

A

GH45-1 MLSL-----KIAVAIILSLAG--VTIAQDLTPIPGGKSGDGVTTTRYWDCCAPSCAWYPRIHTQNGVPIQOTCKADGVTSPSKDLNA-QSGC-
 GH45-2 MKLLVA---IAFLGYVAAGSFGRCPPGDI VPIPGGLSGDGIITTRYWDCCAQTCAHRQNVKTDNGIPVQTC AIDGTTNIITIDQNGIVSGC-
 GH45-3 MKYLIV---ITFLGYVAAS--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 VIKKIPGGLSGVGTTRYWDCCKCATCSWPGNVVEYK--PVKACQADGENAN--DPEN-ESGC-

GH45-1 -EVGGVAYTCTNQSPKINETLAYTFVAASFAGGLDY-ADCCICLVMDPKG-KLAGKRLLAQVTNTGEEA---LQNHFIQMPGGGVGIY
 GH45-2 -RVGGQAFACSNQPPYVVDTLALGWSAASFTGGIDN-SKCCSCLLSFKD-QLAGKQMLVQLVNSGTD---LASNHFLQIPGGGVGLW
 GH45-3 -EQGGVAYTCSNQPSVINDTLAFGWAAASFQGGIDT-SKCCCHILLSFKD-QLAGKQMLVQIVNTGSD---LNENQFLQIPGGGVGIF
 GH45-4 PDHPGNAYCNNSPFVNSTLAYGFAGVSFQGGADV-EHCCHYLLSFKG-KLQGGKMLVQVINTGAD---AVAHHFLQIPGGGVGYN
 GH45-5 -NENGAFTCSNQPFVINSTLSYGFAAVSFGVSTDT-GHCCQCYLLKFGQ-QLKDRELLVQAINTGSD---LTTNQFLQIPGGGVGLY
 GH45-6 --VGGGAYCTNQQRSVNDSIALGFVAAKFIHS-NR-NMCCSIVFRFKPAELAGKQMLVQVNTGDDDPHATHNEFLIAMPGSGVGYI
 GH45-7 -EGGGSAYMCNSQPPAVNSTLAYGFGAASFNGVDV-SLCCACFLLSFKD-QISNKKMIVQVTNTGSD---LSHNHFLIPLPGGGVGIY
 GH45-8 --IGGTSYMCNNQPPFVNETLGYGFAAVSFGVDN-DLCCSCYLLTFQN-QINNKLVLQFTNTGGD---LGSNQFLIPLPGGGVGF
 GH45-9 --ENGTAYTCTNQPFIVNQTYGYGFAAAYLIGGPSTNNFCCACFLNFTD-QIKYKHMVVQVTNSGTN---FDKNEFLIPLPGSGVDH
 GH45-10 -DINGSSFCNNSQPPVNSTLSYGFAASFSGGIDT-SMCCSMLLNFEG-QLKKGQFLVQLTNSGEE---YQTNQFLGIPGGGVGLF
 GH45-11 --IGGQSYICTKQSGFAINSTLAYGYVAARFHGT-TR-NMCCSCLVLSFQPELANKKMLVQVTNTGNA-PETNTNLF IAMPGSGVGYI

GH45-1 NLGCKTQWNA PDDGWGERYGGVTDIKGC-KQLPEQLQEGCRFRFTWMKGVNPPVSYFYQIKCPEYFVGVSKCGDL---
 GH45-2 NHGCDAQWAGENGWGRYDGVSSLEEC-CLLPEVLQPGCRFRFQFMGQVYRPNVTFQEVQCPAELIAVTACGNLNY-
 GH45-3 NLGCMTQWGTGEDGWGRYGGVSSIEEC-SILPEVLQPGCRFRFQFMGQVNDPKVVSFQEVKCPAELVAVSACGDL--
 GH45-4 TQGCRIQWNA PENGWDRYGGVHSEQEC-NQLPWQLQAGCKFRFQFMQGVSNPDVVSFQEVKCPSELVSI TGCGLD---
 GH45-5 N-GCVKQWNA PVDGWGERYGRVTSVEGC-DQLPVQLQDGCKWRFYLEGVSNPSATFYEVKCPSELIAITNCGDRD--
 GH45-6 TQGCSSQWNA DVS KWGDQYGGVHSEIEEC-HNLPAHLQPGCEFRFTWMKGYSNPDIEFDEVVCPKRLTDISGCYPASHP
 GH45-7 TQGCCHDQWNA PWNWGDQYGGVHNRGEC-ATLPQALQSGCYFRDFYQANNPRMHFDQVQCPAEIVARS GCSL---
 GH45-8 NQGCCHDQWNA PWTGWQYGGISSREELSLLPKELQSGCLFRDFDMQANNPQMYFEQVECPAELVKISGCSP L--
 GH45-9 PEGCHDQWNA PWTGWQYGGVHMRSECVTLPEELQEGCKFRDFMETANPLVVSFQQVVCPELVKISGCRIP E--
 GH45-10 PKGCTAQWNA PSTGWGDLYGGVHTEEEEC-NELPEVLQPGCKWRFQFMGQVSNPEVTFYQVQCPRELVERSGCVL---
 GH45-11 TQGCSTQWHTDVSSWGDQYGGVNSLQEC-YNLPQLWEGCAFERNWMLGYSNPDVVSFEEVECPQELLSISGCDPISHP

B

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

GH48-1 FNNAWNLETYIIPVYSSQPTNSFYTPGHPATFIPEQDDPSQYP-SQIDSSVPVGDPLHQELVNAYGSHEVYGMHWLLDVDNIYGFNGT
 GH48-2 -----
 GH48-3 FNEAWEIMEKYIIPVHESQPTNLYNPSHPAGYGEQEYPEDYVPGVPDPPAPVGDIPLYQELVDTYGTSIDIYAMHWLLDVDNVYGFNGS

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

GH48-1 GTIQGTLAKAAKMGDYLRALFDKYFKQVGNCDNRWSCPGGYGKSSAHYLLGWYYAWGGSVDTNGGAWRIGDSSAAHFGYQNPLAAYALA
 GH48-2 -----
 GH48-3 SEITDTLQKAGKLDYLRFCFFDQNFKRIGNCIDPYKCPGGTGKDSAHYLLGWYFGWGGISSEYGYSWRIGDGVAFHFGYQNPMAYALI

GH48-1 NDPNLRPKGATAVSDWQTSLEQLFEYEWLQSAEAGAFAGGATNSINGHYDSSDLTANTFHGMYYDWEVYHNPSPNRWYGMQSWSVDR
 GH48-2 -----GAFGGATNTWNGRYDTPPQELTNTFHGMFYDWEVYHNPSPNRWYGMQSWSTDR
 GH48-3 NEPNMTPKGATAVEDWQISLDRQLELYDYLSVEGAFAGGVSNSWNGRYQPPEELMDNTFHGMFYNWEVYAYDPPSNQWFGMQPWSWDR

GH48-1 LAQYYYVTGDSKAKSVLDKWNWILKETTIEAGKSFKLPSQLSWSGNPNVHCTINAYTTDVGSASGTARTLAYAAKANHAQAKEVAKE
 GH48-2 LAQYYYVTGDATAKTLDDKWKWVISEIKFE-GTGYTHPDHLEWSGQPPNVHVQVTSYSDDVGTASSTA-----
 GH48-3 LAQYYYITGDDKAKKILDKWVSWI IANTYFE-GDDYRIPSTLDWVGVPPNVHCKVYVYGNVGPAAATARTLSYAAARANHAEAKNLAKK

GH48-1 ILDIMWNNFQTSKGVSSPEVADTYTFNEPVFVNGWYGTYPKGDVIQSGATFLSLRSWYKSDPDWNKVQTYLNGGSAPTFTYHRFWAQA
 GH48-2 -----
 GH48-3 ILDSLWNLHRTPLGIAVEEQPEIH--FNQSVYVPKDFHGVYPNGDVIDSDSTFISMRSFYKNDPQWNKIESYMGNGPAPKFTYHRFDWQT

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

C

GH28_1 M--TNLTLLIVFSVIVATIAIPFNST-KNIGDGTISNIWEVENVVKCKNIVVNNLYVPGGQKLELKLHSGTVLKFQGTTFQHSNW-E
 GH28_2 M--ATLTLFLVLCAAVATSALSNST--NVGAGCTISKIGEVNDVVKCKNIVNNSLSPVGGKTLKLDLHPGTTLKFQGTTFQHTNW-E
 GH28_3 MYTITMICYLFLFLFNAALVICKCSP-----TNCBITNFQVSDTVHRCSDIIRNLDVPAGQTLLELDLQOGASLTFFEGITTFDYTNW-E
 GH28_4 M-NLFIIEFNIVVLLNSLFLISCVD----QPCTITNFSQVSEVLQSCKNITISNLNVPAGQQLYLELLNDSVTFEGVITTFGVAQW-K
 GH28_5 M-----SYTKFLIVAFISTVSAN-----NNCTITEFAQVAEIVKECSNIVINDLVVPAYSTLLNLLKNGSRVTFGTGNVLFVEVGYW-E
 GH28_6 M--RTIQLFEYFFLCSAYASNLT-----ASCTISRFDHVDTVVVSQCKSITVESFAVPAGQTLKHLHQYGTTLTFNGNIAFYSEW-D
 GH28_7 MIKTGMSLVFLFVLGVVLAQE-----YDCEINSIDQVLPVIEKCSVITVKNLWVPSGQTLLELSLKDNSHLIFDGNVTVGVKYQE
 GH28_8 -----
 GH28_9 MSSNKLIYSLFVVISAAAKSLNE-----DCCTITEYSQVDPVVETCKNIVISNLRVPANKTLNLLNQDGSSELTFFEGRTYFDYFEW-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-GDKGAVKPKFKIRTT-GSTFDNIHLLNCPQCVSILSSKQTLTLNFNIDVSAAGDIT
 GH28_2 GPLISISGSNLHVSGS-GAVLDGLGSKYWDGK-GDKGAKPKPKFKIRETTGSTFDSIHLNCPHCQVSIQNSKKTTLNWNIDVAAAGDIN
 GH28_3 GPLIRINGSGFTIKGAPGSLNNGQGDLYWDHL-GDKGPKPKPKFKIEAFDGSIIENINLLNCPHHCVVYVKGSDGLTIRGWVIDNSYGDQN
 GH28_4 GHLIVVKGNHVI IQGAPGSLNNGQGQKYWDGQGGGGGVTTPKPFYIETTGGSI FKNIIYLCANWCVIG-SKDVITITGWTIDNTAGDKD
 GH28_5 GPLLEISGDGVEVQGNAGHI INAQGEKYWDGQGGGGVTKPRFVVI STTGGSVLRNIYLLNCVYFCVGIH-ASDLTSLGWTIDAVAGNTR
 GH28_6 GPLMWIKGDGITIQTESHLLNGRGELWWDGHGHSNKKPKQFMLIQATGNSLLKDIKVKNCPHTCIGISDSDHITLQHWITDQDGDITK
 GH28_7 VPLIRISGANLFIEGRKDAVINQGEKYWDGKGIIEGKRNKPVLEISAQ-ESLLKNINIRNCPQKCVNILKSANSSFTGWNIDITDGFKD
 GH28_8 GPLVRFSYIYVQGAKGFLDGGALYWDGMMGGNGGVTTPKPFYIETTGGSI FKNIIYLCANWCVIG-SKDVITITGWTIDNTAGDKD
 GH28_9 GPLVNIITGDDLIVRGAPGHVLDGGQELYWDHL-GGKGIKPKPKFIRLQGN-NSRYENIYLNKCPVHCASVAVS-NSIIDGWLIDVSEGDKN
 GH28_10 -----SILDAQGEKYWDGQGGAGGVTKPKPFYVQTTGGSI LKNIYLLNCAHFVGVG-AKDTTITGWTIDVSAAGND
 GH28_11 GFLVSVAGKNVLVQGAPGSLNNGQGEKYWDGF-GDNGVVKPKFRFVATSSGGSIFRNIYLLNCPHFCVGVY-ATDVTTLTGWITDVLGANTR
 GH28_12 GPRIEKKEENVEVQGASRS LLNAQGEKYWDGHHGSGGGVTKPRFVVI STTGGSVLRNIYLLNCAHFVGVG-AKDTTITGWTIDNTAGDKD
 GH28_13 IWLVTISGNNIKVIGEKGLFHGHGKEYWDGHHGSGGGVTKPKLQILNVNNAHFSNINLKNCPMFCGTGITKAKDLTIDGWNADCAEGDKL
 GH28_14 -----DKGNKPKPKFKIQATGGSVFNINLLNCPHCQVSIQNSKQTLISNWNIDVSAAGDN

GH28_1 HL-ATNTDGFDSLSD-SDGITIENSVVRNQDDCVAVNSGKHYHFNKLNCGHGLSLSVGMKNDSP-----RNHVEDVTFNSCIVSN
 GH28_2 SL-GHNTDGFDLCE-NEEITIQNSIVHNQDDCVAVNSGKHYHFNKLTVCVGGHGLSLSVGTSTTDPSP-----KNYAEDINFSDCSVSN
 GH28_3 NFTGHNTDGFDSLSD-ASNLIIEDSTVINQDDCIAIRHGYNILVRNMYCAGGHGLSLSAGFSYTTFQ-----ENTITNVVIKDSVIAR
 GH28_4 MI-ALNTDGFSLID-SENVLIENSTIMNQDDCIVVRRGNMFTFRNFKCFSHGSLFATGFHETDGFPHGEDDAEDIATDITFEDCLVAN
 GH28_5 G--GLNTDGFIGN-SQNLIIENSVIMNQDDCVVNSGSDMVFRLNLECYGSHGLSFSIIGSDSHNDDA-----AANTIKNIITFSDELVAN
 GH28_6 G--GANTDGFDIK-SYKVTIKDITVRNQDDCICVNVQGHVLFQNMHCIGGHGLSLSAGL-WDTYE-----LNTIYNVTFQNSIVEN
 GH28_7 NV-GVDTGFAVAN-SSDIIIKESNIINQDDCIVVNVQGSDLHFQIIVCRGSQGITVRPEWEY-----ENYIRDVIFDCTVIE
 GH28_8 NL-GHNTDGFVDIY-GENIVIENSIVNQDDCVAINRGNMFLISNLRKYGSHGLSLSVGFSSHRSYK-----HNTVHNVTFIDCVVAR
 GH28_9 NFTGHNTDGFDSLSD--STNLIIQNSIVKNQDDCVVNVGANGILVRNMACYGGHGLSISAGFSKDDFA-----KNSVYNIIFEDSLVHR
 GH28_10 LI-ALNTDGFVSSSDNIIENSVIMNQDDCVVNVQGTNMVFRNLHCVGSHGLSFAVGFGRDKP-----EDDSVASNITFENCWVAN
 GH28_11 G--GLNTDGFGIHS-GRNIVVQDSVVMNQDDCVVNSGTDMI FRLNLCYVGGHGLSFSVGSKTEENA-----EAGIVQNIITFLDSL VAN
 GH28_12 ---GKNTDGFGIAA-GNNIHIENSVDNQDDGIVVNGGTNMVFNKIKCTGSHGLSFSAGSNTNDHA-----KYATINNIITFNSCELKD
 GH28_13 ---GRNTDGFGISW-SQHVIYINNAIHNQDDCLYVNVQGSMDVFTGIHCVGSGNFCATAGFSKTSYE-----ENTTKNITFHNCVLEG
 GH28_14 KL-GHNTDGFDISG-SDGVNFEYCTVQNDDCVAVNSGKLNLFHNMTCVGGHGLSLSIGMSKTDSS-----KN-----

GH28_1 SLNGIHIKT-HSDAGKGYINGVEYRNIILKDIITNYGINVQDDYQGGHSTGYPTSNIPIINGLKLLEGVGTGSLRS----GQPVYIFCGN-NA
 GH28_2 SRNGIHIKT-HTDGANGYIRGVTYKNIKLSGITHYGINVQDDYNGGSSGYATSNIQINGLHLQSVTGLSKS----GKAVYILCGN-KA
 GH28_3 SANGIHVKT-HADAYNGRIQNVTYENIFMSGLINYGINVQDDYVNGSATGVANNIPIYNLNLINIRGTVRDSDEKSPVYINCCK-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---EGRPSGNVKITELDISDVKGNTMDKY---VRSVYIWCGP-DG
 GH28_8 SENGIHVKT-HNDGYLGEIKNVTYKNIIEFVDILNYGVNVQDDYANGTSTGNPTNIPITNLSLINVHGTGKSH---ATGVYILCGS-AG
 GH28_9 SPNGIHVKT-HADSGPGIIQNIYRNIRFEDINNFALNIQDDYVNGEATGIPGTNIPIVGLSLDNI 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 CSNFNWSGISIYGGNEKNGCNYHPNGFSC-
 GH28_3 CHEWSWSNINIAGGSNSSICNYTPDGYQC-
 GH28_4 CSEWIFSNINILGNG-RSYCNYQ-----
 GH28_5 CQNWTWSNINILGGG-KNYCNFQPTFIC-
 GH28_6 CTNWNWSEINVSGAAKPNSCNFTPNGFSC-
 GH28_7 CANWNWSDIDIEAENACNFPNWNWSCW
 GH28_8 CIDWNWSEISITGAKRENSCNYVPSGYHC-
 GH28_9 CDKWEFHNIDITGAQNNSICTFQPEGYSC-
 GH28_10 CDDWKFSGINILGGG-QSYCNYVPEDEFHC-
 GH28_11 CSNWTWSNINILGTG-KSYCNYIPDGFRC-
 GH28_12 CANWQWSNIDISGGA-KDYCNFHTGFDC-
 GH28_13 CSNWI FNDVQVTTGGGVKSSCNYKPSGFNC-
 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; Parsiegla *et al.*, 2008, *J Mol Biol* **375**: 499; van Santen *et al.* 1999, *J Biol Chem* **274**: 30474).