; Ishikawa, T.; Kobayashi, Y.; Todo, T. Functional and structural analyses of cryptochrome- Vertebrate cry regions responsible for interaction with the CLOCK: BMAL1 heterodimer and its nuclear localization. *J. Biol. Chem.* **2003**, *278*, 35620-35628.