

***Fatty acid synthase 2* contributes to diapause preparation in a beetle by regulating lipid accumulation and stress tolerance genes expression**

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Additional information in this file.

Figure S1. Alignments of *C. bowringi* FAS protein sequences.

Figure S2. Gene identification of *C. bowringi* *SOD* and *GST*.

Figure S3. Schematic diagram of deduced domains of FASs of *Tribolium castaneum* (A) and *Bactrocera dorsalis* (B).

Table S1. Primers used in cloning *C. bowringi* cDNAs.

Figure S1

CbFAS1 KU516006 : MTRINLDRDRKNQYTYG---RILAHPPPSEAVVISGISGVVFKCRNVVEELRDSLMNKLDLTAHYREG-FDHABLPKRSGLTNTGLQDFDAGFFGMHENQADPCSIETRIILLESIEAIIIDAGMNFK : 124
 CbFAS2 KX467777 : MPAR-----APEPER-----HLGNSFSDDVVITGISGRLPESNTIEEFKQQLFDGVDLVTDDERRWPSGLYGLPTRTGKIKN-LQYFDATFFGVHAKQANVMDPQLRMLLELTHEAIVDAGMNF : 114
 TcFAS XP_015836196.1 : MSRS-----SEPNHQSFS---RWLSQPPEGDEVVVTGMSGRLPDSLHLLHFDNLFNKVEMVSDDDRWRKLDHKEBTPQRTAKILD-IDKFDTGFFGLHFRQANTMDPMTIRMVLESAMEAIFDAGVNPR : 118
 TcFAS XP_008200285.1 : MPAR-----VPDAQNG-----HHVNAISDDIVITGISGRLPESNTIEEFKQQLFDGVDLVTDDARRWPSGLYGLPARTGKIKD-LSRFDATFFGVHAKQATVMDPQLRMLLELTYEIVDAGVNPN : 115
 AiFAS AGR49310.1 : MPSA-----VTNGAR-----GSEDDIVLTGISGRLPESDTIEEFKQQLFDGIDLVTADDRRWTPGLHGLPERNGKIKD-LAHFDATFFGVHAKQAHLMDPQLRMLLELTHEAIVDAGINFS : 110
 ApFAS XP_008187030.1 : MSRQQAIELKIKTDREIALRAGRRLVKCDPGEIVISGFSGSFNSDGLPDEADNLFNKVDLISDDNRRWTIEHPEIPQRTGKLNQ-VNKFDAFFGVHAKQAHTMDPMCRITLESYEAIVDSGNSFK : 128

CbFAS1 KU516006 : DIESTKTFYLYCYSDIESTLQWTKHKEKRFILTAARFMSVSRVAVFLKLGPTYYQDCSACSSSLHALDHAFKDTRSGECENAVAGANLSMFPGTTLQFAKLGVLSPRCICQFPDKNGDYVVRSEV : 253
 CbFAS2 KX467777 : ELRCSTGTFIVGSDSESSEFWTQDPEKVNGYGLTGCCRAMFPNRI SYTFDLTGPSYALDTACSSSLFAFQAATAIKTGCCDAAIVGGVNLKPTSSSLQFHRLSMLSPQGMCKAFDASGNGYVVRSEA : 243
 TcFAS XP_015836196.1 : ELECTRTGWFISASWSDMENRLLTSISEPERYGITCYLRSLLAQRI SYYLKLGPSHIVDTACSSSGNALEHAFKAIIRSGCCDQALVGCNSLULHPGNSLQFFRLGVLSSQKORVFDQDASGYVRGET : 247
 TcFAS XP_008200285.1 : DIKCKSTGTFIVGSDSESSEYWTQDPDKINGYGLTGCCRAMFNSRISYTFDFSGPSYALDTACSSSLVALQAATAIKTGCCDAAIVGGVNLKPTSSSLQFHRLGMLSPQGMCKAFDASGNGYVVRSEA : 244
 AiFAS AGR49310.1 : ELRCSTGTFIVGSDSESSEYWTQDPDKINGYGLTGCCRAMFPNRI SYTFDLTGPSYALDTACSSSLVALQAATAIRSGHCDAAIVAGCNLCLKFNANLNFHRLSMLSPEGRCAAFDASGRGYVVRSEA : 239
 ApFAS XP_008187030.1 : SLKCKSTGTFIVGACFSSEKTFWFEYKLVQNGFGLTGCCRAMLANRISYWLGNPYSYVSDSACSSSLYALEHAYKAIIRDGHCDSALVGGCNLCLHFFVYVSLQFARLGVLCADGRCKSFDEAANGYVVRSEA : 257

CbFAS1 KU516006 : ITVVLQKARNKRRIYAQVINTKCNSDGFKDNGITFPSSRAQAELIAEVLSESNVQFDNVTYLEGHATGTSAGDPEECAAIDSVIGQ-NRKTPLRVGSVKSVMGHSEPSAGICSLIKVLLISMESGFLFP : 381
 CbFAS2 KX467777 : AVVVYLQKASARRVYATVLGAKINTDGNKEQGITFPSSGQMNKLIREVYEEIGVRFQEVSYVEAHGTGTVGDPQEVNSIADFFCK-NRKPPLIGSVKSNMIGHSEPASGLCSLAKIVIAMBAGMTPQ : 371
 TcFAS XP_015836196.1 : IACVFLQKAKNSRRIYAQIINAKINSDGFKQGITFPSTQAQKILMTEIYDESNVHFNQLSYLEAHGTGTVGDPQEVNAIDCALAK-PRNKTPLRVGSVKSVMIGHSEPSAGICSLIKVLLIAMESGLISP : 375
 TcFAS XP_008200285.1 : AVVVYLQKASVAHRVYATVLGAKINTDGNKEQGITFPAGPMQNQLIRETYAEFGVDNFVSYVEAHGTGTVGDPQEVNSIADFFCTKRKPELMIIGSVKSNMIGHSEPASGLCSLAKIVIAMESGMTPG : 373
 AiFAS AGR49310.1 : AVAVLLQRRGAARRVYATLRLGLRVNTDGAQDQGITFPSSGDMQRRLEAETFAEAKLRFADVAYVEAHGTGTVGDPQEVNAIAELFCK-GRKGFLLIGSVKSNMIGHSEPASGLCSVAKVVVAMBERGITPS : 367
 ApFAS XP_008187030.1 : VCVLVLQKAKNAKRVIYAKVHAKTNCQDGYKEQGITVPSGPLQQRLEEFYEECEIKFSDLAWIEAHGTGTVGDPPEVKALENVFCP-GRITPPLIGSVKSNMIGHSEPASGLCSVAKVVIAMESGFTIPP : 385

CbFAS1 KU516006 : TINYSETRPGISSILEGRLEVVTPEIKITEEHLMAVNSFGFGGNSLSLRSISKKKQNGGEPNSDNLPRLVMSGRNLEAVNSLDSVPSNPLDAEYIRLLQNSFRIDIPNNSFKGYMIISKTTETSR : 510
 CbFAS2 KX467777 : NLHFKSPNDIPALNDGRLKIVAKNEPWNGG--IIAINSFGFGGANAVLVRSNPKPKTLWPVG--PIPRVVGVSGRTEAVNTFLAKVEQKNDEEFLALLDEIHSKNINGHAYRGYVLLKDKQ-AIKE : 495
 TcFAS XP_015836196.1 : NINLKRIKEGMVGFQKRMKAVTEITELEGNEAIVGINNFSGFGGNCNAIVKRFKMKKNGGFPDDNLPRLVCVSGRSEAVQAQILNQVN-LKLDVEFNALLHEIYKDIIPNHMFRGFTLVGKSGPLVT : 503
 TcFAS XP_008200285.1 : NLHFKSPNTDIPALLDGRKIVAKNEPWKGG--LIGVNSFGFGGANAVLILKSNPKPKASWPTD--PIPRVVGVSGRTEAVNTFLDHVEKNKNDDEFLALIDQIHSKNITGHAYRGFTVLSNP-ALRE : 497
 AiFAS AGR49310.1 : NLHFKNANPDIPALSDGRIVVDRNTPWDGG--LVAINSGFGGANAVLIFESEAGGAARTPARYAAPRLVLASGRTEAVQELTQLAAQHREDAGLHALLDAVHRHNIPGHSYRGFVAVLSDP-PVQE : 493
 ApFAS XP_008187030.1 : NINENTPREDITAFYNGRINVVADKTPWNGG--LVGINSFGFGGANAVLNLWNNSKINNGLPEDDLPRLVVASGRTEAVTTLLNDFLSRSLDKYVRLLDVQAEQIPGHYIRGYTIKKDCKANQ : 512

To continue the last alignment

CbFAS1 KU516006 : SFDKI--SLERLPLFYVFGDGR-DIYALQQFSAVPVFAGLQNIQGYLKKKDVVKTTLLSADEEVR--KSYNTLGLSLVIQICLADVLKKNLRPVSATGYSFGELVCAYYDDDLDTLTVLGLCLILN : 634
CbFAS2 KX467777 : VTQLP---GENRPVAFVFSGMGSQWPGMAKDLMLQDFKNSIILKCSDAIKPHGINLEDIILNGTEATFDNVLNSFISIAAMQVALTDVILKTLGTEPDVIVGHSVGEVGCAYADGTFIAGEAVLAAYSRG : 621
TcFAS XP_015836196.1 : SVKLR--RALDTFFYVYFGQFG-RNYKLGQFLMGFPVFCDTIKRIN-----ETLSGKTPPQ--AYQPIILGSLIVQLGLVDLLKALNLSFV--IYGDNWGKLATAYYYKTLLEECI----- : 607
TcFAS XP_008200285.1 : VTEYS---NEKRPVWFVFSGMGSQWPGMAKQLMEVEVFRNSIKRSAEILKPHGINLEDIILVNGTEATFENVLNSFISIAATMQVALTDVILKALETEPDGIVGHSVGEVGCAYADGTFIAGEAVLAAYARG : 623
AiFAS AGR49310.1 : CIELES---GDPRPVWFVFSGMGSQWPGMAKTLMLPFAAASINRSAAALRPHKLDLINIITDAPAAAFDDVINSFYSIAAVQVALVDVILRALETRPDGIVGHSVGEVGCAYADETLIAGEAVLAAYWRG : 620
ApFAS XP_008187030.1 : SMDLQYSGESRSVCFVFSGMGSQWPGMGTSLMLQPLTFNBSISLKSHSILKEFGIDLVKIITSTDANILNNTVNSFVGIAMQIALFDVLVAIGITPDIITGHSTGELVCAYADGCLTSEATTIKVAYYYG : 641

CbFAS1 KU516006 : GEALFNGEKNGLIFG-----SSSTNEKTKIRKDIYTKFSEELKNKQT-----VRRSEAFVDAILRLN----- : 693
CbFAS2 KX467777 : RAILESKLPLGAAAVGLSWEVEKRRCPPEIYPACHNSEDSVTISGPPAAIEKFVAELQAQDIFAKAVKSSGTAHFSKYIADAGPKLRKALDEIIPNPKPRSPRWISSIPESGWTGPMQHSAAAYHV : 750
TcFAS XP_015836196.1 : -----ISATNN-----HGKTPDFAPLPLNGQ-----LRSDSLTHDTLLN----- : 641
TcFAS XP_008200285.1 : RAILESKLIPGQAAVGLTWEAKRRCPDPVFPACHNSEDNVTISGPLDAVNFVDQLTSENIFAKVNVSSNIAFHSKYIAEGGPKLRKALEAIIPNPKPRTSRWISSIPESAWGTPLAQSSAAAYHV : 752
AiFAS AGR49310.1 : RSIYDAKLAPGAAAVGLSWEQCEARCPPDVPACHNANDSVTISGPVDSLEKFVAELSAEGTFARRNVSSGVAFHSKYIAAAAPLLRRSLEKIVITAPKPRTSRWSSSLPRDQWNSDLAKLSDANYHV : 749
ApFAS XP_008187030.1 : LATINSKLPLGAAAVFGIGVNIKDLLPTNVVVAWHNSPDSCAISGLKESVEGFVLKLSKSDISTQMINVLNTPYHSTSIAKKAIPSLLEYLKNIIITNPKLRSGKWLSTSVPEEKWGEDKAKYCSAEYCA : 770

CbFAS1 KU516006 : -----ITSTHDIHSDSLIVEIIGEN---ELMNYDS-EK--TPWEIKLSLFSHFIETFLQ-ILGSLYILGYNASIENLYPTIEFPVSKSTFNISSKIKWNHERKWFTHSQMVLNAKYPAPRHFEDL : 806
CbFAS2 KX467777 : NNLLSPVLFHEALKHVPENAVVIEIAPTGLLQAILKRAL-GPKVTNVSIVKRGHADNIEFLLSALGRIYNAQAQPKLSNLYHPVSFPVGRGTPEMINSMTIEWHSIEWSVANISGKGSRS-GELVVDIDL : 877
TcFAS XP_015836196.1 : -----LKNAFILNNSDS---NLNNRD-----VMITDGIKINFLI-TIGRLYELGHTPQLNQLYPKVEFPVSRGTGMIISPLVKWNHDRSWYTYKREFRITDAEQRDYFISY : 738
TcFAS XP_008200285.1 : NNLLSPVLFHEALKHVPENAVVIEIAPAGLLQAILKRAI-GPKSTNISIVKRHMENNVEFLTSAIGRIYNAQAQPKVGNLYHPVSFPVGRGTPEMIASMTQWDHSTEWAVANICDKGSRS-GELVIEVDL : 879
AiFAS AGR49310.1 : NNLLSPVRFADALREVPARSIVVEVAPHALLQAVLKRALPAPAAAHVPLVRRDAACACAHLLAAAGRLYAAQAQPAVGRLYPAVWVWVPRGTFLASRVWDRLEWQVAHTG-NASRS-GENVIEYDV : 876
ApFAS XP_008187030.1 : NSLLNSVLFDETFEHPKGSVLIIEAPHGVLQDVLNRSK-TNITNVDIASRNYKDGIDVLLSAFGKIFEAGLNPKIISNLYPDIIEFPVSRGTPEMIAPLVRWEHSEDWVYVWVRVQDKIKSGERNISIS : 898

CbFAS1 KU516006 : KNKQSWFVAGHLIDGRLLFPASGYLYLAWQTLGKFPKMLMEYIVTFRNCRFIRAINVPLDGSVALDVTIQP-SGHFEVLEGESIVVAGEIT----IEQREKAIERLPV--IPSDSNMINSKDIYKELR : 928
CbFAS2 KX467777 : SKESDQYLVGHTIDGRVLPATGYLTLVWKTFAKLRNEDFEQLPVIIEVDVQFHRAITMPKEGSKVFLINIFEGTGFBELCEGGSVAVSGKISVPEDVS-KEALDLPKPHGKTEKDVLPNSADVYKELR : 1005
TcFAS XP_015836196.1 : VYDEYKFMQGHVTDNRNLPATKYLTLVWETFAQSRRLLPEDVSVVFNCRFVRAVTPKTFGFKLLVITIGLNGNFVLEKDTLVVSGKIRTLLEETNQKETDFGPIDL--GSDCTQIEHDEIYRELY : 865
TcFAS XP_008200285.1 : SKEDDQYLACHAIEGRVLPATGYLTLVWKTFAKLRNEDYEQLPVIIEVDVQFHRAITMPKEGTVRFLINIFEGTGFBELCEGGSVAVSGRISVPEDVS-KELLHLPKPTPEVTKDLLPNTADYKELR : 1007
AiFAS AGR49310.1 : SRNDSFITGHNIDGRVLPATGYLTLVWRMFAKLRNKRPEETIVMSENIQFRRALIVSRDTPVRFLINVLVDTGFBFDVCEGGAVVIGTVRLADDPAGERLKDLDCPPREDGLLPVTDIYKELR : 1005
ApFAS XP_008187030.1 : KDEEHEYLSGHVIDGRNLPATGYLVMAWETLALMRGELYSEVPVVFENVRFRRAINIPKDGNEFIVMVKQSGSTFEVVEVGAPVVTGRLYIPTDANYEMIDMPPHPD--EPSDIDLN-IKDIYKELR : 1024

To continue the last alignment

CbFAS1 KU516006 : LRGYNYNGEFGAIREVNLDAHLITWNNWITFIDNMFQMKILKSDSRLLYVPTFLAKITIANKYHERFVAGLLGEKSGVLPVHYYPEVDITRCGGIEVHDLKASSIPRK-KVTATPVLETYQFLPN- : 1055
 CbFAS2 KX467777 : LRGYDYGGIFRGITESDNWGISGKIKWENNWISFIDTMLQFSILGQDTKELYLPTRLQRAFINPKEHLKATSELRESE--GVPVHMYRNIQVIKSAGIELRCMKASLAPRRQQSQAPPKLEKYQFVPE : 1132
 TcFAS XP_015836196.1 : LRGYNYSGLFKGIKAKNVEGSSGLVKEENWCTFTDKMLQLKILQNDTRLLYVPTVGIQKMWVNPVKHKFAEQLGEE-ALIPVYCYKDNVIKSAGIELGLQAKSIKAK-KQRLEPVLEKYQFVPE : 991
 TcFAS XP_008200285.1 : LRGYDYDGMFRGIAESDNKGIACKLKWENNWISYIDTMLQFSILGQNTRELYLPTRLQRCVINPKEHLQYLNGLKE-E--DPSVYMYRNIQVIKSAGIELRCMKASLAPRRQQSQAPPKLEKYQFVPE : 1133
 AiFAS AGR49310.1 : LRGYNYGGIFRGIRASDPRGTCGELAWDDNWSFMDTMLQFGIIGVDTRELYLPTRLQRALIDPAAQLAAVAALGEGG--TLPVRMHRDIDVISAAGIEFRGVKTSLAPRRANPNAPKLEKYVFLPYD : 1132
 ApFAS XP_008187030.1 : LRGYNYKGMFRSLNRVNLDAIVGRVGFNWNWAFMDNMLQIQILKEDTRALFVPTSLQKLFIVKKHATILQTLPEDK-PEFPVYVPEIDLQSGGVEIRGLHANVIAKR-KPLADPVTEKYTFVPE : 1151

CbFAS1 KU516006 : -----YIELSTADSVRVNAQIILEN-TLLRKIKSLEIIEDETLPEDYQVLSITLIDCLGDQPMIQPEAAIQI-----TAEINVDVTIINKLVP---EDEYTLITAINISKV--VKLLGEASNA : 1163
 CbFAS2 KX467777 : NNQPLTEDSDKAKTHALTVLLQTVIENSSGALKIKVAEVTGDKPIE---AILAPTIKNILESEPMIESTDVTVVTG--GPVDTTSLEANDVKKHVIDVNSNTVAQDAHLVVASDLIMYDRRVLDNAVAS : 1256
 TcFAS XP_015836196.1 : -----SITLSLGDSTRVNTQIILEN-SLESHFKSVEIIDEETSQ---LTPLSPLFCKSLDDVPMITPNVITSTK-----KTLEEIPGVKIEDFVITP---ESNLLIIGIKLQR--PTIPKLYFQA : 1098
 TcFAS XP_008200285.1 : NNTALSENQDKAKTHALTVLLQTVIENSSGALKIKVAEVSGRPVV---AIIAPSVKDIIDEREPMIESTDVTVVTG--GPVDTTSLEANDVKKHVIDVNSNTVAQDAHLVVASDLIMYDRRVLDNAVAS : 1257
 AiFAS AGR49310.1 : NAAVATEDIISRSKRDAITVSLQLVLEN-AGALKIKLAEALDRPAE---ALLTPQALAVLESEPMIESTDVTVVTG--GPVDTTSLEANDVKKHVIDVNSNTVAQDAHLVVASDLIMYDRRVLDNAVAS : 1257
 ApFAS XP_008187030.1 : I-----EIDYILEQIVRISLHLVLEN-LMDIKVKTVETIINKTFNP-DVQILSPIILDVADLPIIQPEVSLSDG--THPQLKEIGSNITVEDKRLSS---DQSVLITVSGSVLQD--SVLLEQVFAT : 1265

CbFAS1 KU516006 : IRENGFLICRESPDFENMP-----QSIGLSVITVHRNPKETLVLNKLKSKKKK-TVFDFTEDPQFDWLPKIQDKIKWAIKKN-EEIILQSTKNSKSGLLGFVNCNLRREPEGIVKCVLVLDETE-DF : 1283
 CbFAS2 KX467777 : LKPGGFILLEELKSPIDM---NKLDG--LELISKQLTDTKIYLLLRKPTVEPTDATVIQVTENN-FSWVEPLKDKAMKQAESDG-RKTYLYVHGEELTGLVGMVNCNKQEPGGANLRSTFVQ--DSKAP- : 1375
 TcFAS XP_015836196.1 : LSSKGFLLSRESKDFHSEN-----IEN-LEILTEFTTSDEKLIMFRKNCAIPV-PHFVKIGPET-EDWLPBLQK---SLKNH-DSVIAFAQNETPEGILGLVSLRPEPTGNKYRCYFLMDESP-EF : 1212
 TcFAS XP_008200285.1 : IKDGGFVLEEPKGAINS---GKLSTTEIIVYSTQVPTPKSYVLLRKPVDVRSSTAIQITENN-FAWVEPVKDKAMKSEGDG-SKIYLYVQGEELTGLVGMVNCNKQEPGGVGRVAVFIQ-DTNAP- : 1378
 AiFAS AGR49310.1 : MADSCMLLEEPHKALDDRAAQEMLRAGLSPVSRQVAASCEYVLLRRAPALPAQHVVVDVADTTSYAWVDALREALARAEGED-MRVYCVAR-TPNSGVLGCTCLRGEACGRALRCYFLP-GAREPF : 1383
 ApFAS XP_008187030.1 : LKPGGFLLTREKLNVEYS-----QGSVEVCLDASLEQERLMLVRKPLEQNI-VPIIVKISSTEFVLPVQLKLDKADASVSQKIVLVGEKDPKNGIVGLLNCIRKEPCCRVRVCFIMDKCAPIF : 1385

CbFAS1 KU516006 : DPNVKLFADQLKGLAINVYQNGSWGTYRHLILK---KPEVVKSDHCFVAQTVRGLDSSLTWFEGLNRDMLK--EPEKRIIKIHYSSLNFRDIMTASGKINVDAITTNRLQEQCGGCFEFGIDQSQ : 1407
 CbFAS2 KX467777 : KFSISAYENQLKDLVHNVMKNNTWGCFRHIMLENYDSDGKLVHEHAYINTLTRGLDSSLRWIEGPLETYKGG--DAKSELCHVYYAPLNFRDIMLATGKLPDAPGLAGQDCILGLEFGSGRDSKGR : 1502
 TcFAS XP_015836196.1 : DPENSLFAAQTRKDLAFNVYKDGTYRHLILE---ELEBVESEHCYANVTYRGEIQLSLKWLCEPMRKSQSVI---KKNVMIILNYATINFKDVMSSGRINVDVITSDRREQEALGFEEAGRDLRGR : 1336
 TcFAS XP_008200285.1 : KFSLSAYEQQLKDLVHNVMKNVWGSFRHILLDHDHDGKLVHEHAYINTLTRGLDSSLRWIEGPLETYKGG--DAKSELCHVYYAPLNFRDIMLATGKLPDAPGLAGQDCILGLEFGSGRDSKGR : 1505
 AiFAS AGR49310.1 : RPDAAPIAAQVRRDLAVNVLRAGVWGCYRHLPLG--DAEAQLQVEHAYVNTLTRGLDSSLRWIEGPLETYKGG--DAKSELCHVYYAPLNFRDIMLATGKLPDAPGLAGQDCILGLEFGSGRDSKGR : 1510
 ApFAS XP_008187030.1 : SLDEPLYKQKLNKDLILNVYKKNVWGSYRHLILE---PPSLIEVQHSVCNTSIRGLDSSLKWFQSGIVPFTPK--PAESDLVHVVYALNFRDIMLATKLAPEVIARGRINQESVIGFEYSGRRENCE : 1509

To continue the last alignment

CbFAS1 KU516006 : RVMGIIPHGALSTLAYADNHLWVRPDBWSLAEASVPVYGTTVYALAIRCGMKRCDLSILHSCTGGVQAAIRYALYHGCTVFTTVGNQAKRDFLKQLYPQLTDKNIGTSRDSFVKMVMKRTKGRG : 1536
CbFAS2 KX467777 : RVMGMVAAKSLAITVYADPGFLWEVPEKWSLEEAATIPVYGTSSYALVVRGGLKPGQSLLVHAGTGGVQASISLALHMGCTVFTTVSSQAKRDFLKKTFPQLKDEHIGNSRDTSFQQLVMTQTNGRG : 1631
TcFAS XP_015836196.1 : RLCCGMDNSAFSSHISADPTLLWEIPDSWSLEDGATIPVYGTVLYALLMVRKLRPGSSILHSATGGIGLAAINVCLYYKCCQIYLVGTQEKRDYLRKMYPPQIPQTRIGNSRDTSFEEIMKRETNGRG : 1465
TcFAS XP_008200285.1 : RVMGMVEARSLAITVYADTGFLEWVPEKWSLEEAATIPVYGTSSYALVVRGGMKPGESLIHAGTGGVQASIALALHMGCKVFTTVSSQAKRDFLKKTFPQLNDDCIGNSRDTSFQQLVMTQTNGRG : 1634
AiFAS AGR49310.1 : RVMGMVAACGLASTVYADKGFLEWVPAKWSLEEAATVPVYATAYALAVRCRMQRGDSVLVHAGTGGVQAAVALALHAGCTVFTTVGTDPKRAFLRERFPTLPPENIGNSRDTSFQQLIKRRTRGRG : 1639
ApFAS XP_008187030.1 : RIMGMITSRALTNILVHDKYLAWKVPDSWSLEEAATVPVYGTVYALIVSRMCRKCDLSVLHAGTGGVQAAITIALYECIFFTVGTAEKRFIKTHFPQIPESHIGNSRDTSFQQLIMMETDGGK : 1638

CbFAS1 KU516006 : VDIVLNSLAEDKLLASARCLGKGRFLEIGKYDLFANSPLSLLEKEASFHGIIVLDALFNSQP--SEKLTLYKLGEGIRSGSIKPLGTTVFKTNEIECAFREHMTRGCIHMGKVLVEVQKEEKIETKRP : 1663
CbFAS2 KX467777 : VDCVLNSLAGSQLQASVRCLEIGGRFLEIGKYDLSNNSPLGMSIFLKNITFHGILLDALFDSSES--PBKRWVFNLYSEGIKTGAVRPLPKSVFNEHQVECAFREMASCKHIGKVLVLIQREESRKTQRP : 1758
TcFAS XP_015836196.1 : VDIVLNSLSEKLMASVRCVAPGGRFLEIGKFDLANNTQLGLLMEKGISYHGVMLDQIYNNSP--ELKRELISQIVSDGKIGFKPLPRVVFKRPEIEAHRVMMTGRHMGKVMKIRHEEPKTAHIP : 1592
TcFAS XP_008200285.1 : VDIVLNSLANHQLQASVRCLEIGGRFLEIGKYDLSNNSPLGMSIFLKNITFHGILLDALFDSG--PDKREVVRLINEGIANGAVKPLPSTVFNENQTECAFREMASCKHIGKVLVLIQREESRKAQRP : 1761
AiFAS AGR49310.1 : VDIVLNSLAADKLLQASVRCLEIGGRFLEIGKYDLSNDTALGMSIFLKNITFHGILLDALFADSENDSKAAVRCVTDGIAAGAVRPLPATVFSDFQLECAFREMATCKHIGKVLVLRVDEE--AAGARP : 1767
ApFAS XP_008187030.1 : VDIVLNSLAEEKLLASVRCLEIGGRFLEIGKFDLANNSMIGMELFLKEISFHGMVLDLTFESPD--EWKEVFQRQVQENIDSGAIRPLVRIVFESDQVEPAFRVMAAGKHIGKVLVLIQREEDDRFIRP : 1765

CbFAS1 KU516006 : D---IRGIIPRYNCHADKCYIIVGGLGGFLELTDWLILRCARKIVLTSRGGIRTYGQRSRIRLRWSYGMVLAISTSDVTTNDGCKELIEEANKLGPICAFNLAAVLQDAAFENQRKMYEISLAPKAY : 1789
CbFAS2 KX467777 : ATKTYAATPRTYMDPEKSYVLVGGGGFLELAKWLIVRCATKIVLTSRSGVKTGYQSLOVRRWREKGTQVCTISTADATTEKGAARLLEEANALGPVGGIFNLAIVLVDAMMENQSEADFKTVCKPKVD : 1887
TcFAS XP_015836196.1 : NDQLFKVHPRFYANGSRVYIIVGGLGGFLELADWLIVRCATKIVLTSRHGVTTYGQNRQTIWKSYGQVVIISTHDIITKLCQLIKQAATMGPIDGFNLAGVVLKDALFEDQNEESFKLSRAPKST : 1721
TcFAS XP_008200285.1 : KPKTVAATPRTYMDPKSYVLVGGGGFLELANWLITRCASKIVLTSRSGIKTYGQSLOVRRWVDSGMKVLISTADATTEKGAARLLEEANALGPVGGIFNLAIVLVDAMMENQTEADYKTACKPKVD : 1890
AiFAS AGR49310.1 : ASKLYSAIPRTYMPKASVYLVGGMGGFLELAQMMVKRCCTRLVLSRSGVRTGYAWCVRRWREAGVRLVSTADACSAAAGARALLREAAALGAVGGVFNLAIVLVDADFQTPADFKQAVAKPKID : 1896
ApFAS XP_008187030.1 : RSINVKAYPRVTFDKNSSCLICGGLGGFLELADWMLRNSRNILITRTGIRNGYQALRKRWRWESYGANVISTADITTEEGVQQLNEANKLGPVSTIFNLAIVLVDALFENQTEEDFKASFGPKAI : 1894

CbFAS1 KU516006 : ATKCLDEVSRSLCPBELSDFVVFSSVSCGRGNPGQTYGMANSVMERICBQRRRDGYFALATQWGAIVGLVAEMQELHSELEISGTLPRQRISSCMEVMDIALRQKSATIVSSMVVAEKRSSANSA--- : 1915
CbFAS2 KX467777 : GSKHLDAASRALAPHLDYFVNFSSVSCGRGNAGQANYGLANSAMERIAEFAQAAGLPGVATQWGAIGVGLILETMGGN-DTEVGGTLPQRWSSCLTMDIFLQCC-PHSHVASMVLAEKHKGTGSGSQV : 2014
TcFAS XP_015836196.1 : ATRFLDEITRVSOPELRHFVVFSSVACGRGNCGQTYGMANSIMERICBKRKNKGFALATQWGAIGVGLVAKMKENRELVIIGTLQKQISSCLEVLDRLKQ-GNPVVSMMVVAEKHNRNENL--- : 1846
TcFAS XP_008200285.1 : GSKQLDAASRALAPHLDYFVNFSSVSCGRGNAGQSNYGMANSAMERICBARQAAGLPGVATQWGAIGVGLILETMGGN-DTEVGGTLPQRWSSCLTMDIFLQCC-PNAVVSMMVLAEKHKAGADANQV : 2017
AiFAS AGR49310.1 : ATKILDAATRELAPELEYFVVFSSVSCGRGNPGQSNYGLANSAMERICBQRQADGIPGLAVQWGAIGVGLIVETMGGD-ETVVGTVPRQIASCEALGALLAL-PHAVAASMLADKRR-SAAAPQQ : 2022
ApFAS XP_008187030.1 : ATSLDKYSRTMCPBLKHFVVFSSVSCGRGNAGQTYGMANSVMERICBIRHSEGLFALAVEWGAIVGLVADMAEDNQEVVIGGTLQKQIGNCLEILDLLTQKNNPIVSSMVVAEKRSSNAG-- : 2021

To continue the last alignment

CbFAS1 KU516006 : SLSGTVLDIIGIKDIKSVSIQSTLAEIAGMDSMTGVEIRQVLERBFDVFLSAKELRRLTVARLMKLEEEK-QNQMTENKHN-----FSLKBEIMSLLPDNDKGAIVILELBSRISD-----TEGAPL : 2029

CbFAS2 KX467777 : SLTDAVGNILGIKDTSTVAPSATLADLGMSLMAEIKQTLERNYDLVLSAQEIRGLTFGHLELSSGGSAGAPTETPGLQD-----NN--IQFDKTAETMPKKTIVQMPSKT-S-----DNKRTP : 2127

TcFAS XP_015836196.1 : SAVEAVALVLGIKDIKTVSQHATLAEIAGMDSMMGTVEVIQLEKBYEYITAKDVRSITFAKLRREIADRSEVKASDTKTS-----KGTNLLMKYIPDSKTSHLPTIRLESRVKE-----SANAPT : 1961

TcFAS XP_008200285.1 : SLIDAVANILGIKASTVTASASLADLGMSLMAEIKQTLERNYDLVLSAQEIRALTFGKLTLELSSGGAAPVETSAP-AGD-----NQ--VQFDKNAEIMPSKCLVQMKSKG-G-----DSKKNP : 2129

AiFAS AGR49310.1 : DLLHAVANILGIKDPKTVSDSANLAEIAGMDSLMAEIKQTLERGVYDVLGVQETIRGLTFSKLRGMAGGEDAAAGDAAPAATE-----SADQVQFAALGELMPKQVLVKLPSAAPA-----GSELRP : 2138

ApFAS XP_008187030.1 : TIVDTVINILGLRDLKTIISLHSTLAEIAGMDSMMAVEIKQTLERQTEVFLTPQDIRSMTFAKLRQETIGSSDDKEKKADVDSKSIQVQPDVGLGYLIRAIGEESAYNSVMRIPSLCEDGSVVEQPTTKLNT : 2150

CbFAS1 KU516006 : VFLLGGIEGYSEALRTEITRQLNARTISFQYDYDNPNDNIVKMAALYSYITEDNITKDDPFCITVAISYGCAGLEVVSVLESKGYKGLVSDIGSPSVLQT-LASLIS--HENVK-IFEVSIIRETTNSY : 2154

CbFAS2 KX467777 : VFVLLHPVIEGVVKALEALAKNIDAPVYGLQCTATTPLTSTIVDLAKHYIAQIKTVQPKG-PYVLIQYSFGACVAFEMGLWLEKNNKVKLLLDGSHSYVATHGKAR--SKIQGGTAVEQSEVLVYFMMQ : 2253

TcFAS XP_015836196.1 : IFLLAGIEGVFHPANITKNLNAHIFGQYDYNPEDTITFEVALKLLPHTEANLPQNRQFKIIGYSFGAAVGLVVSLEKMGKLGKMMTIDGSPSYLTASAKEYLP--EVDEA-EFQTALIFKILAVL : 2087

TcFAS XP_008200285.1 : VFVLLHPVIEGVVDALQVILASNTEAPVYGLQCTKDTPLTSTIGDLAQYNNKQIKTVQPKG-PYTLVGYSGACVAFEMGVQLNSGEQVKLLFIDGSPYVATHGKARNTKSLQGNTAAEQSEALVYFALQ : 2257

AiFAS AGR49310.1 : VFMVHPVIEGVVELLRGVAAAWRAPVYGLQCTQAAPLEDMAALARHYVTHVRAMQAA-PYTLVGYSGAGVAFEMALQLEQAGCETRLVLDGSPAYVATHTRGKK-KRTTRSAETDEADALAYFVQL : 2265

ApFAS XP_008187030.1 : LFIIPGLEGISSMLEPLSRNLNMQVLCQYDILGTASTIEEMAATHYTLIQERLSADQEFSTIVGYSGGLIAIEVLKMLEKNNRTGKLVLDISAPQFLKMTTELAIRGDKAQDQ-EIQVQLILRFLDLV : 2278

CbFAS1 KU516006 : VENDVISRYIPELMEIESLDERLERTADIVK-EYLPYEKEFIKSLYKGLIKRMWALKMYT-PTFTKINSKVIILFKPTEQILKEYLYDLGLSLTCGNPVEVIEIEGNEHLSILG---DENLANRINSL--- : 2276

CbFAS2 KX467777 : FKDIDQQAVVSEELASLKSWEERLQAVQLLS-GATPYKAEIISDAATSFYGKLVVADKYT--PSGKFGSDVTLVKAIDNYVQM-GDDYGLSEVCKQKVNVESLKGNEHRSILAGNSVEKLTADILN-KLIKV : 2378

TcFAS XP_015836196.1 : VPIDLLVAFKDKLLKCKDMNERCDLVLEMLP-IEVEIKQKMEKQAALTYKRFKAVIGYK-FEHEKIKSPVHLVKAKFAMVNE-EDDYQLSKCES-VEFSTVNGDHTILD---QEBLVKKVEGFL-- : 2208

TcFAS XP_008200285.1 : FKDIDQQAVVTELMSLKTWEERLVARATQLVS-GAAYPKPEQLAAAAASFYKLVVADKYK--PNMQFKGPTLIRAIDNYVQM-GDDYGLSEVCKGKLVQALEGNEHRSILGGSTVQKLANITHNDFIKA : 2383

AiFAS AGR49310.1 : FKDVDAANVSSLELERLPSWEARLAHTTALVGAAGPHGAEALAAAAASFYKLVVADTYK--PAGRLRAPVTLFTARDNYVTL-GEDYGLREVCAEGLHTQQLAGTHTILAGDAAAAIAQHLSQMLAH- : 2391

ApFAS XP_008187030.1 : WPHN-KTKITTELYQINSWDERLNYFIEGVP-DDVIYSKIYQKQLLNCAYIKLKALINYGKPNGSLKTRTLLIRPTEQVLPVPI-SEDYGLSEYFNSAVMVHFVEGNEHYSILE---NKKVAELLSQSSSFKDL : 2404

Figure S1. Alignments of *C. bowringi* FAS protein sequences. Alignment was performed in MEGA 4.1 and Genedoc Version 2. *C. bowringi*, KU516006, KX467777; *Tribolium castaneum*, XP_015836196.1, XP_008200285.1; *Agrotis ipsilon*, AGR49310.1; *Acyrtosiphon pisum*, XP_008187030.1.

Figure S2

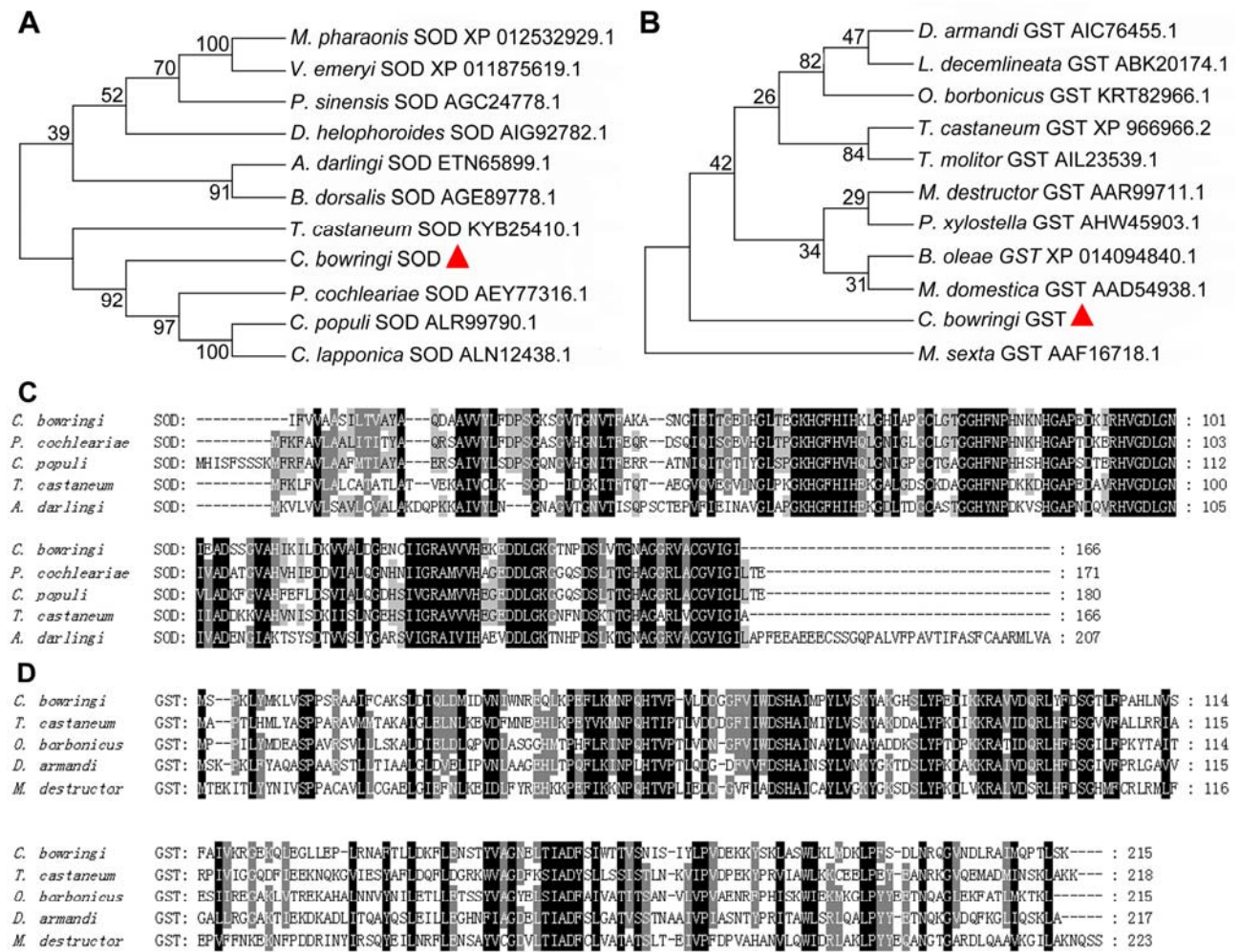


Figure S2. Gene identification of *C. bowringi* SOD and GST. Phylogenetic tree analysis of SOD (A) and GST (B). Red triangles denote *C. bowringi* SOD and GST proteins. Alignment was performed in MEGA 4.1 and Genedoc Version 2. The proteins of SOD are as followings, *Monomorium pharaonis*, XP 012532929.1; *Vollenhovia emeryi*, XP 011875619.1; *Pelodiscus sinensis*, AGC24778.1; *Dastarcus helophoroides*, AIG92782.1; *Anopheles darlingi*, ETN65899.1; *Bactrocera dorsalis*, AGE89778.1; *Tribolium castaneum*, KYB25410.1; *Phaedon cochleariae*, AEY77316.1; *Chrysomela populi*, ALR99790.1; *Chrysomela lapponica*, ALN12438.1. The proteins of GST are as followings, *Dendroctonus armandi*, AIC76455.1; *Leptinotarsa decemlineata*, ABK20174.1; *Oryctes borbonicus*, KRT82966.1; *Tribolium castaneum*, XP 966966.2; *Tenebrio molitor*, AIL23539.1; *Mayetiola destructor*, AAR99711.1; *Plutella xylostella*, AHW45903.1; *Bactrocera oleae*, XP 014094840.1; *Musca domestica*, AAD54938.1; *Manduca sexta*, AAF16718.1.

Figure S3

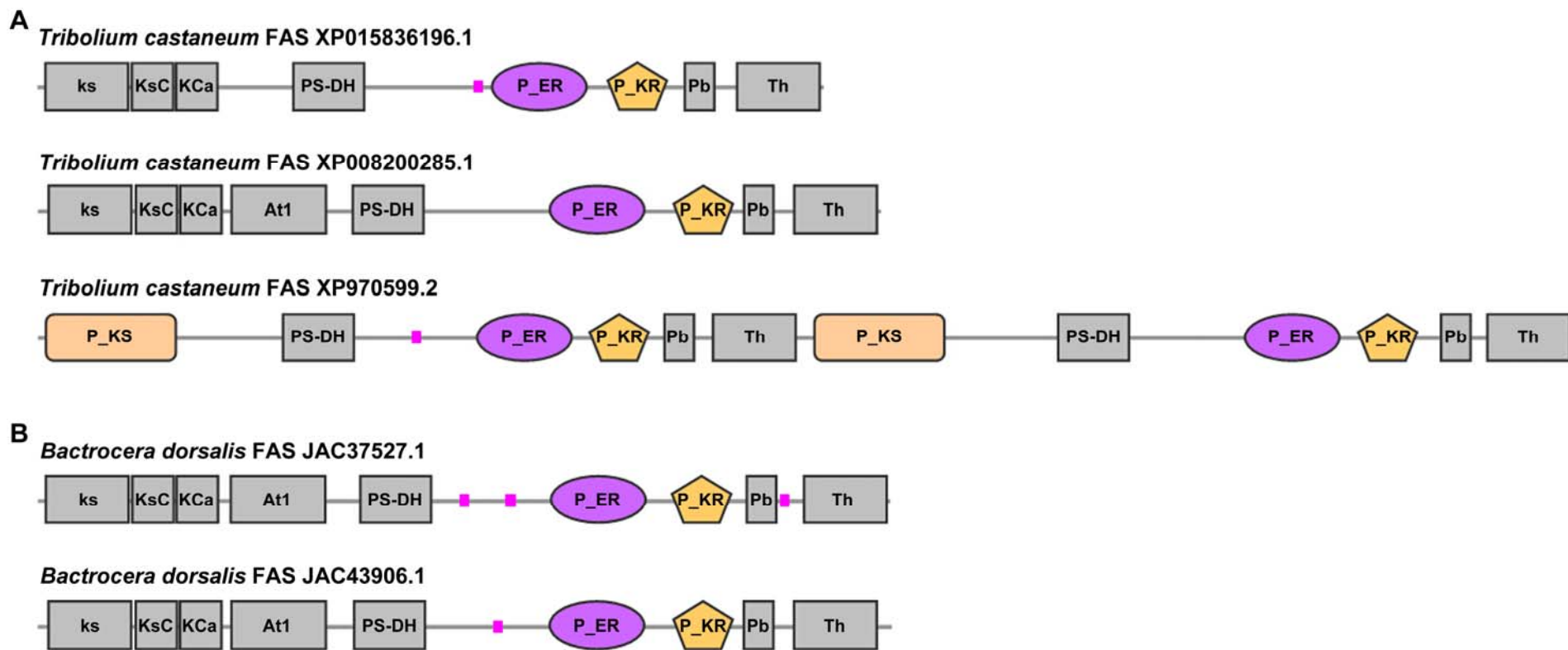


Figure S3. Schematic diagram of deduced domains of FASs of *Tribolium castaneum* (A) and *Bactrocera dorsalis* (B). FASs protein sequences were download from NCBI database and the protein domains were predicted with SMART tool. ks, ketoacyl-synt (pfam00109); KsC, Ketoacyl-synt_C (pfam02801); KCa, KAsynt_C_assoc (pfam16197); At1, Acyl_transf_1 (pfam00698); P_ER, PKS_ER (smart00829); P_KR, PKS_KR (smart00822); Pb, PP-binding (pfam00550); Th, Thioesterase (pfam00975); P_KS, PKS_KS (cd00833).

Table S1. Primers used in cloning *C. bowringi* cDNAs.

Primers	Sequences (5'-3')
FAS2-cloF	gttcctaacaggcaaaattg
FAS2-cloR	ttcggttccccaatagaaca
SOD-cloF	atattcgtggtgcagcttc
SOD-cloR	tattccgatgactccacagg
GST-cloF	atgagtccaagttgtacatg
GST-cloR	cttgacaatgttggttgca