

**Table S1:** CCE transcripts of *S. littoralis*

C L A S S I F I C A T I O N	Sequence name (RNAseq)	sequence (aa)	a a l e n g t h
C l a s s e 0 1 6	SlitCXB67	MRLITTVGVLIILCVIHNISCDDDVTLVEVEQGQLRGQVLDVAVVGDFQYLSYKGI PYAKPPVVKLRFKDPEYLD SWE GVLNATEHGSVCPQFNPI TAVYTSGSEDCFLNVYTRNLTPDAPRPVVVFIHGGAIFGSGNTDLYRPDYLLANDV IVVTINRYRLGVLGFLSLGNEDVPGNAALKDQVTALKWVQNNIEKFGGNPNSVTI VGD TAGGASVTLHMLSPMSKGL FHKAVAMSGSATCDFGLTYKHVEKAKIFGSALKCENVEDSAALLDCLQAADYNAFYSITPTVLASEEITDVLFKME HFTFPVIEKKTGNNFLTEDYYSALTKGHVNKD VDFIIGYSSQEA VLLIDLFNASYVDLYSR YKELFTPSEILIKSTP DTNLNVAKS VKEFYFGEKPVKTENLNL FVKYSSSSASIGYHAQRYANKWANFGKKT YFYIFDGF TDWNFFGQQGVKY GIEKASHFDITYYLFYPESLNWSIDTDSVEYQVTKQLTSLTNFAKSSDPV DGV TWPQYSESSKAYVTFGNDGPV VGYPDEDDYNFWAGVYKSAGIPF	5 5 6
	SlitCXB54	MMSTVLRIALLCVVLSEALAMVQVRVSDGLLEGEVHVNEYGGTYFSFLGIPYAQPPLGDLRFKAPQPPKPWDGVR AKEFGPKCFQYDLFVDKGHVTGSEDCLYLNVYTPDVTVPVKPLPVMVWIHGGGLVSGAGDDQEYGPFLVRQDVILV TLNRYRLEVLGFLCLDTE DAPGNAGMKDQVAALRWVKENIANFGGDPDNTIFGESAGGVSVTYHMLSPMSKGLFQR AIAQSGVSVSYWAQAYKPRERGFALARKLGFYSDDVKDVYEFLLKQPIENLIKTKVPITYSEKERTNVEVYFSVVE EKQFGDNERFFYGDMIDAVSNGIHEGVDMITGYTAD EGI LSLAIFGDISASLEQARNFPQLFISY PMSLTLSTNDQLELGRKIREYFKNSISVPD LELGNRLKEYYFKEQIRVPDHWESLKD FYSMDIFVFP TMRWIKLSARSKKNKIYLYKFTCYTELNI VSELMGVGH VGNGKPVVAHSDDLMYLFSARNQTKLDMNSEEKQIEVVT KLW TNFAKYG NPTPDDSPGVAWAPYSLENQDYLDIGN ELKAGQAPDDEEIKFWENLLTEYGQKLY	5 6 0
	SlitCXB55	MVQVQVNEGWLLEGEVVQNEYGGSYYSFKGI PYAQPLGELRFKAPQPPKPWDVRS AKQFGSKCYQYDAFFEKGKV CGSEDCLYLNVYTPSIKPDKPLPVMFVIHGGSFISGAGDDDVYGPFLVRQDVILVTFNRYRLEVLGFLCLDTE DVP GNAGMKDQVAALRWVNKNIANFGGDPNNITIFGESAGGASVTYHLISPM SKGLFRRAIAQSGTNVGYWAQAYKPRE RGFALARKLGFYSDDPKQVYEFLLKEQPLEALIKAAVPITYSEKARTYTEFYFSVAAEKQFGNSKQFFCGDVLDSVS NGIHEGVDMITGYTAD EGI LSLAIFGDISASLEQARNFPQLFISY PMSLTLSTNDQLELGRKIREYFKNSISVPD DWEKLEKFYAADLFVFPANRWIKLCAQSKKNKVYFYKFTCVSELNMI SQMIGVGD LKDKPVVAHADDDL LYLFTPN TSPIIDRNSKTFQHVEKVTKLW TNFAKFGNPTPDDSLGVTWTPYSVANKDYLDIGNELKPGHAPDDEEVQFWENVL TEFNQKLY	5 4 0
	SlitCXB56	MVQVQVNEGWLLEGEVVQNEYGGSYYSFKGI PYAQPLGELRFKAPQPPKPWDVRS AKQFGSKCYQYDAFFEKGKV CGSEDCLYLNVYTPSIKPDKPLPVMFVIHGGGFISGAGDDDVYGPFLVRQDVILVTFNRYRLEVLGFLCLDTE DVP GNAGMKDQVAALRWVNKNIANFGGDPNNVTIFGESVGGASVTYHLISPM SKGLFRRAIAQSGTNVGYWAQAYKPRE RGFALARKLGFYSDDPKQVYEFLLKEQPLEALIKAAVPITYSEKARTYTELYFSVAAEKQFGNNERFFCGDVLDSVS NGIHEGVDMITGYTAD EGI LSLAVFGDVSTSLAQARNFPQFFISY PMSLTLSTNDQLELGRKIREYFKNSISVPD DWEKLEKFYAADLFVFPANRWIKLCAQSKKNKVYFYKFTCVSELNMI SQMIGVGD LKDKPVVAHADDDL LYLFTSPN SSPIIDRNSKTFQHVEKVTKLW TNFAKFGNPTPDDSLGVTWTPYSVANKDYLDIGNELKPGHAPDDEEVQFWENVL TEFNQKLY	5 4 0
	SlitCXB57	MVQVQVNEGWLLEGEVVQNEYGGSYYSFKGI PYAQPLGELRFKAPQPPKPWDVRS AKQFGSKCYQYDAFFEKGKV CGSEDCLYLNVYTPSSKPDKPLPVMFVIHGGGFISGAGDDDVYGPFLVRQDVILVTFNRYRLEVLGFLCLDTE DVP GNAGMKDQVAALRWVNKNIANFGGDPNNITIFVGESAGGASVTYHLISPM SKGLFRRAIAQSGSNVGYWAQAYKPR ERGFALARKLGFHSDDPKQVYEFLLKEQPV EALIKAAVPITYSEKVRDNEIYFNVTAEKQFGNNEQFFYGDVLDSVA NGTHEGVDMITGYTAD EGI MSLAVFGDISANLEQARNFPQFFITYPMSLTLSTNDQLELGRKIREYFKNSISIPD DWEKLEKFYAACQFLFPANRWIKLCAQSKKNKVYFYKFTCVSELNMI SQMIGVGD LKDKPVVAHADDDL LYLFTSPN SSPIIDRNSKTFQHVEKVTKLW TNFAKFGNPTPDDSLGVTWTPYSVANKDYLDIGNELKPGHAPDDEEVQFWENVL TEFNQKLY	5 4 0
	SlitCXB63	MVQVRVNEGWLLEGERVDNDYGGSFYSFKGI PYAQPPVGD LRFKAPLPKPSWDGVRSAKEFGPRSFQNDILMKTGLV GEDCLYLNVYTP EIKPDKPLPVMFVIHGGGFYCGSGNDDLYGPEFLIRHGVLVTINRYRVDVLGFLCLDTE DIPG NAGMKDQVQALRWVNKNIASFGGDPKNITIFGESAGGSSVSYHLISPM SKGLFKRAIAQSGVSTCAWAQAI EPRER ALALARSLGCHSSEDDKELYDF FKNQPKESLVGVQCPVATFEAFKGLDIYFNVANEEKFGDNERFFYGDMLDVISN SVHEGVEIMMGSTTEEG LISYADSEDI IKTLLAKIYPEYFVNKL VAFSLPLKQQLKIGKEVRKFYFNDQINVPDD WDKLINFTSMQNFVYPERQWAKHSAQGKHKLYLYKF SCKTERNFIAKMRGMTEMLGNREVTCHADELTYLFNPKL MPTKLDTASETFQ LMERLMKLW TNFAKYG NPTPDDSLGAKWAPYTLENQEYLDIGNELKTGTAPDAEETQFWDKLY EKYGL	5 3 7
	SlitCXB64	MVQVRVNEGWLLEGEQVDNHYGGSFYSFKGI PYAQPPVGD LRFKAPLPKPWDGVRTAKEFGPKSYQNDIFMNVGRV GEEDCLYLNVYTPSIKPDKPLPVMFYIHGGGFYSGSGNDDLYGPELLVRHGVLVTINRYRVDVLGFLCLDTE DIPG NAGMKDQVQALRWVNKNIANFGGDPKNITIFGESAGGASVSYHLISPM SKGLFKRAIAQSGASTSPWAQAVEPRER ALALARSLGFYSEDDKELYEFFKHQPMESI VGVVPVSATFEAFKGGIDVNTVVNEKKFGGENERFFYGD MIDAVSN GVHEGVEIMTGT TTEGLIAMGDLKDTTKALELARTYPEI FMNKYEAYNLPLKQQLKIGREIRKFYFNDQVINPDD WDKLMNFLSMQMFVYSTMQVVKYCVQAKKHKLYLYKF SCKSERNVMSFLRGQTEMLGSRRTVCHADELTYLFNPKL MPKMDTASATFKMVERILT LWTNFAKYG NPTPDDSLGVNWPYTLENQEYLDIGNELKAGTAPDAEETQFWDNLYE KYEL	5 3 6
	SlitCXB108	MHTKISFFIIFTFLQWIFCEYVEVEVAQGRLRGERLETVTGEAAYYSFKGIPYAKPPVGT LRFKDLPLPPEWDGV RDTAQHGSVCPQVELLNNI VIPGNE DCLFLNVYTPILTPTPLPVMVFIHGGGFKFGSGNVDVYGPDLVAKDVIV VTMNYRLDVLGFLALGTKEVPGNAGMKDQVVALRWVNENIENFGGDSRNITLFGESAGATAVAYHLVSPISKGMFQ RAILQSGATSLDCFI PYKPRERAFVLGNSLNI TTKNSTELL LSLQELPAVELLNRTAYLFASESITHIQKF TPTPT PVIEEDFGQDMRFVSEDPFDSL DNGNVNDVDMF SYNKHETLIMLPFYVNDNFRIYQRYNRYPELLVPSKILIKAN TDDIYYLWNKINDFYFGDKSISVENMPEFIKYSSFASVVYDVHRRFIRRWPSVGNVYLFKFESYSSRSYYGLQGASY GIGPAHFDDL FYVFDPKIMQFSLP INSTEYKVMVQM TTI FTNFAKYG NPTPDKSLGVFWPQYNRSRQAYAIADN ITIGYKPKADKIKFWKEVLEYAHIKF	5 5 8

	SlitCXE86	MGDADCLPSGDPSARLPILHWISCEYVEVEVAQQQLRGELLDVTVTGEAKYYSFKGIPYAKPPVGDRLRFKDPQPPEP WDGVRNATQHGSVCPQIDLLNSIVVPGSEDCFLFNVTYTNLTENPLPVMVF IHGGGFKFGSGNVVDVYGPDLVPAK DVIIVTMNYRLDVLGFLALGTKEVPGNAGMKDQVLALRWVNENIESFGGDKQNIITLFGSAGASAVGYHLVSPMSK NLFQKAILQSGVPSMDPHIPYRTVERAFVLGNSLNIITKNSTELLSSLQELPAVELLNRTAFLFASESITHIVFKF TPFTPIIEEDYQGEMIFVSEDPFDTLDSGNVSNVDIMFSYNKYEMLIMLPYVNNTRYIQRYNRYPELLVPSKIL MKASDDIYYLWNKINDFYFGNKSISVENMPEFIQYAGFASLVYDVHRFIRRWVQGVNVYLFKFECISSRNFYGLP GAAYGLNGPSHFDDLFFYVFPDKSLQFPLPTDSKEYKLVQQIATVFTNFACYGNPTPDSLTVGSWVPQYDKSKQAYAI IADNITIDYKPDADIKFWRKVLEYAHIKF	5 6 2
	SlitCXE42	MQWQTCVLLLCVTTAILADDEWREVKTAQGPVVRGRKHPTEDIYTFYNI PYATAPVGVDFKFKAPLPPPVWLESYEAVD EQVICPQPALPFQDLEIKNELPLVKQENCLIANIYVPNTNKKNSLVVYVHGGGFVTGWGELFKATQLLKKKDIIV VTFNRYRLGVHGFLCLGTEDAPGNAGMKDQVALLRWVQKNIASFGGNPDDVTIIGYSAGSASVDLLMLSESTGLFH RVIPESGGNLAAFSIQRDPVEIAKTFARQLNFTNVDDIYALGEFYKTAPLELLTSDPFDRTDSTLMFSPCVERNM GEETFLTESPLTILKNGKYKKLPMLYGFANMEGLFRVNFPLWKQKMNDKFSDFLPADLRFSEEEEREDVANKVKR FYFGDEPVSEVNIVEYVNFDTVMFAHSMWLATKLQVEAGNNQIYLYEYSFVDKDVPEVPHTNIRGATHCAQSMAI LDGKNLTHTSHTDESATPEFQMKKTMREIWNFIKTGKVPVEGSSLPAPWPAARANRSPYMSLDQKIELRGVLL ERTRFWEIDIYQKHYLEPVPPPTPPPKPRSEL	5 6 3
	SlitCXE46	MWKILLLSVVTLGYCDDGEWKQVRTAQGEVVRGRKDPAGGLYAFNLIPYAKVPVGTDRFKAPLPAPIWLEPLDAID RGIIICMQPPSPFLDTSKVMQEDCLITNVYVPDTPDDKNLPVIVYIHGGAFFIIGFGNMMTPKHLVKNKKVIVVNFNY RLGVHGLCLGTEDAPGNAGLKDQVALLRWVNKNIASFGGNPDDVTIAGYSAGSVSDLLMLSKAGLFTNKVILE SGVSVGFIAIQRNPIENAKTYAKMLNFTNVNDFYLMQEFYKSAPMKSMFMTFLGRKDSVTFLFSPCIERRRQNAF LDESPYNI I KSGKYNKIPLMIGISNMEGSLQMHHVGIWKDSMNTKFSDFLPVDIKFQSNDRDIVSNKIKEFYFGG QPVGEEITILAYLDYFGDIMFGYSTLRVAVKLHLEAGHKQIYLYEFSFVDDSPVPIPNTNERRAQHCAQTMVLEGPV DGKTLSEERYNLKSVIREMWSNFAIHGTPVTEDSSLPWTTPTSAGGSPYMSGKAVEIKESFLGEHGKFWNKIYEK YYSAPVAVAPPPSQAYHNEL	5 5 2
	SlitCXE49	MWKLVLVLLFCCLAIVLGDDSRVSTAQGPVVRGRLLPGGGVYGFYNI PYASAPTADRYKAPLPPTWVTIFEAEDR KIICPHRRSGDPMNAREDCLVVNVFVPTDNTNLPVHI FVHDGAYQFGFGLQKTFTELVRQNIISVSFNRYRLGVH GFLCLGTGEGAPGNAGLKDMVALLRWVNTNIASFNGNPDDVTLSLSSAGSGSLDFTLVSSLTDLGLFKKVIQESGTVI GAVGAQVDP IQNARNYATVLFNDVNDFNSLEEFYKNVTIEQLISRTDAILNNEGVTARFGPCVERDLGQEIFS SPMNLSSRGNYTKVPRMYGFTTMDGSVRLSIFDTWREMMNEKFSDFLPSELHFDSEEVKEQVAKVKQFYFGDSPV DDHNIIVSYLNYNTDVLFAFPMLRTLSTRVGALGDP IYLFYFSFIDENSVPVLPQTDENGARHCSQERIVADGDTVAA TNEYKRMQEIMRDYWMNFI SNGYPSSSDPSLPTWTPANAQRSPHMSLGRQIVLRDSSPIPERAAFWDELDFEYFRG PIVMDPVPTPTTPAPGAASSLVMSNIIFVSLLLSFYFTLYLN	5 7 5
	SlitCXE50	MWKCVLVLFVCSILILVQGGQDDWLQVNITQGPVVRGRKDPNGGLYVFYNI PYATAPTGRDRFKAPLPPPVWMSPLDAV NRNIRCPQPNVLEHTQEDCLVVNLVFPDTPDTNLPVLVVFVHGGAFQNGHGLSDQYRELVRTRNLIAVSFNRYRIGVH GFLCLGTGEGAPGNAGIKDQVALLHWVNTNIAKFGGNPQDVTLAACSAGSGAVDVLTLSSATTGLFQKAILSEGSST GAVGVIDPIQNAKNYAKVLNFNDVDDLSLEEFYRNAPFQLLTSRVDIEVDNKDTAVRFAPCVERDIGQERVITD APMNVIKRGNYTKVPLLYGFTNMEGAMRLPYFDDWKVQMNEKFSDFLPAELHFDNDEEKEKVAHRVKQFYFGDS SDTMEQFLLYFTDVLFAYPMLKSLARVEALGDTIYLFYFSFVDEDTPSFPHTNVRGAAHCFQSRRAVRDQDLTGR TDAYRRMVQIAREYTLNFI LTGSPSTSDARFPLWRPANAQRSPHMSIGPVIELKDDILGDRAAFWDSIYEEHYRGP LVDPGYTGAASSIMISKIILMAVTVGMLNW	5 6 3
	SlitCXE40	MQISKIDGNNNKNTLMKASLLFGHANEVCEAEGIMQYRSKVASVFGEPRVDPLVLISSQGLVMGHRATDGDYSM FLGVPYARVDAADPFGPSREIQPFEBIIFNANDGTVRCPQLGESSIDCLRLNIYVPFKASSNPLPVLVWIHGGNF VRGSAGDYGVRLVRHDVVVTVNRYRLGPYGFMCCLDTPRVPGNQGLKDQYTALNWRINSIASFGGNPNYNTISGH AGATSVLLHMYADNLKLFNKVIESGTPSEGFMVNSDENMAIKIAEHLGVNTTDGNEALEFLINSPHNLVAGAAH ELNLPLGPCKEKSFSGIEFNVENDPYALTNAKVRNTPVILIGYTSRERDSLSADYFSDSPFYEKLKNNFNLNQQL ENAAATFVRRFYIGDNPVTSVSTQLQNFESDFVINHPSERIITRLDENVGSVYEYLFYSYTGSTNDGAGHSELNY LFNDGSGNIVRSEDDQLIADRISTLWTNFVKYGDPTPQTSDLLPVKWPTVTISSRPTMVIDTDIRMDSRVENQRMA FWDLFYSVYGSYSNLARECSFTDCC	5 5 7
	SlitCXE41	MTSLGRISVALLVLFHHTQCLPRVDPLVDTKVGLIRGLRADDGNYSKFLGIPYAQVNPDPNPFGEESTPQPKFEETFE AYDESAVCPQWYWWTGEIDGNPDCLQLNVYVPDTANSNNRPLPVMVWIYGGAFERGEFSQKLYGPTYLVKHDMVMA INRYRVGPYGFMCCLDTPETIAGNQGLKDQHLGLQWVKDNI EAFGGDANQITLFGLSAGGHSIDLHLLSQRREVIY NQKVIQSGSSLAATVLYEPDKLAHIKLAQLHGFETDTTNEAISFLAKSDSNLVIAATLDLGIIFKPCVENSFEVGEPLN SSWIHAGTPKVRNMPVLTGYNEHGLASFHNKDEEYFKNLNIISDYMKRI FNFGEELQEMSDSIAHFYIGDEAIS SDVKLALIMDSDFTYIHPIQRSIQYLEARNRVYVFSYLGGRNAILDNGGVEDNSSNVCCAAHADELPLYL MVNKPPTTEHDEIVIERMTTMTWNTFAKYGDPTPQTSDLLPVKWEPLTKESFTYMDIGSELSLGRPPAHD RMAYWDLFYKLNQDKHK	5 4 3
	SlitCXE69	MWIVGLLVLLCGLVQGLYRVDPLVSTNKGLIRGLRSNEGQAQFLGVPAVVDKNNPFGPSVPHPGFDDIYEAYESN VCPQVSSDEAIGTIDCLTMNIYVPSAATTQNRPLPVMVWIHGGAFVTGSAQTEGNPNFLLRNDVIVVAINRYRLGAYG FMCLDIPVPGNQGLKDQVLALRWINENIEAFGGDVSTQITVFGESAGGMSVNLHLLSSYERLFQKAI IQSGPASSP WLIVESDKTIPIKLANFLDFETEDTLEALEYLASVDVHTLIKVAHDLKITDSTGTKNPGTLPCIEKEIDGESFIT NHPMNINTPKVRNTPVII GHTNNELPFQYGLADSDFFANYDFSLLSNAFDLEDDWEDAVNDVRHFIYIGDEAANKNV ADKITDFASDFVFNHPTQRMADRILDIGGRTVYRYVFSYSGNRNLLKVLFNLNATGAIHADDELGYLFDNVELFGEQ VTPQDQLMIDRLTTLWTNFAKYGDPTPATSDLLPVKWQPI TKTSQPYLNLSDSLTLGARPPHDMAFWDLFYKLYG NQQYKGLSGK	5 4 2
	SlitCXE100	MWSVILLISFCGLVQGLSRVDPLVSTKSGLIRGLLTDSGYAQFLGVPAEVNKSNNPFGPANPHPGFNDIYEAYKSN VCPQVSYNVTVGTIDCLTLNIYVPSAATSKNRLPVMVWIHGGYFIVGSGDAVRIPDYLLRNDVIVVTINRYRLGAYG FMCLDIPVSGNQGLKDQVLALRWINDNIDAFGGDVSTQITVFGESAGGMSVNLHLLSSYEPFLQKAI IQSGPAVSP WVMKGTDNVPIKLAELNFPDSDVSEAI AFLSTIEVHTLIRLAHDLKLTFFMSLEDSPTVPCVEKKMEGVEHFL TEYMTIES TKLKNVPVILGVTSNLEFMGYTADDEFFRNFDFTVLNTAIDLGEKFDVAEDIRHFIYIGDEDTSEK VKDEITNFASDVLFNHPTERMAKRLLELGAKSVMYVFSYSGGRNVIKIRLNLNGTGAVHADELGYLFDSELTGD IAPEDQLMIDRITTTMTWNTFAKYGDPTPSTSGLLPIKWEPI TRTTHPYLNLSDLSLESRPFHSRMAFWDLFYKVYV N	5 3 3
C   a d e 0 0 1	SlitAchE1	MRVLAALATALAARALAGPHEHRRARHHAPEHPPHPAPAPPQPYRGHGEAVRYNPELDITLPRLEDHETSSKRAK EDAETSSKRAKYDERFYSNHERADEEPMADEPQLGPEDDDDPLVVRTRKGRVRGITLTAATGKKVDANWFGIPYAQK VGDRLFRHPRPAESWGDEIILNTTTLPHSCVQI IDTVFGDFPGAMWNPNTDMQEDCLFINI VTPRPRPKNAAVMLW VFGGGFYSGTATLDVYDAKILVSEEKVVVYSMQYRVASLGFLFFDTPDPVGNAGLFDQLMALQWVKDNIAYFGGNP	6 9 5

a d e 0 2 7		HNITLFGESAGAVSVSLHLLSPLSRNLFSSQAIMQSGAATAPWAIISREESILRGIRLAEAVHCPHSRTDMGPMIEC LRKKSPDELVNNEWGTLGICEFPFVPIIDGSFLDELPARSLAHQNFKKTNLLMGSNTEEGYFIFYLTELFPKEE NVGISREQYLQAVRELNPHYVNDVGRQAI VFEYTDWLNPDPIRNRNALDKMVG DYHFTCGV NEMAHRYAETGNNVF TYYYKHRSKNNPWPSWTGVMHADEINYVFG EPLNPGKNYSPEEVEFSKRLMRYWANFARTGNPSINPNGESTKIYW PVHSATGREYLSLAVNSSTVGHGLRVKECAFWQKYL PQLMSATNKPEPPKNCTSSAAPIKVPYEIIIGVGVIATGL AKTTMFKYIV	
	SlitAchE2	MISNTKIVFTKLLCCIVSGAWTRSWANHHD TTTSTQTTPPTSQAPKNFHN DPLIVETKSGLVKGYAKTVMGREV HIFTGIPFAKPPLGPLRFRKPVPIDPWHGVLEATAMPNSCYQERYEYFPGFEGEEMWNPNTNISEDCLYLN I WVPQ HLRVRHHQDKPLTERPKVPILVWIYGGGYMSGTATLDLYKADIMASSSDVIVASMQYRVGAFGFLYLNKYFSPGSE EAPGNMGLWDQQLAIRWIKDNARAFGGDPELITLFGESAGGGSVSLHMLSPEMKGLFKRGILQSGTLNAPWSWMTG ERAQDIGKVLVDDCNCNSSLAADPSLVMDCMRGVDAKTISVQQWNSYTGILGFPSAPTVDGVFLPKDPDTMMKEG HFNHTEVLLGSNQDEGTYFLLYDFLDYFEKDGPSFLQREKFLEIVDTIFKDFSKIKREAIVFQYTDWEEITDGYLN QKMIADVVDYFFVCPTNYFAEVLADSGVEVYYYYFTHRTSTSLWGEWMGMHGDEMEYVFGHPLNMSLQYHTRER DLAAHMQSFTRFALTGKPHKPDEKWPLYSRSSPHYTYTADGTSGPAGPRGPRASACAFWNDFLNKLNELEHMPC DGAVTGPYSSVAGTTLPIVLLTTLATTVAL	6 3 8

**Table S2:** Spodopteran GSTes reconciled nomenclature, with new annotations combined with previous studies.

<b><i>Spodoptera litura</i></b>				
This study	Zhang et al., 2016	Cheng et al., 2017	Genbank GCF_002706865.1	chromosome
<i>SlGSTe1</i>	AAS79891	SWUSI0010470 _SlituGST14	LOC111364724	Chr1
<i>SlGSTe2</i>	ACZ73898	SWUSI0064760 _SlituGST05	LOC111351682	Chr14
<i>SlGSTe3</i>	ACZ738999	SWUSI0064770 _SlituGST08	LOC111351684	Chr14
<i>SlGSTe4</i>	KF482955	SWUSI0064780 _SlituGST07	LOC111351681	Chr14
<i>SlGSTe5</i>	KF482956	SWUSI0091750 _SlituGST24	LOC111355027	Chr20
<i>SlGSTe6</i>	KF482957	SWUSI0010470 _SlituGST15	LOC111347873	Chr1
<i>SlGSTe7</i>	KF482958	SWUSI0108040 _SlituGST10	LOC111357178	Chr24
<i>SlGSTe8</i>	KF482959	SWUSI0040720 _SlituGST23	LOC111349356	Chr9
<i>SlGSTe9</i>	KF482960	SWUSI0040700 _SlituGST17	LOC111349355	Chr9
<i>SlGSTe10</i>	KF482961	SWUSI0040720 _SlituGST22	LOC111349356	Chr9
<i>SlGSTe11</i>	KF482962	SWUSI0005590 _SlituGST38	LOC111364883	Chr1
<i>SlGSTe12</i>	KF482963	SWUSI0038410 _SlituGST12	LOC111348828	Chr8
<i>SlGSTe13</i>	KF482964	SWUSI0038420 _SlituGST13	LOC111348827	Chr8
<i>SlGSTe14</i>	KF482965	SWUSI0040710 _SlituGST18	LOC111349355	Chr9
<i>SlGSTe15</i>	KF482966	SWUSI0038400 _SlituGST11	LOC111348844	Chr8
<i>SlGSTe16</i>		SWUSI0040730 _SlituGST16	LOC111349158	Chr9
<i>SlGSTe17</i>		SWUSI0064750 _SlituGST06	LOC111351683	Chr14
<i>SlGSTe18</i>		SWUSI0005600 _SlituGST25	LOC111364904	Chr1
<i>SlGSTe19</i>		SWUSI0040750 _SlituGST21	LOC111349160	Chr9
<i>SlGSTe20</i>		SWUSI0040740 _SlituGST20	LOC111349159	Chr9
<b><i>Spodoptera frugiperda corn strain</i></b>				

This study	V6 genome assembly (Gimenez et al., 2020)	chromosome
SfCGSTe1	SFRUCORN610000010054	Scaffold_107
SfCGSTe2	SFRUCORN610000007603	Scaffold_116
SfCGSTe3	SFRUCORN610000007603	Scaffold_116
SfCGSTe4	SFRUCORN610000007603	Scaffold_116
SfCGSTe5	SFRUCORN610000003468	Scaffold_118
SfCGSTe6	SFRUCORN610000010054	Scaffold_107
SfCGSTe7	SFRUCORN610000012733	Scaffold_114
SfCGSTe8	SFRUCORN610000013771	Scaffold_47
SfCGSTe9	SFRUCORN610000013772	Scaffold_47
SfCGSTe10	SFRUCORN610000013771	Scaffold_47
SfCGSTe11	SFRUCORN610000018645	Scaffold_107
SfCGSTe12	SFRUCORN610000029704	Scaffold_93
SfCGSTe14	SFRUCORN610000013772	Scaffold_47
SfCGSTe15	SFRUCORN610000029703	Scaffold_93
SfCGSTe16	SFRUCORN610000013771	Scaffold_47
SfCGSTe17	SFRUCORN610000007603	Scaffold_116
SfCGSTe18	SFRUCORN610000018646	Scaffold_107
SfCGSTe20	SFRUCORN610000013771	Scaffold_47
SfCGSTe21	SFRUCORN610000013771	Scaffold_47
<b><i>Spodoptera frugiperda</i> rice strain</b>		
This study	latest V3 genome assembly (Gouin et al., 2017)	chromosome
SfRGSTe1	SFRURICE00000011418	Contig162
SfRGSTe2	SFRURICE00000005971	Contig39
SfRGSTe3	SFRURICE00000005971	Contig39
SfRGSTe4	SFRURICE00000005971	Contig39
SfRGSTe5	SFRURICE00000026315	Contig2
SfRGSTe6	SFRURICE00000011418	Contig162
SfRGSTe8	SFRURICE00000030251	Contig524
SfRGSTe9-1	SFRURICE00000030253	Contig524
SfRGSTe9-2	SFRURICE00000026789	Contig830
SfRGSTe10-1	SFRURICE00000030251	Contig524
SfRGSTe10-2	SFRURICE00000030251	Contig524
SfRGSTe11	SFRURICE00000014441	Contig697
SfRGSTe12	SFRURICE00000003921	Contig401
SfRGSTe13	SFRURICE00000003921	Contig401
SfRGSTe14	SFRURICE00000026789	Contig830
SfRGSTe15	SFRURICE00000003920	Contig401
SfRGSTe16	SFRURICE00000030251	Contig524
SfRGSTe17	SFRURICE00000005973	Contig39
SfRGSTe18	SFRURICE00000014439	Contig697
SfRGSTe20	SFRURICE00000030251	Contig524
SfRGSTe21	SFRURICE00000030251	Contig524

## Sequence retrieval

*Spodoptera* coding sequences for detoxification genes were retrieved from the latest genomic datasets: for *Spodoptera litura* datasets (Cheng et al., 2017) were combined to the chromosome-level assembly from NCBI (Genbank: GCF\_002706865.1); sequences for *Spodoptera frugiperda* Corn strain were from the latest V6 genome assembly (Gimenez et al., 2020) and from Gouin et al., 2017 for the Rice strain (V3); sequences for *Spodoptera exigua* were from the chromosome-level genome sequences from NCBI (GenBank: GCA\_011316535.1). Given the absence of genome assembly for *Spodoptera littoralis* candidate detoxification cDNAs were identified from a de novo transcriptome (Poivet et al., 2013). Reciprocal tBLASTn and exonerate (Slater et al., 2005) searches were performed against the different datasets to generate complete repertoires for all detoxification gene families.

## Multiple sequence alignments and phylogenetic analysis

Amino acid sequences were aligned using MAFFT (using L-INS-i option) (Katoh and Standley, 2013) implemented in the Geneious software (<http://www.geneious.com>, Kearse et al., 2012). Phylogenetic trees were constructed using PhyML (Guindon et al., 2010) based on the best substitution model as determined by the SMS server (Lefort et al., 2017), using Nearest Neighbor Interchange (NNI). Branch supports were estimated by a Bayesian-like transformation of aLRT (aBayes) (Anisimova et al., 2011). A dendrogram was then created, annotated and colored using FigTree software (<http://tree.bio.ed.ac.uk/software/figtree/>).

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