Supplementary Files

Figure S1. Predicted amino acid sequences of the 105 protease genes identified from the Hessian fly *(Mayetiola destructor)* genome. The sequences are listed in order of putative trypsins, chymotrypsins, trypsin/chymotrypsin homologues, truncate trypsin/chymotrypsin-like proteins, cysteine proteases, and homologues of cysteine proteases. Bold sequences at the N-terminal indicate putative secretion signal peptides. Truncated proteins were indicated by red notes.

Trypsins:

>MDP3
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CTAAIGNVASRISIYMGASSNKQGGFEHHVKRIVQHKRYNSRNIDFDFSLLELEEAVSYTDSVQAVALPDFGELTAD
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LDGKPILVGVVSWGYGCAQPMYPGVYSRVIAAREWIYEHTGI
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DSDPERITVKSGTNFHQHGTESKVKRIIEDPKYFRPTRTYDFALLELENELKLDETRKAIKLAESNDHHVDGSMCLV
TGWGKTKNASESTHMLRGVEIPIVPQNECNKAYEEISDITSSMICAGYMEGGKDTCQGDSGGPLVQFKNGEPILIGV
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SGWGNTLSSNESRAILRGAFVPIVNQEKCVEAYRRMNNVTPRMICAGYEKGGKDSCQGDSGGPMTLFSKKGPRKLIG
IVSWGYGCAQSNYPGVYSRVQAARQWIQLVTGV
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>MDP25 (5’truncate)

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Chymotrypsins:

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GRNSFPTPPGLSPLPDILQFAPAKTLSPEECESEFQATIYAHYLSETNVCTVNPKGRGACHGDSGGPLISNDKALVG
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Trypsin and chymotrypsin homologues

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CCISVTEFVMDIELAGGGGGGYNKLMKSNQFMDDTPPIRYNSMMSKSKTKTKTKHMISPPAPYLKHNALRRRMDEMD
MMNQYECGVPRTSQNTIQKRIIGGRVAPFAAIPWQAHIRIAEYQCGGVLVKIL
>MDP88
MKVIILALFAIVAVACVSGQGAVLLQDPLKTISEAGKSATDAANGGVKSATETVTGSGKSATDAVTGAGKQAAGTVN
GGVKSATGAVTGAGKQAADAVTGAGKQAADTVNGGVKSATGAVTGAGKQAADTVTGAGKQAANTVNGDGPLPSELHE
VPVPILNNTSCEGMYRNAGYRENIPSHLFICAGHIKGGRDSCAGDSGGPLVIEREDKRFLLAGVISWRINCAEPNQP
GVYTRISEFRGWINQILQF
>MDP89
MNEFGVATFMECVHSMHDSIVVNEILILQTLSLGSLLQCEPKIICGIHTFFKYVFFFNFQSSRQSTVWRSTIVGGNV
TTINDYPWAALFQYHHQEKQLDTWGCSGAYIGGRTVVTAAHCVDESSRRDLGELRIVRLGEYDTETNPDCVKHGTDD
EQDCNETPFDATPEKIIIHPKRADDSKQYDIAVIILETKPPYTDFIRPICLPEVAERDLIDSNEIIYVTGWGWTHGF
IRSPSNVKRHVRINLVHQNICQQQYPAIPVNPVSSKMELFGTNWVNVYKIISFHLNP
>MDP66
MLFIEIIIMGIFLVLQTTNGHLHLYLNDKCLMAHSNDSGICQYVENCPIVVKLFRQQHINPTLCGFERDKQIVCCPK
EIETRFSDNATEVNILRKTISSQKCVEYQNVCSESTSIDWESDQITAKQFPFMAAIGVLEQKRGREDKIVWSTGGIL
ISKNFVLLTTKRLKNNSP
>MDP87
MDWKIFFIGILWCLATTDAQDSLAGSLFSTFLDSITTSVESKDCPGSCVHSLATLLCQSVDEAAQCPNNLKCCIETN
STSSEDETQSETQRPTRITTTMKPATKTTQKLEKPTKFDSNKAESTNCVGVCVPHHLADYCEAYLTTNGLCKGEMRC
CVSRENYSDKMPNDLHIPMIQVHSNHTVSSKPTKSNSPRPKQPTKTATSRPTKPQEPSRESIDGNHIGGQRRCDGEC
VGSLIALFCEKTDGDAYCPNDETCCFVNDNNDNIKETTQKPQIVSGPGMNVYCKFVYLNFIIHRLNSETVQASALHL
YSVHFDYREECPGSCIVSLLSFTCFRNAEMTDVFKCKKSGTTCCAPKSRIHEVQMMHRNDTYPQFVGPQQQQQIPQY
LPNNYQPQNYQPIPPNNYAPIPNPYQPIPAQPINNYQPIPSQNNYISQPQPVPQQPIQHIQQAPIISNNYPAPPQNY
PNPNANVYQPNVVIGNPSVNLSPAYSTPATQPTTTTTTTTTTRSPSGCTNTSCGHYLHSSQSQQSNIRQ

Truncate trypsin- and chymotrypsin-like proteins

>MDP40 (3’-truncate)
MKPKYVLCCAAIFWFGQAYGQTDNVNVEQVFHDGSTQATAKSTEITDTTDITSNSTTAADNCENGTECIPYYLCANG
SIITSGEGILDVRLGAEDDPEPGQHPCSDFFETCCTHISKEITTKSQFSISEKCGVRNKRGNGFEVLPRDNEAQFAE
FPWAAAIIHKVHDGDNVVNVYKCSGSLIHPKVILTVSHCVIDLKPEDIKVRC
>MDP53 (3’-truncate)
MKQNSALAVLIKTFLNIFILLNVLCVAQDRISSQKCTEYQSSCPKYSDPFNIKGGEAASKEFPHMAAIGYENVYKNN
GIHWLCTGSLISVNFILSAAECTRRVGSLIPKYVRLGDSDIRSYNDDARPQQFNIIETFAHPSHSPGAKYNDIAL
>MDP55 (3’-truncate)
MKQNLAVAVLIKTFLNIFILSNVLCAAQDRISSQKCTEYQSSCPKYSDPFNIKGGEAASKEFPHMAAIGYENVYKNN
GIHWLCTGSLISVNFILSAAECTRRVGSLIPKYVRLGDSDIRSYNDDARPQQFNIIETFAHPSHSPGAKYNDIA
>MDP31 (5’-truncate)
CGELYTRANRIVGGHSTSFGSHPWQAALIKSGFLTRKLSCGGALVSNRWVVTAAHCVATTPNANMKVRLGEWDVRDQ
DERLNHEEFGIERKEVHPNYSPTDFQNDVALVKLDRNVVFKQHILPVCLPPKTSKLIGKKATVAGWGRTRHGQSTVP
SVLQASILTIHSKWTFAVHNAHDVPFKKRIIFFPNLLQEVDVEVISNDRCQRWFRAAGRRETIHDVFLCAGYKEGGR
DSCQGDSGGPLTMALEGRKTLVGLVSWGIGCGREHLPGVYTNIQKFVPWIDK
>MDP36 (5’-truncate)
EWDTQTSNEPFPHQDRKVTEIKIHEHYRPGSHFNDVALLILDKPVDLAENVNTVCLPPQDFNFNDRRCIATGWGKNK
FGSTGLYQVILKKVELPVVPSDQCQKILRTTRLGRYFILDPSFICAGGESGKDTCQGDGGAPLICSIDNNKNEQNYQ
AGMVAWGIGCNDPIPGVYVNVAKFRNWIDHAMDNLKLEKKFYTL
>MDP50 (5’-truncate)

NVAEQIKYPTFTSKYKYNDIGLLRLETTITFNEYIWPACLPEFTAIGFQATATGWGRLDNNGPLSSTLRKVELDLYT
HKECDDLYTAIKSRQIDRGILNDTQLCAGSHSGRGDTCQGDSGGPLQKFHDSLTCMYTIVGVTSFGQYCGSRLPGIY
TRVYSYVEWIEGIVWPN
>MDP56 (5’-truncate)
CVEYQAPLYEHVANPLSFGSNNIEQSVLRCPLSSVPLVVGGQNAIPKEFPHMALIGFEDLSKPNNITWGCGGSLISD
RFILTAGHCINTRSGLPKSVLLGEYVLDMDTDDAQPKQFDVIETIRHPDFKSPVKYNDIALIKLNESVEFSQYIRPI
CLPESNTIETDRVLASGWGKLNYTGQSADILQKVLLEIFTNEECNEKYQPHINRYISRGILNETQVCAGSHEFRKDT
CQ
>MDP63 (5’-truncate)
KALGYEKMITTEIRNDTEPNTRYVRVLDPKSAEISFVRTSCEKKQALWVSCSNLDCGVQPMLGSGSAMSLSKMANVG
DWPWHVSLHRDETHVCDGTLVSENWVLTTESCFQGQSKAAWIAVVGNIRLNSHTPWTQRRRIIGMIKSPVEGSTSAL
VRLDTPITYSDYVRPICLPDALTIDKTETAAQTANGSTTSSDISVSRTKKGGRNDVTENRDYFFGPDDFQIKADEMD
DEFGARKVRAIPTEFMSTPVSVPANEKTNATKNDDSHMKSATETSKPTQWATCNTLGWQTQREHVQR
>MDP64 (5’-truncate)
RCASKFNTDQYCFRLESSHQIIHSLNINALIIIFKMGFHMLWITSMLFVSTFAQNKLNDQCQVARSGSMGHCQYLES
CSVVLKEISEQGLFPNFCTTQDRKQLVCCPLPPTKRTTKKPSKPNRISAQSMFQIENKLIEKALKVLILFL
>MDP65 (5’-truncate)
RCANKFNTDQYCFRLESSHQIFRSLNINALIIFKMGFHMLWITSMLFVLTFAQNKLCKVARSGSMGHCQYLESCSVV
LKEISEQGLFPNFCTTQDRKQLVCCPLPPTKRTTKKPSKPNRISAQSMFEIENKQAEKALKVLILF
>MDP68 (5’-truncate)
GFEYAKMQKIPLNTITNTECNQVYANRDRIALPNGIDKNTQICAGSRLGERDACRGFSGAPLLNTKQKKSCLYEIYG
LNSISLVCGSGYPSVYTRVSAFLDWIENIVWLNGTEKVPDIPITHPPTTKSPKADRTFVKKCNEYHNSLFGPNRIEQ
NVCTFAVSPYIVDGEVAEAKEFPHMALIGFDGKNKIAWACGGTLISENFVLTAGHCLNVTGYGVAKYVLLGDLDYSR
DDDDARPLQ
>MDP69 (5’-truncate)
GFEYAKMRKIPLNTITNTECNQVYANRDRIALPNGIDKNTQICAGSRLGERDACRGIFRCTIIKYKGKKILFVRNLW
FEFDKFGVWIRVSIGIYTSLCIS
>MDP70 (5’-truncate)
KIQIVNGRIASIENNPWHVAVIEYPWWRFYSWSYACGGAIIGKRWILTAAHCPLDNYWYGIRTGSVHHADGGKVYNV
KKITKHPEAKKNSNDIAIFELDEDIEYNDRTRNIIMANKNETIENYVLASVRATGWGRTCLRCPISDVLLETEVLKI
LNPCTFQPLNICVFDNVGEAAPCRGDSGGPLSVGNSEKDGTLIGVISSVDNDCNASYPSIGPFIPLYRDWIQSITGI
>MDP81 (5’-truncate)
NSLHSAHNLQMSQHINLTSVLKYQAANNSTKQNGPHSMHKIQAAHFNQRPHSNQINWQGLPRGTQPNEAAFGEFPWQ
AMILRESTKTILCGGAIIDKNMVATAATCVDGLRTHDILIKAGEWKLGSNEEPKPFQTVRVKQIVLHPAYQPTNLES
DIALLHLENDLKYDKHIGAICLDDSDLEPAGSNEECVTSGWGKENIKYHIAGAIPHSLAIEPVSPNECQASFSSYNP
NSAVCGRAQGNPCDVDVGSALACTRGNGRYLLKGIYSAQSGCGPDQVMSFTKMDVNFIRGHSEKTHPNTPFNHSPSQ
FKSNQPTSTSFSHQTPTPSVLGVRGYLPPNLK
>MDP94 (5’-truncate)
PQTRIVGGSESSPGDWPFLAAILGGPEEIFYCAGVLISDQWVLTASHCIGNKSLHSITNWTIQLGITRRNSHTYYGQ
KVKVQRVIPHPHYNLDVMHDNDIALFQLATRVAFHEHLLPVCLPPPSIREIKPGTLCTVIGWGKKE
>MDP32 (both ends truncate)
YRAESCFTTNIQPQNSRTAFQNMVFRNLLAKEQITNVVPSLFQNRPITLLFLTESSFGRWPWQISLRQWRTSTYLHK
CGAALLNENWAITAAHCVDNVPPSDLLLRLGEYDLAEEEEPYLYQERRVQIVASHPQFDPRTFEYDLALLRFYEPVV
FQPNIIPVCVPETDENFIGHTAFVTGWGRLYEDGPLPSVLQEVSVPVINNTLCEGMYRNAGYIEHIPHIFICAGYRK
GGYDSCE

Cysteine proteases

>MDP95
MNKLLIVLFGLVSAANAVSFFDLVKEEWNAFKLEHAKNYESDTEERFRMKIFMENKHKIAKHNQLYHKGQLSYKLAI
NRFADLLHHEFVGGMNGFNRTTAMKLYKGETKPVERSLTYIEPANVEIPDSVDWRTKGAVTEIKDQGHCGSCWSFSA
TGALEGQHFRKTNTLVSLSEQNLVDCSAAYGNNGCNGGLMDQAFQYIKDNGGIDTEKTYPYEGVDDTCKYNPKESGA
TDRGFVDIPQGDEKKLKSALATVGPVSVAIDASHESFQFYSSGVYYEPQCDSQQLDHGVLTVGYGTDESGQDYWIVK
NSWGT
>MDP96
MKFVFLLFGLISLGYATPVAELLNEEWIEFKLEHSKEYKHEEEELFRLKVFLENKYKIAKHNQLYDQKRVSFRLAMN
KFGDLLNDEFSKLMNGFHGANVMKWDELEVPTWKIGMSHSEQINENFTDSMDWRKSGAVTDIKDQGQCGSCWAFSAT
GALEGQHFRSTGVLVSLSEQNLIDSKHNQLYDQKRVSFRLAMNKFGDLLNDEFSKLMNGFHGANVMKWDELEVPTWK

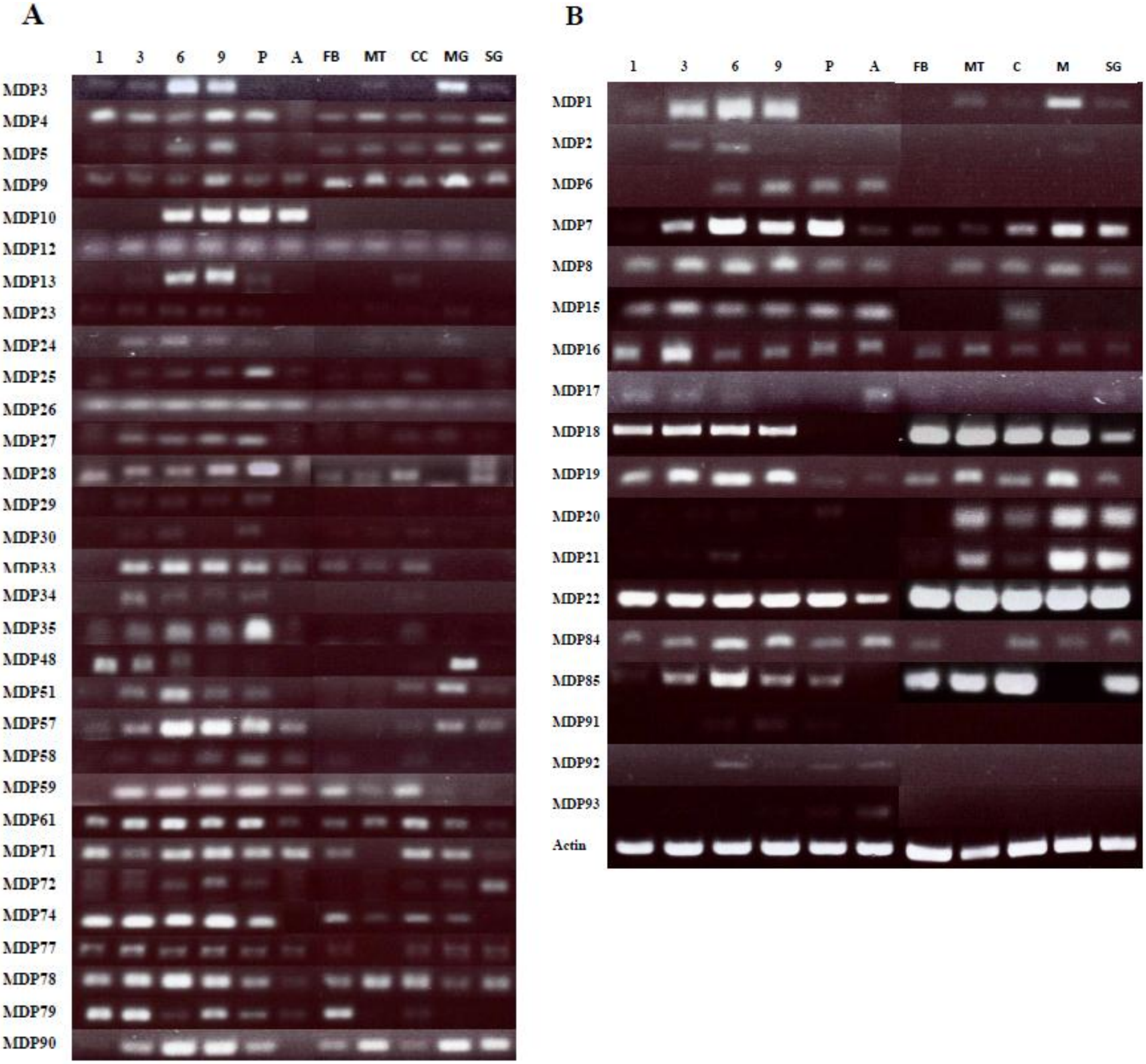
IGMSHSEQINENFTDSMDWRKSGAVTDIKDQGQCGSCWAFSATGALEGQHFRSTGVLVSLSEQNLIDCSGKYGNQGC
NGGSMNKAFQYVKENGGIDTEKSYPYRGYEHSSCKYNPREIGATDCGYKTIESGCETCLTSAISSVGPISVGIDAGH
RSFQFYSKGIYYEPACSTYNLNHAVLAVGYGTDVINEEYYILKNSWSPGWGENGYMKMARNRGNSCGIATMASYPLV
CANV
>MDP97
MNRGSITLLFILIWGCGVVVSGFPVLNAVTNAISRMGRNFVERFTSNFMNRRNSNLFPDEWADFKKTNNKTYSRAEE
NLKRMKIFMENRKRIRQNNLLYQQGKVPFRMRANSFSDLSRLEFSQQMKGFLKGLKFGTEPIYESTKNNETQLPKSV
DWRTEGAVGAVHKQGKCGACWAYSAAGALEGQQKIKTGKLVPLSVQHLVDCSKENSGCGGGLPSRAFNYIKRNGINA
ESSYPYTGRNGVCKFDPENNAATATGYITIGKDEDLLAEAVATIGPISVIIDSDHESIQLYESGIYYEPKCNSNSLD
HAVLVVGYDTDKNGKDYWIVKNSWGENWGLKGYIHMARGRGNNCGIASRALYPTI
>MDP98
MKTNVFILLSAFCISALATKPPRWDLLHHVKAVLYIPYAEIVEPFEAWFDKNTNRSRIDYYNGMVKTYQLGRNGPYG
TLLKIAPVTTKEKSNEITCLQVNGTSENRVEPQSVLPDCKQFSLADTLEFRNWNCNKFTFEEMIGEKKNQYTIYVRY
VKSPKYPASLQPIPVRYEMRGFNTLLGSHYDHYYIDYDSYVHDDIPDDIFEYDTEDKPCIAFPGPGNGHYATFNPMK
EFVHPADVSHVDIEQARFINKHGVVYATTEERMRRHHVFMHNLRYIHSKNRQNLGFSLTVNRFADRTDDEMKALRGF
RRTVGYNGGRPFPYHLNVTILADLPDDYDWRLYGAVTEVKDQSVCGSCWSFGTTGAIEGAWFLKNGGNLVRMSQQAL
IDCSWGQQNNGCDGGEDFRAYQWVKENGGIPTEESYGGYLGQDGYCHVNDKNVTLVAPVTGWVNVTRNNPNALKVAL
IYKGPISVAIDASHKSFSFYSHGVYFEPKCGNKEEDMDHAVLVVGYGLMNGEQYWLVKNSWSNMWGNDGYILMSARD
NNCGVLNDGTYVTFD
>MDP99
MKCSKGFWIFLLLVLVCFLAVPIHFGLKQYYVPHRLADQLFRNFTQKFNKSYLQPEEFQNRLNIFTQTLKKIVELNT
VQNPSAHYGVTKYSDLSSDEFASLHLNKNMSHIIGARLKSIKENPKSNIPKIVNTKDINYKFTYNVTLDSYQAFYSL
DLLHKNVNFIPLKVDWRNNKVLHPVRSQGNCGICWAHSVISMIEANLAIHKNISVALSVQQMVDCARNGNNACSGGD
SCLLLEWLVENKIKIRTEEDYKPSISGMNETCKVPLSDNGAGLKTFQSNDFVCNNFTNNEDEMLEIIANYGPVAVAV
NALPWQHYTKGIIKDNCNGNADDLNHAALIVGFDRSGTVPYYIVQNSWGTDFADEGFVNISIGNNTCGIASEVSMVQ
M
>MDP100
MKCSKGFWIFLLLVLVCFLAVPIHFGLKQYYVPHRLADQLFRNFTQKFNKSYLQPEEFQNRLNIFTQTLKKIVELNT
VQNPSAHYGVTKYSDLSSDEFASLHLNKNMSHIIGARLKSIKENPKSNIPKIVNTKDINYKFTYNVTLDSYQAFYSL
DLLHKNVNFIPLKVDWRNNKVLHPVRSQGNCGICWAHSVISMIEANLAIHKNISVALSVQQMVDCARNGNNACSGGD
SCLLLEWLVENKIKIRTEEDYKPSISGMNETCKVPLSDNGAGLKTFQSNDFVCNNFTNNEDEMLEIIANYGPVAVAV
NALPWQHYTKGIIKDNCNGNADDLNHAALIVGFDRSGTVPYYIVQNSWGTDFADEGFVNISIGNNTCGIASEVSMVQ
M
>MDP104
MRRLKNVVFVAIFAFAAASAATDPLSDEFIAEINEKATTWKAGRNFHPSTPKVYIHNLMGVHPDSKNYLEAPKFMGS
IREDLPENFDAREKWQHCPTIQEIRDQGSCGSCWAFGAVEAMSDRECIHSEGQSHFHYSAEDLVSCCHTCGFGCNGG
FPGMAWSYWVHKGLVSGGNYDSHQGCQPYIIKPCEHHVNGSRGPCAGEGGGTPKCEHKCEDGYTTPYEKDKHYGKKS
YSITKNPDDIRQEIFENGPVEGAFTVYEDLLSYKSGVYQHVHGKALGGHAIRILGWGVENGTPYWLIANSWNTDWGD
NGFFKILRGEDHCGIEGEISAGIPRTAK

Cysteine protease homologues

>MDP101
MLSKYPCSVWILLILCINYIGCDRLVGNVGDADDTDKETVRELLIDSLKQLKGEENGIELNLIRISSVKSQVVAGKK
YTIQGEFATNDNSIKKNCEVSLWHKAWTGFRETSFNCDDATKYKVTKQSRKKRSAIGGPVDVEPDTLDELRKNITNS
FSQLGASDASKQLKLKQVYGAQRKIVAGILYTVRAEVETNEGVKNCSIEVWEKPWIHFRRVTVDCENGQQFEVIHDG
STPKKATFETQNDHETEIDDMDTLNVNEADTATLFEQYKRHFGRLYTDANEESIRYRIFQQNLYLIKQLRKFELGTA
EYGLTDFADLTEEEYKMRIGLRPELRSNENAIPNPPADIPDIVLPEAHDWRDHGAVTPVKNQGI
>MDP102
MKFLVLCLVFVLIFGIDANAFDGVLGGPKEITDTDKRTHLLDQIKKHLETLSSKPNHPQLEYVGHSSATYQIVAGTL
YKMNGTLKENDQEVICALTLWEKPWMNFEKFTAHCGEEPVRTYESTVGEERRRKRAILLGGPQNVPEEEWPEIHTKL

LNAFDQFHAKHENFDYNYKNIVEATKQTVAGIKYAVKVIVNVGKSKDQTKECNISVWEKSWEQFYKFTFECDDDTYE
YTSSPATSASINE
>MDP103
MKLLGLCLVFVISAMTVDAHHITHAELEKLLNKIKRHLVILSNKPNHPQLEYVNHSSVKYQLVAGSLYTMKSTLKEN
HHKVKCLLEFYEKVWDNFEELRVTCGKKPKRKYKSVKGEEDPPQDVTEEDS
>MDP105
MANIVLSIGILLMFDCVSITVNGYMRDFPGPYCAQRRGGCCDSRKDECSVPISTTLCYCDEFCDRTINGDCCPDYES
FCLNISPADELTVRCKHKDTIFNPFEQIKDNCNLCTCQGNGHTVCEQNTCLIDDSLVNNVNTISHTLGWTAYNYSEF
WGRKYQEGLDLRLGTKEPTYRVKAMTKLSNKPESLPRDFNAIDHWPGFISEVRDQGWCGSSWAVSTSSVASDRFAIQ
TKGKETVELAPQHLLSCVRKQSGCQGGHLDWAWNYIRKIGLVDDECYPYTAEATRCKIRRTDTLSSAGCKLPQKVPR
DHLYRVGPAYSLNNESDIMAEIYESGPVQATMRVFRDFFAYHRGIYRHSAASRAEPSGFHSVRLIGWGEERSGYDVT
KYWIAANSWGKWWGENGYFRILRGSNECEIENYVLATWPHAHLKPKIPSNRVSKSRRPFY

Figure S2. Original reverse-transcription PCR results for figures 3 and 4. A. PCR results for the 31 putative trypsin genes. The six lanes on the left side of the figure were samples to determine developmental stage-specific gene expression. The numbers 1, 3, 6, and 9 represent samples from whole body of 1- 3-, 6-, and 9-day old larvae, whereas the letters P and A represent samples from whole body of pupae and adult flies, respectively. The five lanes on the right side of the figure were samples to determine tissue specific expression of genes. The letter combinations FB, MT, CC, MG, and SG represent fatty bodies, Malphigian tubules, cascades, mid-guts, and salivary glands from 3-day old larvae, respectively. B. PCR results for the 18 putative chymotrypsin genes. Denotations are the same as panel A. C. PCR results for the seven putative cysteine-protease genes. Again, the denotations are the same as panel A.



C

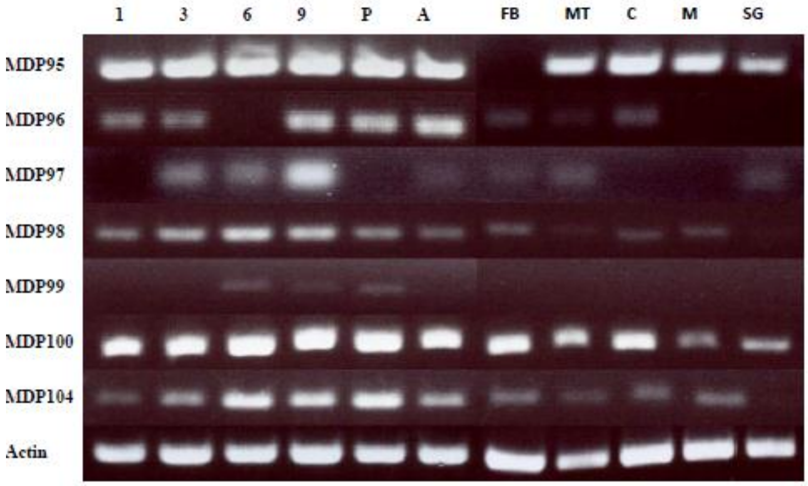

1
3
6
9
P
A
FB
MT
C
M
SG
MDP95
MDP96
MDP97
MDP98
MDP99
MDP100
MDP104
Actin

Figure S3. Original reverse-transcription PCR results for figure 5. A. PCR results for the 31 putative trypsin genes. N1 and N3 represent samples from whole body of 1- and 3-day larvae living in the susceptible wheat Newton, whereas M1 and M3 represents samples from whole body of 1- and 3-day larvae living in the resistant wheat Molly, respectively. B. PCR results for the 18 putative chymotrypsin genes. Denotations are the same as panel A. C. PCR results for the seven putative cysteine-protease genes. Again, the denotations are the same as panel A.

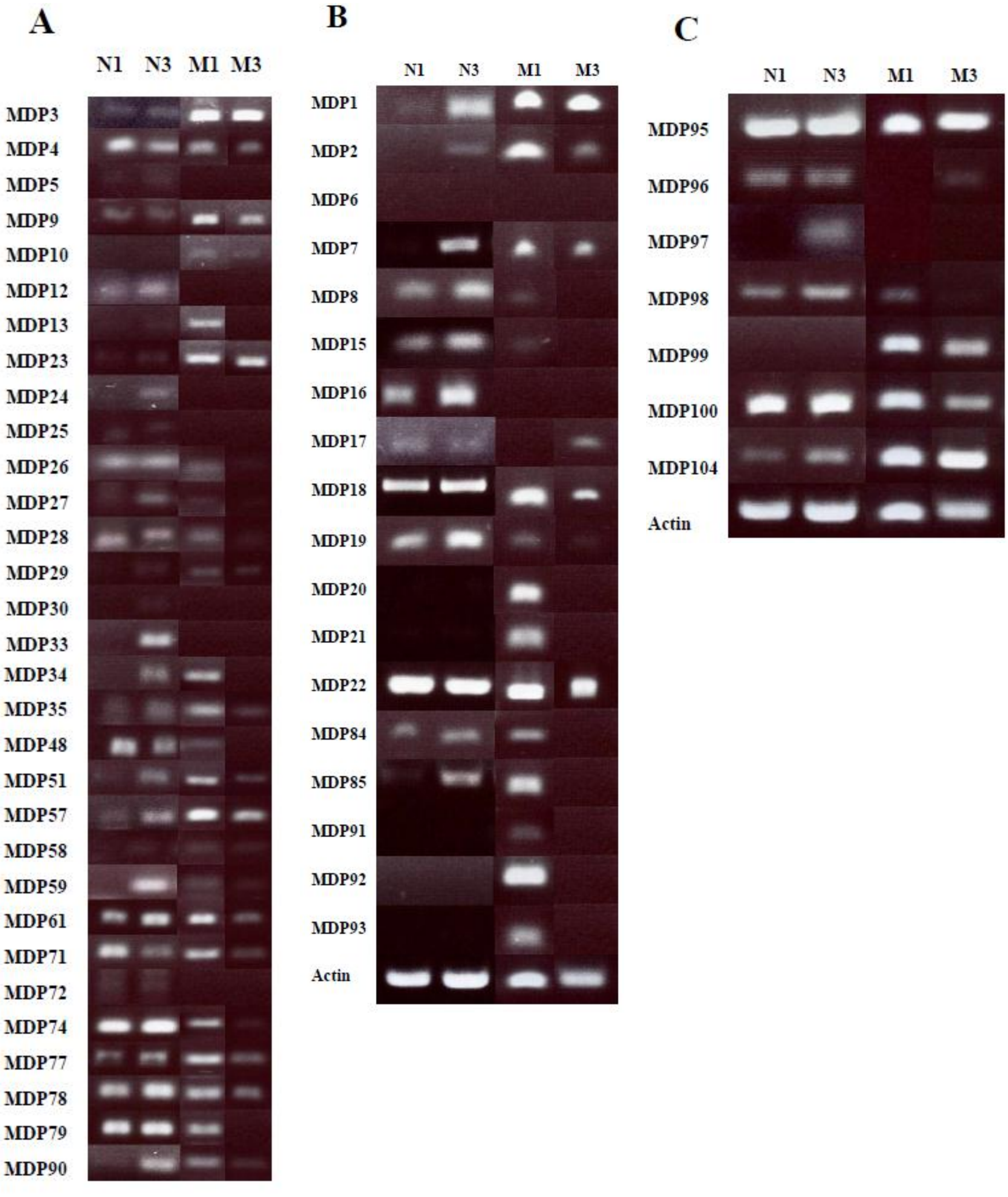


Table S1. Primers used for Semi-quantitative PCR analyses.

	Sense Primer	Anti-sense Primer
18 Chymotrypsins		
MDP1	5′-GTCCATTGATTTCAAACGATA	5′-GTGTGATATTTGATGGTACTG
MDP2	5′-CCTACAATGATAACGAACC	5′-GTCCAGCACAAATCATAC
MDP6	5′-CTCTGTTCAGCAATGGAA	5′-GCGAGTCTCAGTAATAGG
MDP7	5′-GTGGTTCAATGGTTAGAA	5′-CCCATCCAGACAATTTAC
MDP8	5′-TCGGAAATCAAAATGTCTAAAG	5′-AACGCTGAAATTCCGAAA
MDP15	5′-ATCGTGGAACCTTACAGCAATGC	5′-GACGAATTTTGAAATAATTGG
MDP16	5′-CGACCAAATCAAATTAATGA	5′-GAAGCCACTACATATACC
MDP17	5′-CGGTAGATCGGAGTATAG	5′-TGTCGGTAATAATGTCATC
MDP18	5′-CCATCAGAGACAATAAGC	5′-CCGACCAAAACTTTATCA
MDP19	5′-GGTCAAATGGATGTCATA	5′-GTCTGATATTGAAGCTTTC
MDP20	5′-GCACCATTTCAATGTTCTATG	5′-CAGGACGTTGACCACTAA
MDP21	5′-TGGCTAGTTTTGTTTCAC	5′-TCCGATACTCTTAACAGC
MDP22	CGTGCAAATAATCTAACTGA	5′-GCATCTTTTGTTTCAATCG
MDP84	5′-CTGTGATACCATTAACAAAA	5′-GTCTGCCGTAGATTATTC
MDP85	5′-CAGCTTATGGATATGGAAC	5′-GAGCGAGTTTAAGACAAA
MDP91	5′-GTGGTTAATTGATTACATTGG	5′-TGGACTTGTGATAGGAATA
MDP92	5′-GTGTCGTGATGGATCTGA	5′-GTGCTGCACAATATTTCAC
MDP93	5′-AACCGATTCAACAAATGC	5′-AGCAGATGGCATAAATGA
7 cysteine proteases		
MDP95	5′-CCATGAATCATTCCAATTCTA	5′-CCCATGAGTTCTTTACGA
MDP96	5′-TGGGATGAACTAGAAGTG	5′-CCTTGATCTTTAATGTCAGTA
MDP97	5′-CGGTATTAAATGCTGTCA	5′-CTACGATTCATAAAATTCGAAG
MDP98	5′-CCAGTTACAACGAAAGAA	5′-CTTCGAAAGTGAATTTATTACA
MDP99	5′-GAAGCGAATTTAGCCATC	5′-GCATGTTTCATTCATACCA
MDP100	5′-GAAGCGAATTTAGCCATC	5′-GCATGTTTCATTCATACCA
MDP104	5′-GATCGAGAATGTATTCATAGC	5′-CCTGATGTGAATCGTAATTG
31 trypsins		
MDP3	5′-CAATCTCAACACCACCAACAATTCG	5′-CTGGTCACAATACGTGTTA
MDP4	5′-CACGCATATCAATTTATATGG	5′-GCTGTACAATCCTTTTCA
MDP5	5′-GCAACTCAATTCTTATTTGTTG	5′-TGGTCATATTTCATTGGAGA
MDP9	5′-AGTGCTCCATCAATGATA	5′-CACTCAATTCCAATAATGAATA
MDP10	5′-TTCCGAAATGAATAACTATGA	5′-CAACCGATTGTAGAACAG
MDP12	5′-GCAAGCGTATATCGAATA	5′-TCCACCTTTATCAGAATATG
MDP13	5′-GGCAAGCATATATCGAATA	5′-CCTCTATTGCAATATGATGA
MDP23	5′-GCATCACTAATAACATCCG	5′-ACACCAACTATTGAGCTA
MDP24	5′-TGCACCTATAATTTGAAAA	5′-CGTCATTATTTAGATTGTCC
MDP25	5′-GCCACAGGATTTAAATGATA	5′-GCTGAATGAGTTTCGATC
MDP26	5′-GCGTAATAATCGAATTGTTG	5′-TCCTCTAAATAAACCAACCA
MDP27	5′-AGTCCAAACAAAATGAGG	5′-TGCAGTACAAATGTTTAAC
MDP28	5′-GCCACAGGATTTAAATGATA	5′-GCTGAATGAGTTTCGATC
MDP29	5′-CATCGAAATATCCAATAAATAAACC	5′-TGGGAATTTTGATGTCGC
MDP30	5′-CGTCATCAACATCATCTG	5′-TCTGGCTTTGGTCTATTC
MDP33	5′-ACTCGTATTCCAACAAGA	5′-GTGGTTTCATCAGGTCTA
MDP34	5′-CACACATATCTATTTACACG	5′-GTTGGTCTCTTAGGAATC
MDP35	5′-GGCGTCATGTTGTTACAG	5′-CTGGCAATGGTTCAACTG

MDP48	5′-GCGTATCTTATCAGCCAA	5′-CAAGCCCAATCAATTCCA
MDP51	5′-AACCGAATACATTGAATGAA	5′-CAGTGTATGTTGTAGTTCAG
MDP57	5′-CGTCGTTGATGATATTGTC	5′-GGAACTGGTGTTGTAGTA
MDP58	5′-CAACCGATAACAACAAGA	5′-GGACGAGAATAATACGAAG
MDP59	5′-TCCAGTTGTTGATATACCA	5′-CGAAGCAATGCAATATCA
MDP61	5′-CTTGGGAATACTTGTGCC	5′-GTCGAATGTAATCCGTGTA
MDP71	5′-TCCGGTTTATAATAATGTAGTG	5′-GCCGATTAGTAACTGGTA
MDP72	5′-GCGATGAATTTCCAAATG	5′-CCAAGTGTTTCTGAGATAC
MDP74	5′-GGTGTTCTCATGGTTCAA	5′-CGGAATTGGAATGTGTTTG
MDP77	5′-CTGGATGGGGTAAATTACA	5′-GCATCTACAATTTGATAGGC
MDP78	5′-GGTGGTACTTATTCTCAAC	5′-CACCATTTCCATTACTAATTAC
MDP79	5′-GCTCAGCTTGGTACATATAATG	5′-GAGACCAGATCCGCTATC
MDP90	5′-CTGCTCGTATGATTTGTG	5′-TCACCAAACAGTACCATA

Table S2. Pairwise comparison of the 31 putative trypsins in the Hessian fly genome. Sequence identities (%) are shown in the upper right corner, while phylogenetic distances are shown in the lower left corner.

Percent Identity

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31		
1	■	46.7	43.0	42.9	46.1	32.1	34.9	32.9	38.1	32.6	31.3	32.2	31.8	31.1	31.2	31.2	27.6	30.5	26.7	26.9	31.4	25.6	31.4	33.8	30.7	34.2	25.6	22.9	61.3	50.2	61.3	1	MDP3
2	89.1	■	41.1	40.8	48.5	34.8	35.0	34.0	40.5	33.8	34.7	36.2	34.2	35.6	32.6	35.7	27.9	31.5	27.4	26.6	37.6	27.7	35.0	32.0	33.1	34.1	27.3	26.4	49.2	55.6	48.4	2	MDP9
3	100.9	107.4	■	40.6	43.9	32.5	34.3	32.6	33.5	31.9	34.5	34.8	33.0	36.3	32.0	31.4	30.3	33.2	30.3	28.0	31.6	26.4	31.8	31.0	32.5	36.3	24.4	24.6	42.7	42.6	41.8	3	MDP10
4	101.1	108.5	109.1	■	66.1	30.9	35.1	33.2	38.7	31.4	34.2	32.5	31.8	34.5	32.0	31.1	29.4	29.2	30.5	24.5	31.0	30.0	29.3	32.2	33.1	31.9	24.0	22.8	41.0	41.2	40.6	4	MDP12
5	90.8	84.0	97.8	44.9	■	33.3	39.4	36.8	36.9	33.5	35.6	35.8	37.3	33.9	35.2	33.9	28.1	31.4	30.2	29.0	32.0	29.2	31.6	32.4	30.6	32.9	23.7	22.8	45.3	42.9	43.8	5	MDP13
6	147.3	133.6	145.1	154.4	140.9	■	38.0	28.8	33.7	29.4	33.2	33.3	27.1	32.4	29.5	30.0	30.0	29.2	30.9	29.3	31.8	27.4	33.0	31.0	28.6	29.6	24.7	25.3	34.4	31.2	34.9	6	MDP23
7	133.1	132.4	136.1	132.3	113.9	119.5	■	29.0	32.5	28.7	31.2	32.1	28.6	28.4	26.6	30.8	27.3	29.0	26.5	24.9	28.4	25.9	31.8	29.2	33.2	27.6	28.3	23.9	34.8	33.2	34.0	7	MDP24
8	143.1	137.3	144.6	141.6	124.4	167.8	166.5	■	45.6	51.2	48.2	42.8	32.9	34.9	36.0	34.1	32.6	35.5	32.9	31.7	38.3	35.3	38.0	38.5	32.2	32.1	30.0	23.3	35.4	34.4	32.9	8	MDP25
9	118.9	109.6	140.0	116.4	123.8	139.2	145.1	92.4	■	44.0	44.4	43.0	34.5	33.8	34.0	38.8	34.0	30.2	33.2	32.5	32.1	33.0	37.1	38.4	35.4	30.0	28.6	26.8	36.8	36.8	35.6	9	MDP26
10	144.5	138.7	148.4	151.4	140.1	163.8	168.5	76.8	97.4	■	44.7	41.5	34.6	40.4	39.1	37.4	35.2	34.2	39.5	33.1	41.2	34.6	38.4	40.1	32.4	33.6	27.3	24.1	33.5	32.1	33.5	10	MDP27
11	152.2	134.2	134.9	136.4	129.6	141.7	152.5	84.9	96.2	95.3	■	44.7	38.0	36.0	36.4	36.1	32.3	33.5	33.9	32.3	38.5	33.0	35.9	37.2	32.8	36.2	28.3	25.0	32.3	33.3	32.3	11	MDP28
12	147.2	127.3	133.5	145.5	128.8	140.9	147.5	101.5	100.8	106.0	95.3	■	35.5	37.9	37.5	38.2	30.5	32.6	33.5	34.2	34.6	31.4	35.9	38.8	33.2	31.9	30.0	23.8	34.2	35.9	33.5	12	MDP29
13	149.4	136.5	142.4	149.2	122.2	180.6	169.5	143.0	135.1	134.7	119.4	130.4	■	47.6	42.2	36.8	28.0	29.5	31.4	25.7	34.2	26.8	30.5	33.3	30.4	33.9	23.7	22.2	33.9	32.1	35.2	13	MDP30
14	153.5	129.6	126.7	134.9	137.8	145.9	170.6	132.9	138.5	109.8	128.0	119.6	86.4	■	39.8	34.9	29.9	30.0	30.4	31.3	34.5	29.1	34.8	34.1	30.0	35.0	22.6	23.8	34.9	34.4	36.5	14	MDP33
15	152.8	144.5	148.3	148.1	131.6	163.4	184.6	128.1	137.7	114.8	126.2	121.4	103.3	112.1	■	37.2	30.3	27.8	29.4	26.5	33.9	28.7	38.5	34.2	29.0	30.1	26.2	24.0	32.5	32.1	32.4	15	MDP34
16	152.8	129.6	151.3	153.4	137.9	159.7	155.2	136.9	116.2	121.9	127.5	118.5	124.3	133.3	122.6	■	33.1	27.8	30.9	28.0	33.1	30.1	35.6	35.3	31.2	32.9	24.3	21.7	33.5	32.7	29.4	16	MDP35
17	176.8	174.1	158.2	163.9	172.6	160.2	179.0	144.7	137.6	131.6	146.4	156.9	173.5	160.8	158.4	142.3	■	39.8	48.0	40.7	35.8	33.1	32.4	34.2	30.4	26.6	24.6	23.7	30.6	26.4	28.9	17	MDP48
18	157.1	150.8	141.7	165.1	151.5	165.4	166.3	130.1	158.8	136.4	140.1	144.9	163.4	159.9	174.7	174.7	112.4	■	40.2	41.6	38.1	34.0	30.5	36.1	32.3	28.4	25.9	25.0	31.2	29.7	29.5	18	MDP51
19	183.8	178.4	158.2	156.6	158.6	154.4	185.6	143.2	141.7	113.5	137.8	140.1	151.5	157.2	163.8	154.2	85.4	110.6	■	48.2	38.0	34.0	34.6	34.6	32.3	28.8	27.0	24.8	28.8	25.1	27.6	19	MDP57
20	182.0	184.5	173.4	200.0	166.4	164.4	196.0	149.7	145.1	142.3	146.2	136.5	191.8	152.0	185.3	173.9	108.8	105.7	84.9	■	35.8	32.4	29.2	37.0	26.9	31.5	24.0	20.7	29.2	27.3	26.9	20	MDP58
21	151.4	121.2	150.2	154.0	148.0	149.4	171.0	118.3	147.6	107.2	117.2	134.4	136.6	135.1	138.2	142.3	128.9	119.1	119.3	128.8	■	41.4	37.0	39.9	30.8	33.5	29.2	24.5	33.5	32.0	33.1	21	MDP59
22	192.6	176.1	186.0	160.2	165.1	178.1	190.5	131.3	142.5	134.6	142.4	151.2	182.7	165.6	168.7	159.2	142.3	137.3	137.4	145.8	106.3	■	34.6	33.6	28.6	27.3	25.9	23.4	25.9	26.1	25.2	22	MDP61
23	151.6	132.5	149.4	164.2	150.6	142.4	148.9	119.5	123.0	117.9	128.3	128.4	156.6	133.7	117.4	129.9	146.0	157.1	134.7	165.3	123.7	134.3	■	36.1	30.8	29.0	28.8	24.7	35.9	31.3	32.2	23	MDP71
24	138.7	147.9	153.8	146.9	145.6	153.6	165.0	117.5	117.6	111.2	122.6	116.3	140.9	137.2	136.3	131.1	136.5	127.8	134.5	123.4	111.8	139.5	127.7	■	32.9	33.5	28.1	22.6	34.5	34.2	31.5	24	MDP72
25	155.8	142.4	145.4	142.3	156.4	169.0	141.7	146.7	130.8	146.0	143.9	141.6	157.3	159.7	166.7	152.5	157.6	146.2	146.2	181.9	155.0	169.1	154.8	143.0	■	30.0	25.4	25.6	29.8	31.8	30.3	25	MDP74
26	136.4	137.1	126.7	148.7	143.2	162.2	176.9	147.7	160.3	139.4	126.9	148.8	137.9	132.8	159.2	143.1	184.3	170.8	167.7	150.8	140.2	179.0	166.6	140.1	159.9	■	25.0	24.3	39.6	34.9	32.5	26	MDP77
27	193.3	179.0	200.0	204.0	207.0	198.0	171.1	160.2	169.0	178.7	171.7	159.9	206.0	216.0	187.9	200.0	199.0	190.3	181.2	203.0	164.9	190.6	167.7	172.5	194.4	195.0	■	24.2	26.6	25.2	24.7	27	MDP78
28	213.0	186.3	199.0	215.0	214.0	195.5	204.0	210.0	182.8	203.0	195.0	205.0	221.0	206.0	203.0	227.0	206.0	195.0	197.0	237.0	200.0	209.0	198.0	216.0	192.8	201.0	201.0	■	23.1	22.5	25.4	28	MDP79
29	53.9	82.0	101.6	107.6	93.5	135.4	133.8	130.5	124.4	140.2	146.4	136.4	137.9	133.3	145.2	140.2	156.0	152.7	167.7	165.3	140.1	190.6	128.4	135.1	161.3	113.2	184.6	211.0	■	51.9	60.9	29	MDP5
30	79.3	66.2	102.0	107.1	101.1	152.5	141.7	135.4	124.6	147.4	140.9	128.3	147.7	135.6	147.3	144.4	185.7	161.7	197.4	179.0	148.2	188.2	152.2	136.6	149.1	133.0	196.3	217.0	74.9	■	50.4	30	MDP4
31	54.0	84.1	104.9	109.4	98.2	132.9	137.7	143.1	129.6	140.2	146.4	140.1	131.7	125.6	145.9	163.6	167.3	162.9	176.8	182.0	142.3	196.4	146.8	151.0	158.4	145.5	198.0	194.6	54.7	78.8	■	31	MDP90
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31		

Table S3. Pairwise comparison of the 18 putative chymotrypsins in the Hessian fly genome. Sequence identities (%) are shown in the upper right corner, while phylogenetic distances are shown in the lower left corner.

Percent Identity

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18		
1	■	27.9	31.4	30.7	30.8	21.1	21.5	28.6	69.1	45.8	38.2	33.1	30.5	22.1	20.4	24.7	25.4	28.6	1	MDP1
2	174.0	■	52.2	63.9	53.4	26.6	26.3	26.9	29.7	32.3	26.4	25.0	27.1	20.7	20.2	22.1	25.3	26.3	2	MDP2
3	151.4	74.3	■	43.9	50.6	29.2	27.4	30.1	34.9	34.1	30.9	28.1	31.2	23.8	24.3	25.1	24.4	31.0	3	MDP6
4	155.4	48.9	97.9	■	47.7	23.3	23.2	25.1	31.6	31.0	28.5	26.3	26.4	21.2	18.3	23.0	23.8	26.6	4	MDP7
5	155.2	71.3	78.3	86.1	■	26.5	24.7	31.9	32.9	35.1	29.2	25.6	25.7	21.8	20.2	22.0	21.9	27.2	5	MDP8
6	232.0	184.1	165.1	209.0	185.0	■	81.5	41.1	24.0	26.1	21.9	18.7	22.0	20.4	18.5	22.7	24.1	25.7	6	MDP15
7	229.0	187.2	178.2	211.0	197.0	21.3	■	42.1	24.5	25.9	23.2	19.0	22.3	18.6	16.9	20.4	21.3	24.2	7	MDP16
8	169.0	182.1	159.2	197.5	148.7	107.4	103.7	■	27.1	23.6	25.6	21.7	25.1	18.9	21.4	21.1	25.3	24.2	8	MDP17
9	39.7	162.0	133.3	150.6	143.0	204.0	200.0	180.5	■	48.0	37.9	34.5	33.2	23.5	23.1	24.8	26.0	27.2	9	MDP18
10	91.9	146.5	136.8	153.5	132.3	188.3	190.2	208.0	85.2	■	35.2	29.9	31.6	23.8	21.7	22.0	22.8	27.0	10	MDP19
11	118.7	186.0	154.4	169.9	165.2	224.0	211.0	192.8	119.8	131.7	■	28.5	28.5	21.4	20.5	21.7	22.4	23.8	11	MDP20
12	142.3	195.0	172.8	186.7	192.9	262.0	260.0	226.0	135.2	160.5	170.3	■	62.7	23.9	23.5	20.3	21.2	24.3	12	MDP21
13	156.6	180.2	152.3	185.8	192.0	222.0	220.0	197.4	141.6	150.6	170.3	51.1	■	22.6	22.6	22.6	20.9	26.2	13	MDP22
14	221.0	238.0	205.0	231.0	224.0	241.0	265.0	260.0	208.0	206.0	230.0	205.0	217.0	■	67.8	16.8	18.5	21.4	14	MDP84
15	240.0	243.0	201.0	268.0	244.0	265.0	291.0	229.0	212.0	227.0	239.0	209.0	217.0	41.9	■	16.8	18.9	18.9	15	MDP85
16	198.0	221.0	197.5	212.0	223.0	216.0	241.0	233.0	197.0	222.0	226.0	241.0	217.0	292.0	292.0	■	52.7	30.5	16	MDP91
17	194.4	195.6	200.0	206.0	224.0	202.0	230.0	195.6	189.6	215.0	219.0	232.0	236.0	267.0	261.0	72.8	■	30.0	17	MDP92
18	169.1	187.1	154.1	184.5	179.3	192.4	201.0	201.0	179.3	181.3	206.0	200.0	187.8	230.0	260.0	156.7	159.9	■	18	MDP93
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18		

Table S4. **Pairwise comparison of the 7 putative cysteine proteases in the Hessian fly genome.** Sequence identities (%) are shown in the upper right corner, while phylogenetic distances are shown in the lower left corner.

Percent Identity

	1	2	3	4	5	6	7		
1	■	63.1	53.0	42.0	30.1	30.1	27.7	1	MDP95
2	50.4	■	49.2	34.5	28.3	28.3	26.9	2	MDP96
3	72.1	81.9	■	34.7	30.9	30.9	25.7	3	MDP97
4	104.3	134.8	134.1	■	23.2	23.2	22.9	4	MDP98
5	159.1	171.4	154.2	210.0	■	100.0	22.8	5	MDP99
6	159.1	171.4	154.2	210.0	0.0	■	22.8	6	MDP100
7	176.1	182.2	192.1	214.0	214.0	214.0	■	7	MDP104
	1	2	3	4	5	6	7		