SUPPLEMENTAL MATERIAL Figures

Higher expression of the strawberry xyloglucan endotransglucosylase/hydrolase genes *FvXTH9* and *FvXTH6* accelerates fruit ripening

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Figure S1. Expression levels of putative XTHs in Fragaria vesca varieties.

- Figure S2. Phylogenetic tree of XTH candidate genes from *F. vesca.*
- Figure S3. qPCR analysis of FvXTH9 and FvXTH6.
- Figure S4. Amino acid sequence alignment of group I/II XTHs.
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- Figure S8. Amino acid sequence alignment.



Figure S1. Expression levels of putative XTHs in *Fragaria vesca* varieties Reine de Vallées, Hawaii 4 and Yellow Wonder.



Figure S2. Phylogenetic tree of *XTH* candidate genes from *F. vesca*. The tree was constructed using Genious v5.6 software with the Neighbor-Joining method with 5000 bootstrap replications. Amino acid sequences were retrieved from the *F. vesca* Genome Browser database and their accession numbers are as follows: gene00216, gene00661, gene00663, gene01781, gene01986, gene05197, gene05204, gene05205, gene05220, gene05221, gene05591, gene09279, gene09672, gene12291, gene13718, gene17597, gene17598, gene18893, gene19553, gene19781, gene19782, gene19783, gene24600, gene24869, gene24871, gene28698, gene28699, and gene28700.



Figure S3. qPCR analysis of *FvXTH9* (a) and *FvXTH6* (b) at different fruit maturation stages (small green, large green, white and ripe fruit) as well as other tissues (young leaf, old leaf and flower) of *F. vesca.* Hawaii 4. Relative expression levels are normalized to the reference gene (interspacer gene).

| | | | | | | | | | | | — Section 1 |
|---------------------|----------------|--------|------------------------|-----------|----------|-----------------|-----------|-----------|------------------|------------------|-----------------------|
| | (1) | 1 | ,10 | | 20 | | 30 | | 40 | | 55 |
| At-XTH10 | (1) | M | FLINR | SKPFVL | LVGFS | IISSL | LLWVS | QASVV | SSGDFN | IKDFFVI | WSPTHVN |
| At-XTH6 | (1) | 1 | MAKIY | SP-SFP | GTLCL | CIFTL | LTLMF | IRVSA | RPATF | /EDFKAA | WSESHIF |
| At-XTH7 | (1) | M | VVSLF | SRNVF | YTLSL | CLFAA | L Y | QPVMSI | RPAKFE | EDDFRIA | WSDTHII |
| FvXTH6 | (1) | M | YPSLR | SG-SVI | ASISL | CFLSL | FS | LSAFAI | RPATFI | QDFQVI | WSDSHIF |
| SI-XTH7 | (1) | MATLTO | CCSLKI | NS-AFV | LILVY | ALTFS | FS | LVS-AL | RPATFI | QDFKIA | WSDSHIK |
| At-XTH9 | (1) | | MV | /GMDLF | KCVMM | IIMV | -LVVS | CGEAV | SGAKFI | DELYRSS | WAMDHCV |
| FvXTH9 | (1) | | M2 | ASASLF | LSVIL | GLS | -LFLG | 3PV8 | SSAKFI | DELFQPY | WASDHFI |
| At-XTH8 | (1) | METI | ERRII | rscsam | TALFL | FMTAL | MASSS | SIAATP | rqs-fe | EDNFNIM | IWSENHFI |
| SI-XTH1 | (1) | | MG | LIKGVL | FSIVL | INLSL | VVFCG | YPRRP | JDVPFV | VKNYEPS | WASHHIK |
| SI-XTH4 | (1) | | | -MKGVL | VAFVL | INLSI | LASCO | APRKV | L DVPFV | VNNYEPS | SWSSHHIK |
| At-XTH4 | (1) | | -MTVS | SSPWAL | MALFL | MVSST | MVMAI | PPRKA | DVPF | GRNYVPI | WAFDHQK |
| At-XTH5 | (1) | | -MG-RI | SSTLC | LTFLI | LAT | VAFGV | PPKKS | INVPFO | GRNYFPI | WAFDHIK |
| Fc-XTH1 | (1) | | MASS | OCTLL | LSIML | MGS | VTMAA | PPKRP | JSVPFO | GRNYMPI | WAFDHIK |
| Md-XTH1 | (1) | | -MASCI | XOWTVF | LSLLC | LVS | ΑΤΊΛΑΑ | PPKKP | JAVPEC | RNYMPT | WAFDHIK |
| PHTXET16A | (1) | | -MAAA' | ZPWTLF | LGMLV | MVS | GTMGA | ALRKPY | IDVAFC | RNYVPT | WAFDHIK |
| Consensus | (1) | | | SVL | LSLLL | TLS | L | in Dicici | F | NY PT | WA HTK |
| conscribus | (1) | | | 511 | | 1110 | 5 | | - | | — Section 2 |
| | (56) | 56 | | ,70 | | ,80 | | 90 | | 100 | 110 |
| At-XTH10 | (52) | TSNDG | RSRTLI | KLDQES | GASFS | SIQTE | LFGQI | DMKIKI | LIRGSS | SQGTVVA | YYMSSDC |
| At-XTH6 | (50) | QMEDGI | KAIQLY | /LDQST | GCGFA | SKRKY | LFGRV | SMKIKI | IPGDS | SAGTVTA | FYMNSDI |
| At-XTH7 | (49) | QIDGGI | RAIQLI | KLDPSS | GCGFA | SKKQY | LFGRV | SMKIKI | LIPGDS | SAGTVTA | FYMNSDI |
| FvXTH6 | (48) | OTDGGI | RATOL | /LDONS | GCGFS | sкнку | LEGRV | SMKTKI | TPGDS | SAGTVTA | FYMNSDT |
| SI-XTH7 | (51) | OLDGGI | RGTOL | LDONS | GCGFA | SRSKY | LEGRV | SMKTKI | VPGDS | SAGTVTA | FYMNSDT |
| | (44) | NEGI | EVTKLI | LDNYS | GAGEE | SRSKY | LEGKV | STOTKI | VEGDS | SAGTVTZ | FYMSSDC |
| F _V XTH9 | (41) | YEGI | ELTHM | LDNYS | GAGES | SKNKY | MEGKV | νπνοτκι | VEGDS | SAGTVTZ | FYMSSDC |
| | (53) | TSDDGI | ETWNT | | GCGEO | ткних | REGWE | SWKIKI | VGGDS | SAGUVTZ | VVMCSEN |
| | (49) | FINCC | י דמששם | TIDDCC | CACEO | QVVQV | TROUT | CMVMDI | VCCD | | EVI COM |
| | (45) | VINCC | נודים ביים. השאימים | TDKGG | CTCEO | GKDGA | TECHE | CMKMKI | | | EVI COM |
| | (50) | OFNCC | | | CIGICIC | OKCON | TROUT | CMUTU | | | |
| | (30) | VINCO | апалатт. | | GIGPQ | ardan Serger | TEQUE | OMUTRI | | | TLIPSIN |
| | (47) | VENCO | | | CIGEQ | I GRUGAL | TROUT | UMOTVI | | | T I LOOV |
| | (40) | TENGGI | истоти | | GIGPQ | SKGSI | LIGHT | ' TMQIKI | JPPGDS | AGIVIA | AFILSSIN |
| | (48) | YFNGGI | KEIQLI | ILDKYT | GTGFQ | SKGNY | LFGHF | THMQIKI | IVPGDS | SAGTVTA | IYYLSSQN |
| PTTXETI6A | (48) | YFNGGI | NEIQLI | ILDKYT | GTGFQ | SKGSY | LFGHF | SMQMKI | - V PGDS | SAGTVTA | FYLSSQN |
| Consensus | (56) | NGG | ΤQΓ | LD S | G GFQ | ISK Y | LFG F | SMKIKI | JV GDS | SAGTVTA | AFYMSSDN Coction 2 |
| | /111) | 444 | 10 | 0 | 1 1 1 20 | ` | 1.4 | 0 | 150 | | - Section 3 |
| | (111) (107) | DNI | | V X | VNCOD | VILOT | NUVAE | | UCL THTQTS | | |
| | (107) (10E) | | | PEFLON | DRCOD | I T T O T | NTEAU | | PODVNI | WFDDGN | |
| | (104) | | ים זפת ב | EFELON | DGCOP | | NVENE | ICKCDDI | | WEDDOL | |
| | (107) | ייזגם | | N DL 1G N | DUGOD | | NTVPAD | IGAGDE | | MEDESE MEDESE | |
| | (105) | DAVI | ים ים חר | EFLGN | DUCOD | I T V Q T | NUVVV | | | WEDDCZ | |
| | (07) | UIU | | PEFLGN | RTGQP | TTVQT | NTYTE | IGKGDKI | I O D T NT | WEDPSA | OF HTYTT |
| | (97) | PNI | | PEFLGN | TTGEF | T T V Q T | NIXIN | GVGNR | JONT DI | WFDP1''I | DBUQYCT |
| | (94) | PLI | | PEPLON | TTGEP | I SVQT | NUVVVV | | INDUCT SORLDI | MEDPRI'I | |
| At-XTH8 | (108) | GAGPEI | | BFLGN | RTGQF | TTTD. | NVYKN | GTGNR | IODIU | MLDDJ.R | UTHTYS1 |
| SI-XTH1 | (103) | AEI | DETDI | FEFLGN | KTGQP | тгдт | N V F'T'C | GKGNR | SQRIYI | "MED B.L.R | GYHSYSV |
| SI-XTH4 | (100) | AEI | DETDI | TEFLGN | RTGQP | тгот | NVF'I'G | GKGDR | SQRIYI | WFDPTF | DFHSYSV |
| At-XTH4 | (105) | NEI | DEID | FEFLGN | RTGQP | AILQT | NVFTG | GKGNRI | SQRIYI | WFDPSK | AYHTYSI |
| At-XTH5 | (102) | SEI | DEIDI | FEFLGN | RTGQP | YILQT | NVFTG | GAGNRI | EQRINI | WFDPSK | CDYHSYSV |
| Fc-XTH1 | (103) | AEI | DEIDI | FEFLCN | RTGQP | FILQT | NVFTO | GKGDRI | EQRIFI | WFDPTK | CEYHSYSV |
| Md-XTH1 | (103) | NEI | | FEFLGN | RTGQP | YILQT | NVFTG | GKGDRI | EQRIFI | WFDPTA | AYHSYAV |
| PttXET16A | (103) | SEI | DEIDI | FEFLCN | RTGQP | YILQT | NVFTC | GKGDRI | EQRIYI | WFDPTK | CEFHYYSV |
| Consensus | (111) | EI | DEIDI | FEFLGN | RTGQP | YILQT | NVF | GKGNRI | EQRI I | JWFDPTK | OFHTYSI |
| | | | L | | | | | | | | |

| (166) | 166 | 180 | 190 | 200 | 210 | 220 |
|-------------------------|------------------|---------------------------|----------|-------------|---------------------------|--------------|
| Δt-XTH10 (159) | LWNTHOTVEMVD | TPTRLVRNF | IGEKGVA- | -VPRLOPM | SVOASLWNG | ESWATRGGH |
| At-YTH6 (159) | TWCHKHINEANDI | VDIBEVKNN | IGUKGVA | -VPTSOPM | GVVSTIMENI GVVSTIMENI | DDWATRGGI |
| At-XTH7 (157) | GWNHI DIVEVVDA | | IFADKUD- | -VDPFODM | | DWATROOL |
| | TWNUUUTVEVVDI | | EARCED | VDKLODM | GVISILWEAI GVEGUIWEAI | DWAIRGGI |
| | EWNNHILVFIVDI | TDTDUVVNN | EARGIP- | FDKEODM | GVESILWEAD | DWAIRGGL |
| SI-XTH7 (159) | FWNHHQAVFSVDO | - I P I R V I KNI | EAKGIP- | -FPKFQPM | GVISTLWEAD | DDWATRGGL |
| At-XTH9 (149) | EWSKRSVVFMVD | T. PIRVQKNI | EEKGIP- | -FAKDQAM | GVISSIWNAI | DDWATQGGL |
| FVX1H9 (146) | FWNQRQVVFLVDF | STPIRVHTNE | IESKGLP- | - F PKDQAM | GVYSSIWNAI | DDWA'TQGGR |
| At-XTH8 (163) | LWNNHQLVFFVDF | RVPIRVYKNS | 3DKVPNND | FFPNQKPM | YLFSSIWNAI | DDWATRGGL |
| SI-XTH1 (155) | LWNTYLIVIFVDI | OVPIRAFKNS | SKDLGVK- | - FPFNQPM | KIYSSLWDAI | DDWATRGGL |
| SI-XTH4 (152) | LWNTYQIAIFVDI | DADIBALKUS | SKDIGVK- | - F'PF'NQPM | KIYSSLWNAI | DDWATRGGL |
| At-XTH4 (157) | LWNMYQIVFFVDN | JIPIRTFKNA | AKDLGVR- | - FPFNQPM | KLYSSLWNAI | DDWATRGGL |
| At-XTH5 (154) | LWNMYQIVFFVDI | DVPIRVFKNS | SKDVGVK- | -FPFNQPM | KIYSSLWNAI | DDWATRGGL |
| Fc-XTH1 (155) | LWNLYQIVFFVDI | DIPIRVFKNS | SKDLGVK- | -FPFNQPM | KLYSSLWNAI | DDWATRGGL |
| Md-XTH1 (155) | LWNLYQIVFLVDI | DIPIRVFKNS | SKDLGVK- | -FPFNQPM | KLYSSL <mark>W</mark> NAI | DDWATRGGL |
| PttXET16A (155) | LWNMYMIVFLVDI | OVPIRVFK <mark>N</mark> C | CKDLGVK- | -FPFNQPM | KIYSSL <mark>W</mark> NAI | DDWATRGGL |
| Consensus (166) | LWN YQIVFFVDI | OVPIRVFKN | DLGV | FP NQPM | VYSSLWNAI | DDWATRGGL |
| | | | | | | — Section 5 |
| (221) | 221 230 | 240 | į | 250 | 260 | 275 |
| At-XTH10 (212) | DKIDWSKGPFVAS | SFGDYKIDAC | IWIGNTS | FCN | GESTEN | WWNKNEFSS |
| At-XTH6 (211) | EKIDWSKAPFYAY | YKDFDIEG | PVPGPTF | | CPSNPHN | WWEGYAYQS |
| At-XTH7 (210) | EKINWSRAPFYAY | YKDFDIEG | PVPGPAD | | CPANSKN | WWEGSAYHO |
| FvXTH6 (209) | EKINWSKAPFYAY | YKDFDIEG | SVPGPAN | | CASSAON | WWEGTAYOA |
| SI-XTH7 (212) | EKINWSKSPFFAY | YKDFDIEGO | AMPGPAN | | CASNPSN | WWEGPAYOO |
| At-XTH9 (202) | VKTDWSHAPFVAS | SYKEFOTDAC | ETPTTD | T. | SKCNGDOKFU | WWDEPTVSE |
| EvXTH9 (199) | VKTDWSHGPFVAS | SYKGEDINAC | ECPASVA | GAENAKKC | SSSNGDKKY | WWDEPVLSE |
| $\Delta t_{XTH8} (218)$ | EKTDWKKAPEVSS | SYKDFAVEG | RWKDDED | ACV | STTTEN-I | WWDOYDAWH |
| SLYTH1 (208) | FKTNWANADETA | SVTSFHVDC | FAATDOF | VOV | CNTKCMKI | |
| SI-XTH4 (200) | EKTNWANAFFIA | | EAATFQE | VQV VOV | CNTNCMKI | |
| 3FXTH4 (203) | EKINWSGAPPIAC | VVCENTDC | LAVIPUL | VQV | CAROCRM | W DQKAFQD |
| AL-XIN4 (210) | EKINWANAPPVAS | VDCFHVDC | VASVE | ALI | CETOCKDI | WUQKEFRD |
| AL-XTH5 (207) | EKTNWEKAPFVAS | VDGFHVDGC | EASVN | ARF | CETQGKRI | WUDOKEFOD |
| FC-XTH1 (208) | EKTDWSKAPFVAI | TIRGFHIDGC | EASVQ | ARF | CATQGKR | WWDQKEFQD |
| Md-XTH1 (208) | EKTDWSKAPFIAS | SYRGFHIDGC | EASVE | AKY | CATQGKR | NWDQKEFQD |
| PTTXE116A (208) | EKTDWSKAPFIAS | SYRSFHIDGO | EASVE | AKF' | CATQGAR | NWDQKEFQD |
| Consensus (221) | EKTDWSKAPFVAS | SYK F IDGO | E | | C TQG V | WWDQ FQD |
| | | | | | | —— Section 6 |
| (276) | 276 | 290 | 300 | | 317 | |
| At-XTH10 (259) | LTRVQKRWFKWVF | RKAHTIADAC | QDYGRFN | NKLPKECS | LPKY- | |
| At-XTH6 (256) | LNAVEARRYRWVF | RVNHMVYDYC | TDRSRFP | -VPPPECR. | A | |
| At-XTH7 (255) | LSPVEARSYRWVF | RVNHMVYDYC | TDKSRFP | -VPPPECS. | AGI | |
| FvXTH6 (254) | LNALEYRRYKWVF | RMNHMIYDYC | SDRSRYP | -KPPPECV | AGL | |
| SI-XTH7 (257) | LSPVQARQYRWVF | RMNHMIYDYC | TDKSRNP | -VPPPECR. | AGI | |
| At-XTH9 (250) | LSLHQNHQLIWVF | RANHMIYDYC | FDATRFP | -VTPLECQ | HHRHL | |
| FvXTH9 (254) | LNVHQNHQLVWVH | KNHHMVYDYC | TDSARFP | -VTPVECV | HHRH- | |
| At-XTH8 (265) | LSKTOKMDYAWVO | RNLVVYDYC | KDSERFP | -TLPWECS | ISPWA | |
| SI-XTH1 (256) | LDALQYRRLRWV | RQKYTVYNYC | TDKARYP | -VPPPECT | KDRDI | |
| SI-XTH4 (253) | LDGPEYRKLHRVF | RONFXIYNYC | TURKRYP | -TLPLECT | RDRDL | |
| At-XTH4 (256) | LDAEOWRRLKWVF | MKWTIYNYC | TDRTRFP | -VMPAECK | RDRDA | |
| At-XTH5 (253) | LDANQYKRLKWVF | RKRYTIYNYC | TDRVRFP | -VPPPECR | RDRDI | |
| Fc-XTH1 (254) | LDAYOWRRLRWVF | ORFTTYNYC | TDRTRYP | -TLPAEVO | RDRDI | |
| Md-XTH1 (254) | LDAOOWRRLRWVF | RKFTTYNYC | TDRVRYP | -SMPPECK | RDRDT | |
| PHXFT164 (254) | LDAFOYRRI.SWUL | OKYTTVNVC | TDRSRVD | -SMPPECK | RDRDT | |
| Consensus (276) | L A OYRRI.RWVF | S HWIADAU | | V PPEC | R | |
| | - T T ATTUTUTUNI | · | | × I I I C | ±1 | |

Figure S4. Amino acid sequence alignment of group I/II XTHs using AlignX Vector NTI Advance V.11.5. software. Sequences correspond to the following GenBank accession numbers: *A. thaliana* (At-XTH4 (NP 178708), At-XTH5 (NP 196891), At-XTH6 (NP 569019), At-XTH7 (NP 195494), At-XTH8 (NP 563892), At-XTH9 (NP 192230), At-XTH10 (NP 179069), *S. lycopersicum* (SI-XTH1, BAA03923), SI-XTH4 (AAG43444), SI-XTH7 (AAS46243), *M. × domestica* (Md-XTH1, AAN07897), *F. chiloensis* (Fc-XTH1, ADE42488) and *Populus tremula × Populus tremuloides* (PttXET16A, AAN87142). Identical amino acids in the sequences are shaded in black. The red box indicates the conserved motif and asteriks (***) mark the N-linked glycosylation motif.



Figure S5. Purification of FvXTH9-His and FvXTH6-His. M, protein marker; CE, crude extract; FT, flow through; A4-, A5-, and A6-fractions were eluted with 250 mM imidazole. Target protein (33 kDa) is shown by arrow.



Figure S6. pH optimum of FvXTH9 (a) and FvXTH6 (b). No XET activity was present in control PYES2. Different buffers were used as follows: sodium acetate buffer (pH 3.6, pH 4.0, pH 4.6, and pH 5.2), sodium succinate buffer (pH 5.0, pH 5.5, pH 6.0, and pH 6.5) and sodium phosphate buffer (pH 6.2, pH 7.0, pH 7.4, and pH 8.0). Each assay was performed as 4 replicates; error bars are standard deviation



j.

i.



Figure S7. Metabolite analysis of *F.* × *ananassa* fruit after agroinfiltration. Relative concentration (% equivalent of internal standard of the dry weight) of (a) pelargonidin rutinoside, (b) epiafzelechin pelargonidin glucoside, (c) ellagic acid, (d) kaempferol glucoside, (e) kaempferol glucuronide, (f) kaempferol malonyl glucoside, (g) quercetin glucoside, (h) quercetin glucuronide, (i) catechin, (j) epicatechin dimer, (k) epiafzelechin-epicatechin, (l) p-coumaryl glc ester, (m) ferulic acid glc ester, and (n) caffeic acid glc ester. The data were obtained by analysing 4-6 fruits (10 DPI) for each sample. Control fruit was infiltrated with *A. tumefaciens* AgL0 contained pBI121 empty plasmid. The asterisk indicates statistically significant differences (p < 0.05) between agroinfiltrated fruits with *XTHs* and the empty plasmid.

| 190 Westone | 95 11 FSDE 98 98 98 98 89 89 89 89 89 89 89 89 89 | WATEG | MATQG 310 과 운동 | -AGL 293 1HRH | |
|-------------------------|--|---|--|--|--|
| IVT & FY | TVTSFY TVTTFY TVTAFY TVTAFY 200 | LWRADD 193 LWDGSY LWDGSY LWNGET LWEADD LWEADD | PreEC | P P E C V H | |
| 90 GRSAG | 85 G NS A G 77 G NS A G 88 G D S A G 79 G D S A G G D S A G | QVEST TVHAT NVHLS GVFST | FPKGF 293 FPKGF YPNGF 284 | YPKP-1284 284 FPVT-1 | |
| SAK LAR | DARLVD MKLIS MKLIS XIKLIP ZIKLVE 2 IKLVE | KSQRM 183 183 176 176 176 178 178 178 | kdqam ~D eeR adgwr ydtki | CSDRSR | |
| Ge €≈01 | G E F S V (67 G Y E NMH G R V S MH G R V S MH G K V T V (| ADLPYI ADLPYI IGVPYI KGIPYI | КGLРF 290 М≪ҮрҮ(LSYNY(LSYNY(260 LKYDY(260 274 | М I Y D Y C 274 МV Y D Y C | |
| <u>skyk</u> F | (AKYLF (SNYLF (HKYLF (NKYMF 180 | FKNAFA FK KY 173 FK KY 166 FP NNEA KKNNEA 178 KKNEA | 1 T NMES 30 VX&NU 73 VAERNC 50 VVRENY 34 | VVRMNH 84 VVKNHH | |
| 20 CESS | SGFKSK GSVVSK GSVVSK 68 868 AGFSSK AGFSSK | VPVRTI VPVRTI RAVRSI VPIRLY | LKTVAV 28 SESSE SESSE 27 LKTVAV 27 ASSIQV 28 ASSIQV 20 20 20 20 20 20 20 20 20 20 20 20 20 | YRRYKV 26 NHQLVV | |
| DevSG | DKVSG DKNSG DQNSG DQNSG DVYSG | FLVDR | ЕТ V D E 270 Е LN SEP 263 263 21 D E E D 240 240 254 254 254 254 | LLNALE 254 3LNVHQ | |
| 60 Kt.S.L.e.L | 2 FA L E1 47 LL 2 L T 47 Δ L 2 L T 47 A I 2 L V I 58 A I 2 L V I 49 LL H MK I 60 | NEASU 55 NPKNII 46 NPCOII 58 NHHHIV 148 | nukuv asoyse amdre qayds | G TA YQA EPVLSE | |
| e EBIE | 5 EGENQ 39 39 39 49 - 0 5 DS 49 - 1 DGGR. - 2 5 DS - 42 - 2 5 DS - 42 - 2 5 DS - 42 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - | | 260 260 250 253 253 253 253 253 230 230 230 230 244 | с <mark>N</mark> WWE 244 сКҮWWD | |
| HUX | Н ІК ҮК ⁴ Н | хАDFH2 145 145 136 136 тар ен 1 148 аар ен 1 38 | TTDFH3 SSSSS | NCASS ^P SSNGD <mark>R</mark> | |
| 40 /*****D | 35 7 IGERD 30 7 EPVPD 40 7 TWSDS 33 33 | LWFDP ZLWFDP ZLWFDP MLWFDP | 250 250 √▲►K≪A √▲►K≪A 1≤7KVE 2235 DSA | PA 234 VAKKCS | |
| or Hara | DDQFDV YGDFQV LQDFQV DELFQ1 | REAR 135 KEHOF 126 RE00F REERV REERV | PPSSS1 | - <mark>P</mark> G 227 - ÅGAEI | |
| ³⁰ ≫≏⊷∆⊭F | 25 AAEYNF 20 MAGF 30 ARPATF 23 VSSAKF | A S G D G K A S G D G K A S G V G N A H G Q G N | L NG VG N 240 10550-1- 233 H P K A P P | P A S V | |
| Levas | LAAAA L-A SLSAF LGP TGP130 | RINE 125 INTNVWI HTNIFI QTNIYI | 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 7 NACECI | |
| rv <mark>⊱S</mark> *f | LAVLAV 15 MLASPK CFLSLF CFLSLF LGLSLF | GPY SE | gerisv 27 23 23 23 15 23 24 25 25 22 22 22 22 22 | YKDFDI 21 YKGFDI | |
| TXTIC | PLLAA FGMLVI IASISL FLSVI 120 | HGNS MGNKS TGNKS TGNKS TGNKS | PFVAS PFVAS 273 273 273 273 273 273 275 205 205 277 277 277 277 277 277 277 277 277 27 | 207 207 5 P F V A S | |
| 10 10 10 | -AAK01 -LGLV1 RSGSV1 -ASA51 | HEDEH 195 195 105 105 108 108 108 108 108 108 | EFDFE RWR Se HWRGDI DW-NSZ | NW - SK / DW - SH 0 | |
| 1-1 M | Т Г Г Г Г Г Г Г Г Г Г Г Г Г Г Г Г Г Г Г | GA⇒HD GSTHD -ANHD DAVRD | 210 210 203 203 203 196 512RI 208 208 | GLEKI 198 GRVKT | |
| Sequen ⁸⁴ | BdXTH8 - EfHTG FvXTH6 FvXTH9 | Sequen | FFVX1H9 Sequen | FvXTH6 | |
| | BdXTH8 | EfHTG | FvXTH6 | FvXTH9 | |
| BdXTH8 | 100 | 38.2 | 35.5 | 35.6 | |
| EfHTG | 38.2 | 100 | 44.6 | 39.1 | |
| FvXTH6 | 35.5 35.6 | 44.6 20 1 | 100 45 7 | 45.7 100 | |
| 1 1 1 1 1 2 | 55.0 | JJ.1 | 40.7 | 100 | |

Figure S8. Amino acid sequence alignment of BdXTH8 (XP_003573584.1), EfHTG (CEH24720.1), FvXTH6 (gene05591), and FvXTH9 (gene01986) as well as pairwise sequence identities using Geneious software with default values.