

**A**

GH45-1 MLSL-----KIAVAIILSLAG--VTIAQDLTPIPGGKSGDGVTTTRYWDCCAPSCAWYPRIHTQNGVPIQOTCKADGVTSPSKDLNA-QSGC-  
GH45-2 MKLLVA---IAFLGYVAAGSFGRCPPGDI VPIPGGLSGDGIITTRYWDCCAQTCAHRQNVKTDNGIPVQTC AIDGTTNIITIDQNGIVSGC-  
GH45-3 MKYLIV---ITFLGYVAAAS--SDRSPEIVPIPGGISGDGITTRYWDCCAPSCAYYGFIKTKNGIPDQTCQIDGVTNSTKDNNNA-QSGC-  
GH45-4 MYTGIVNIFLVSIAIVTASS--KESSPDI VAI PGGLRGDAITTRYWDCCVVSCSWDANVHTKNRQPVKSCQKNGATYSTRENNG-NSVCY  
GH45-5 MKTFTV---FASLIVFGASL--KEPSPEIIPVPGGLSGDAVTTTRYWDCCGVSCSWDGI VHTKNGIPVRSCEKDKGTYSTKENNA-QSTCW  
GH45-6 -----RYWDCCKPTCSWPGNVNYKT--PVKSCQHDGVTAI--DPET-QSGC-  
GH45-7 MKIAILV--SALVALAVATP--LEQSPEIKFIEKGISGETTTRYWDCCKPSCSWRGNVHTPSGVPVASCDRSGVNRV--DANA-KSGC-  
GH45-8 M---IFN--CFIFSVVLAVT--LAYSPEIKKIVGGKSGYGTTRYWDCCKPSCAWKENIKTPDMEPIATCATDGVTVV--NASV-QSGC-  
GH45-9 MIFII----FSLLAFLVGLAP--SIDALELTPVEGGLSGNGSTSRYWDCCKPACAWPSNV-PHSRPRVTSCKADGITPI--NPDA-MSGC-  
GH45-10 MIPLPI---LLVLAVATSIK--AEVSPDI IAVPNGLSGGKITTRYWDCCKPSCAWADNVNTPDKQPLKSCRVDGEAVA--PPND-PSGC-  
GH45-11 MKYTTIS--LLLLAAVVAATSLNNQNI VIKKIPGGLSGVGTTRYWDCCKCATCSWPGNVEYK--PVKACQADGENAN--DPEN-ESGC-

GH45-1 -EVGGVAYTCTNQSPKINETLAYTFVAASFAGGLDY-ADCCICLVMDPKG-KLAGKRLLAQVNTNTGEA---LQNHFIQMPGGGVGIY  
GH45-2 -RVGGQAFACSNQPPYVVDTLALGWSAASFTGGIDN-SKCCSCFLLSFKD-QLAGKQMLVQLVNSGTD---LASNHFLQIPGGGVGLW  
GH45-3 -EQGGVAYTCSNQPPSVINDTLAFGWAAASFQGGIDT-SKCCCHILLSFKD-QLAGKQMLVQIVNTGSD---LNENQFLQIPGGGVGIF  
GH45-4 PDHPGNAYCNNSNPFVNSTLAYGFAGVSFQGGADV-EHCCHYLLSFKG-KLQGGKMLVQVINTGAD---AVAHHFLQIPGGGVGYN  
GH45-5 -NENGAFTCSNQPPFVINSTLSYGFAAVSFGVSTDT-GHCCQCYLLKFQG-QLKDRELLVQAINTGSD---LTTNQFLQIPGGGVGLY  
GH45-6 --VGGGAYCTNQQRSVNDSIALGFVAAKFIHS-NR-NMCCSIVFRFKPAELAGKQMLVQVNTGDDDPHATHNEFLIAMPGSGVGYI  
GH45-7 -EGGGSAYMCNSQPPWAVNSTLAYGFGAASFNGVDV-SLCCACFLLSFKD-QISNKKMIVQVNTGSD---LSHNHFLIAPGGGVGIF  
GH45-8 --IGGTSYMCNNQPPFVNETLGYGFAAVSFGVDN-DLCCSCYLLTFQN-QINNKLVLQFTNTGGD---LGSNQFLIAPGGGVGAF  
GH45-9 --ENGTAYTCTNQPPFIVNQTYGYGFAAAYLIGGPSTNNFCCACFLNFTD-QIKYKHMVVQVNTSGTN---FDKNEFLIAPGSGVGDH  
GH45-10 -DINGSSFCNNSNPPYVNSTLSYGFAASFSGGIDT-SMCCSMLLNFEG-QLKGGKQFLVQLTNSGEE---YQTNQFLGIPGGGVGLF  
GH45-11 --IGGQSYICTKQSGFAINSTLAYGYVAARFHGT-TR-NMCCSCLVFSFQPELANKKMLVQVNTGNA-PETNTNLF IAMPGSGVGYI

GH45-1 NLGCKTQWNA PDDGWGERYGGVTDIKGC-KQLPEQLQEGCRFRFTWMKGVNPPVSYFYQIKCPEYFVGVSKCGDL---  
GH45-2 NHGCDAQWAGENGWGRYDGVSSLEEC-CLLPEVLQPGCRFRFQFMGQVYRPNVTFQEVQCPAELIAVATACGNLNY-  
GH45-3 NLGCMTQWGTGEDGWGRYGGVSSIEEC-SILPEVLQPGCRFRFQFMGQVNDPKVVSFQEVKCPAELVAVSACGDL-  
GH45-4 TQGCRIQWNA PENGWDRYGGVHSEQEC-NQLPWQLQAGCKFRFQFMQGVSNPDVVSFQEVKCPSELVITGCGDL-  
GH45-5 N-GCVKQWNA PVDGWGERYGRVTSVEGC-DQLPVQLQDGCKWRFYLEGVSNPSATFYEVKCPSELIAITNCGDRD-  
GH45-6 TQGCSSQWNA DVSQWGDQYGGVHSEIEEC-HNLPAHLQPGCEFRFTWMKGYSNPDIEFDEVVCPKRLTDISGCYPASHP  
GH45-7 TQGCCHDQWNA PWNWGDQYGGVHNRGEC-ATLPQALQSGCYFRDFYQANNPRMHFDQVQCPAEIVARSGC SL-  
GH45-8 NQGCCHDQWNA PWTGWQYGGISSREELSLPKELQSGCLFRDFDMQANNPQMYFEQVECPAELVKISGC SLPL-  
GH45-9 PEGCHDQWNA PWTGWQYGGVHMRSECVTLPEELQEGCKFRDFMETANPLVVSFQQVVCPELVKISGCRIP E-  
GH45-10 PKGCTAQWNA PSTGWGDLYGGVHTEEEEC-NELPEVLQPGCKWRFQFMGQVSNPEVTFYQVQCPRELVERSGCVL-  
GH45-11 TQGC TSQWHTDVSSWGDQYGGVNSLQEC-YNLPQLWEGCAFRFNWMLGYSNPDVVSFEEVECPQELLSISGCDPISHP

**B**

GH48-1 ---MRLGLFVLFVCTSTALAGTYTDRFLTQYRKIHDSNNGYFSKEGIPYHSVETLIVEAPDHGHETTSZAYSYYVWLEAVYGKVTGDFSS  
GH48-2 -----  
GH48-3 MTPHLHLVLAVIIMNHASCESVYKQRFLEQYNKMHDPNNGYFSSKGIPIYHAVETLVVSSDYGHETTSZAHSSYIWLEAMYGGITNNFSR

GH48-1 FNNAWNLETYIIPVYSSQPTNSFYTPGHPATFIPEQDDPSQYP-SQIDSSVPVGDPLHQELVNAYGSHEVYGMHWLLDVDNIYFGNT  
GH48-2 -----  
GH48-3 FNEAWEIMEKYIIPVHESQPTNLYNPSHPAGYGEQEYPEDYVPGVPDPPAPVGDIPLYQELVDYTGTSIDIYAMHWLLDVDNVYGFNGS

GH48-1 PGNCNLGPSAGGPSYINSYQRGSMESVWRTIPQPTCDNFRFGNGHGLDLFTKDNSYAQQWKF T NAPDADARA IQAAYWAGQWAQQSGQL  
GH48-2 -----  
GH48-3 PGNCELGPNEPGPSFINTYQRGPRENAWKTIPQPTCDSHKYGGPEGFGLFSTGD-HAPNWKYSVAPDADARAIAAAFWASRWATKSGHL

GH48-1 GTIQGTLAKAAKMGDYLRALFDKYFKQVGNCDNRWSCPGGYGKSSAHYLLGWYYAWGGSVDTNGGAWRIGD SAAHFGYQNPLAAYALA  
GH48-2 -----  
GH48-3 SEITDTLQKAGKGLDYLR YCFDQNFKRIGNCIDPYKCPGGTGKDSAHYLLGWYFGWGGISSEYGYSWRIGDVAHFYQNPMAAYALI

GH48-1 NDPNLRPKGATAVSDWQTSLERQLEFYEWLQSAEAGAFAGGATNSINGHYDSSDLTANTFHGMYYDWEVYHNPSPNRWYGMQSWSVDR  
GH48-2 -----GAFGGATNTWNGRYDTPPQELTNTFHGMFYDWEVYHNPSPNRWYGMQSWSTDR  
GH48-3 NEPNMTPKGATAVEDWQISLDRQLELYDYLSVEGAFAGGVSNSWNGRYEQPEELMDNTFHGMFYNWEVYDPPSNQWFGMQPWSWDR

GH48-1 LAQYYYVTGDSKAKSVLDKWNWILKETTIEAGKSFKLPSQLSWSGNPNVHCTINAYTTDVGSASGTARTLAYAAKANHAQAKEVAKE  
GH48-2 LAQYYYVTGDATAKTL LDKWVKWVISEIKFE-GTGYTHPDHLEWSGQPPNVHVQVTSYSDDVGTASSTA-----  
GH48-3 LAQYYYITGDDKAKKILDKWVSWI IANTYFE-GDDYRIPSTLDWVGVPNVHCKVYVYGNVGPAAATARTLSYAAARANHAEAKNLAKK

GH48-1 ILDIMWNNFQTSKGVSSPEVADTYTFNEPVFVNGWYGTYPKGDVIQSGATFLSLRSWYKSDPDWNKVQTYLNGGSAPTFTYHRFWAQA  
GH48-2 -----  
GH48-3 ILDSLWNLHRTPLGI AVEEQPEIH--FNQSVYVPKDFHGVYPNGDVIDSDSTFISMRSFYKNDPQWNKIESYMGNGPAPKFTYHRFDWQT

GH48-1 DIAISNGVYGILFNE  
GH48-2 -----  
GH48-3 DVALGFGVYGLLFDE

C

GH28\_1 M--TNLTLLIVFSVIVATIAIPFNST-KNIGDGTISNIWEVENVVKCKNIVVNNLYVPGGQKLEKLSHSGTVLKFQGTTFQHSNW-E  
 GH28\_2 M--ATLTLFLVLCAAVATSALSNST--NVGAGCTISKIGEVNDVVKCKNIVNNSLSPVGGKTLKLDLHPGTTLKFQGTTFQHTNW-E  
 GH28\_3 MYYTIMCYLFLFLFNAALVICKCSP-----TNCBITNFQDQVDFVHRCSDIIIRNLDVPAGQLELDLQOGASLTFFEGITTFDYTNW-S  
 GH28\_4 M-NLFIIEFNIVVLLNSLFLISCVDF---QPCTITNFSQVSEVLQSCKNITISNLNVPAGQQLYLELLNDSVTFEGVITTFGVAQW-K  
 GH28\_5 M-----SYTKFLIVAFISTVSAN-----NNCTITEFAQVAEIVKECSNIVINDLVVPAYSTLLNLLKNGSRVTFFTGNVLFVEVGYW-E  
 GH28\_6 M--RTIQLFEYFFLCSIAAYASNLT-----ASCTISRFDHVDTVVVSQCKSITVESFAVPAGQTLKHLHQYGTTLTFNGNIAFYSEW-D  
 GH28\_7 MIKTGMSLVFLFVLGVVLAQE-----YDCEINSIDQVLPVIEKCSVITVKNLWVPSGQTLLELSLKDNSHLIFDGNVTVGVKYQE  
 GH28\_8 -----  
 GH28\_9 MSSNKLIYSLFVVISAAAKSLNE-----DCCTITEYSQVPDVVETCKNIVISNLRVPANKTLNLLNQDGSSELTFFEGRTYFDYFEW-K  
 GH28\_10 -----LNDC-----  
 GH28\_11 M-----LFYIKILVLLIVVSIAS-----DICTISNYDLVDEALSSCIDIVISNLTVPVSGKTLNLLNKERSTVTFDGVITFEVFSFR-T  
 GH28\_12 M-----CYFNKFSLLLLLSPLLSKS-----DPCTVTQFSQVAQAVNDCTNLIISNLVVPGGQTLLEHLKYGATVTFEGTTFVEVAHW-E  
 GH28\_13 MGFSVLLFLSLLALISGTSVLQATNNTAVGDSCTITQYSQVDGVLKSCNTNIIISNVEVPSGKSLNLYLRDGSLLTVRGTISFDVGYN-N  
 GH28\_14 -----

GH28\_1 GPLVEITGSNLHVSGA-GAILDGLGAQYWDGY-GDKGAVKPKFLKIRTT-GSTFDNIHLLNCPQCVSILSSKQTLTLNFNIDVSGADIT  
 GH28\_2 GPLISISGSNLHVSGS-GAVLDGLGSKYWDGK-GDKGAKPKPKFKIRETTGSTFDSIHLNCPHCQVSIQNSKTTLNWNIDVAAGDIN  
 GH28\_3 GPLIRINGSGFTIKGAPGSLNNGQGDLYWDHL-GDKGPKPKQFKIEAFDGSIIENINLLNCPHHCVVYVKGSDGLTIRGWVIDNSYGDQN  
 GH28\_4 GHLIVVKGNHVI IQGAPGSLNNGQGKYWDGQGGGGGVTTPKFFYIETTGGSI FKNIYLYQCANWCVIG-SKDVITITGWTIDNTAGDKD  
 GH28\_5 GPLLEISGDGVEVQGNAGHI INAQGEKYWDGQGGGGVTKPRFVVI STTGGSVLRNIYLLNCVYFCVGIH-ASDLTSLGWTIDAVAGNTR  
 GH28\_6 GPLMWIKGDGITIQTESHLLNGRGEWLDGHDGHSNKKKQFMLIQAATGNSLLKDIKVKNCPHTCIGISDSDHITLQHWITDQDGDTK  
 GH28\_7 VPLIRISGANLFIEGRKDAVINQGEKYWDGKGIEGKRNKPVLEISAQ-ESLLKNINIRNCPQKCVNILKSANSSTFTGWNIDITDGFKD  
 GH28\_8 GPLVRFSYIYVQGAKGFLDGGALYWDGMMGGNGGVTTPKFFYIETTGGSI FKNIYLYQCANWCVIG-SKDVITITGWTIDNTAGDKD  
 GH28\_9 GPLVNIITGDDLIVRGAPGHVLDGGQELYWDHL-GGKGIKPKFIRLQGN-NSRYENIYLNKCPVHCASVAVS-NSIIDGWLIDVSEGDKN  
 GH28\_10 -----SILDAQGEKYWDGQGGAGGVTKPKFFYVQTTGGSI LKNIYLLNCAHFVGVG-AKDTTITGWTIDVSVAGNKD  
 GH28\_11 GFLVSVAGKNVLVQGAPGSLNNGQGEKYWDGF-GDNGVVKPFRFVATSSGGSIFRNIYLLNCPHFCVGVY-ATDVTLTGWTIDVLAGNTR  
 GH28\_12 GPRIEKKEENVEVQGASRS LLNAQGEKYWDGHDGSGGGVTKPRFVVI STTGGSVLRNIYLLNCPHFCVGVY-ATDVTLTGWTIDVLAGNTR  
 GH28\_13 IWLVTISGNNIKVIGEKGLFHGHGGEKYWDGHDGSGGGVTKPKLLQILNVNNAHFSNINLKNCPMFCGTGITKAKDLTIDGWNADCAEGDKL  
 GH28\_14 -----DKGNKPKPKFKIQAATGGSVFNINLLNCPHCQVSIQNSKQTLISNWNIDVSGADKN

GH28\_1 HL-ATNTDGFDSLSD-SDGITIENSVVRNQDDCVAVNSGKHYHFNKLNCGHGLSLSVGMKNDSP-----RNHVEDVTFNSCIVSN  
 GH28\_2 SL-GHNTDGFDLCE-NEEITIQNSIVHNQDDCVAVNSGKHYHFNKLTVCVGGHGLSLSVGTSTTDPSP-----KNYAEDINFSDCSVSN  
 GH28\_3 NFTGHNTDGFDSLSD-ASNLIEDSTVINQDDCIAIRHGYNILVRNMYCAGGHGLSLSAGFSYTTFQ-----ENTITNVVIKDSVIAR  
 GH28\_4 MI-ALNTDGFSLID-SENVLIENSTIMNQDDCIVVRRGNMFTFRNFKCFSHGSLFATGFHETDGFPHKEDDAEDIATDITFEDCLVAN  
 GH28\_5 G--GLNTDGFIGN--SQNLIENSIVIMNQDDCVVNSGSDMVFRLNLECYGSHGLSFSIIGDSDHNDDA-----AANTIKNIITFSDLVAN  
 GH28\_6 G--GANTDGFIDIAK-SYKVTIKDITVVRNQDDCICVNVQGOHLVLFQNMHCIGGHGLSLSAGL-WDTYE-----LNTIYNVTFQNSIVEN  
 GH28\_7 NV-GVDTGFAVAN-SSDI I IKESNIINQDDCIVVNVQGSDLHFQIIVCRGSQGITVREWEY-----ENYIRDVIFDCTVIE  
 GH28\_8 NL-GHNTDGFVDIY-GENIVIENSIVNQDDCVAINRGNMFLISNLRKCYGGHGLSLSVGFSSHRSYK-----HNTVHNVTFIDCVVAR  
 GH28\_9 NFTGHNTDGFDSL--STNLIQNSIVKNQDDCVVNVGANILVRNMACYGGHGLSISAGFSKDDFA-----KNSVYNIIFEDSLVHR  
 GH28\_10 LI-ALNTDGFVSSHSDNLIENSIVIMNQDDCVVNVQGTNMVFRNLHLCYGSHGLSFAVGFGRDKP-----EDDSVASNITFENCWVAN  
 GH28\_11 G--GLNTDGFGIHS--GRNIVVQDSVVMNQDDCVVNSGSDMI FRLNLCYGSHGLSFSVGSKTEENA-----EAGIVQNIITFLDSL VAN  
 GH28\_12 ---GKNTDGFGIAA--GNNIHIENSVDNQDDGIVVNGGTNMVFNKIKCTGSHGLSFSAGSNTNDHA-----KYATINNIITFNSCELKD  
 GH28\_13 ---GRNTDGFISW--SQHVYINNAYIHNQDDCLYVNVQGSMDVFTGIHCVGSGNFCATAGFSKTSYE-----ENTTKNITFHNCVLEG  
 GH28\_14 KL-GHNTDGFDISG-SDGVNFEYCTVQNDDCVAVNSGKLNLFHNMTCVGGHGLSLSIGMSKTDSS-----KN-----

GH28\_1 SLNGIHIKT-HSDAGKGYINGVEYRNIILKDIITNYGINVQDDYQGGHSTGYPTSNIPIINGLKLEGVGTGSLRS----GQPVYIFCGN-NA  
 GH28\_2 SRNGIHIKT-HTDGANGYIRGVTYKNIKLSGITHYGINVQDDYNGGGSSGYATSNIQINGLHLQSVTGLSKS----GKAVYILCGN-KA  
 GH28\_3 SANGIHVKT-HADAYNGRIQNVTYENIFMSGLINYGINVQDDYVNGSATGVANNIPIYLNLIINIRGTVRDSDEKSPVYINCCK-SA  
 GH28\_4 GLYGIHIKT-APNGKRGRIENVLFKNIKLSGIQEDGIYIQDDYGD---IGKQDSNVTIKNLTNLKVVYGSLLQGL---TRPIHIFCGNQGT  
 GH28\_5 GLYGIHVKT-KK--GTGVLTDVTYENIRLSGITEDGIYINQDYGD---IGNYSREIEITNLKMSNIYGSVQGVL---TRPVHIVCSN-DK  
 GH28\_6 SRNAIHIKTI PVNKKGEITSITYDNKILIGISYAINVQEDYTDNGPTGHPLGNI PVKDLKIHNVTGTMGTSN---SVKAYILCGS-GG  
 GH28\_7 GQTGRVVT-SPHQPEGYISNVIYRKIHLTGILFRGIDIRQDLDD---EGRPSGNVKITELDISDVKGNMNTDKY---VRSVYIWCGP-DG  
 GH28\_8 SENGIHVKT-HNDGYLGEIKNVTYKNIIEFVDILNYGVNVQDDYANGTSTGNPTNPI PITNLSLINVHGTGKSH---ATGVYILCGS-AG  
 GH28\_9 SPNGIHVKT-HADSGPGIIQNI IYRNIRFEDINNFALNIQDDYVNGEATGIPGTNPIVGLSLDNI SGWMSFNESPTLEALILCGD-GA  
 GH28\_10 GLYGIHVKT-GAVGNKGRRIENVVFRNLIKLSGIQEDGIYIQDDYGN---IGNLESEVKIHNLTVENVTGVSQGVL---TRPIHIFCGNRST  
 GH28\_11 GLYGIHIKT-KK--GSGTIRDVIYENIQLSGITEDGIYINQDYED---IGNYSREFEIHNLKI SNVYGSIQGLL---TRPVHIVCNE-NK  
 GH28\_12 GAIGIHVKT-KR--GTGLITNVTYDHIITMTGMQRDGIYINQDYGD---VGNTRDFQITNLKVSNVEGSIHGKG---ARAVHIVCND--AK  
 GH28\_13 GLTGQVQVIA-MADGGPGEITDIHFQSIILKGVRRQGVYVQMDYGN---DGHPNNNIAVTLGLKLSHVTGTVSGNS---ARPYIYKCG--AK  
 GH28\_14 -----

GH28\_1 CFNFNWSGVSITGGNQSSCNYHPNGYYC-  
 GH28\_2 CSNFNWSGSIYGGNEKNGCNYHPNGFSC-  
 GH28\_3 CHEWSWSNINIAGGSNSSICNYTPDGYQC-  
 GH28\_4 CSEWIFSNINILGGN-RSYCNYQ-----  
 GH28\_5 CQNWTWSNINILGGG-KNYCNFQPTFEC-  
 GH28\_6 CTNWNWSEINVSGAAKPNSCNFTPNGFSC-  
 GH28\_7 CANWNWSDIDIEAENACNFLPNNWSCW  
 GH28\_8 CIDWNWSEISITGAKRENSCNYVPSGYHC-  
 GH28\_9 CDKWEFHNDITGAQNNSICTFQPEGYSC-  
 GH28\_10 CDDWKFSGINILGGG-QSYCNYVPEDEFHC-  
 GH28\_11 CSNWTWSNINILGTG-KSYCNYIPDGFRC-  
 GH28\_12 CANWQWSNIDISGGA-KDYCNFHPTGFDC-  
 GH28\_13 CSNWI FNDVQVTGGGVKSSCNYKPSGFNC-  
 GH28\_14 -----

**Figure S1. GH family gene sequences identified from the *D. v. virgifera* transcriptome.** Amino acid sequences of GH45 (A), GH48 (B), and GH28 (C) are shown in alignments. The labels for partial sequences are shown in italics. Potential residues for the catalytic nucleophile and the proton donor are highlighted with magenta and green, respectively (based on Sakamoto and Toyohara, 2009, *Comp Biochem Physiol B* **152**: 390; Parsieglia *et al.*, 2008, *J Mol Biol* **375**: 499; van Santen *et al.* 1999, *J Biol Chem* **274**: 30474).