

RNAi APPROACH FOR CROP PEST PROTECTION

BACKGROUND

[0001] Insect pests are detrimental to crop production and human health throughout the world and insect control can in some instances consume between 10-25% of a country's gross national product (GNP). ([http World Wide Web internet site "fao.org/3/a-av013e.pdf"](http://www.fao.org/3/a-av013e.pdf)). In the U.S., annual loss due to crop pests is estimated to exceed \$120 billion USD/year. (Polaszek A. (1998) Wallingford, UK: CABI. 530 pp.).

[0002] Within crop pests, Lepidoptera are the most detrimental insect pests of cereal crop cultivation. Chemical control is often expensive, inefficient, and can be associated with negative environmental consequences. Host plant resistance is an attractive option but impeded by lack of robust Lepidoptera resistant germplasm ([http World Wide Web internet site "cnn.com/2015/05/08/insects-feast-on-plants-endangering-crops-and-costing-billions.html"](http://www.cnn.com/2015/05/08/insects-feast-on-plants-endangering-crops-and-costing-billions.html)).

[0003] Since 1996, commercialization of crop plants genetically engineered to produce *Bacillus thuringiensis* (*Bt*) insecticidal proteins have resulted in efficient pest control, increased yield, reduced insecticidal use, and enhanced farmer profits. (Khan ZR, et al. (2014). *Philos. Trans. R Soc. Lond Biol Sci.* 369: 1639).

[0004] Consequently, the cumulative area planted with *Bt* crops worldwide reached greater than 1 billion acres during 2011. Within the U.S., *Bt* Corn, *Bt* Soybean, and *Bt* Cotton accounted for 90% of all the total corn, soybean and cotton acres during 2013 (Tabashnik BE, et al. (2013). *Nat. Biotech.* 31: 510–521). However, evolution of field resistance against *Bt* in lepidopteran pests raises potential concerns about the sustainability of this approach. (Campagne P., et al. (2013) *PLoS ONE* 8(7): e69675. Doi:10.1371). That is further exacerbated by loss of resistance against pyramided *Bt* traits as well ([https World Wide Web internet site dt npf.com/agriculture/web/ag/news/article/2016/08/10/rootworm-resistance-pyramided-bt.html](https://www.npr.org/2016/08/10/388111100/rootworm-resistance-pyramided-bt)).

SUMMARY

[0005] Provided herein is an isolated double stranded RNA (dsRNA) molecule comprising a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of a target gene sequence—wherein the target gene is a MIGGS-IRTG as defined herein—involved in gut microbe clearance and/or containment induced by microbes ingested during feeding and/or

active feeding. In certain aspects, the target gene is critical for insect immune responses and certain aspects provide that it is abundantly expressed in the midgut. In certain aspects, the target gene sequence includes at least one of the protein coding region, the 5' UTR region, the 3' UTR region, and any combination thereof, of a target gene. Further, certain aspects provide that the dsRNA molecule silences the target gene when ingested by an insect. In certain aspects, the target gene is a type 1 MIGGS RNAi target or a type 2 MIGGS RNAi target as defined elsewhere herein. In certain aspects, the target gene is a pattern recognition receptor (PRR) class gene or an insect midgut structural component gene. In certain aspects, the target gene is expressed abundantly in a midgut specific manner during active feeding.

10 **[0006]** In certain aspects, a dsRNA molecule disclosed anywhere herein comprises two annealed complementary RNA strands. In certain aspects, said dsRNA molecule comprises a single RNA strand comprising an inversely repeated sequence with a spacer in between, wherein the single RNA strand can anneal to itself to form a hairpin loop structure.

[0007] In certain aspects, a dsRNA molecule disclosed anywhere herein comprises a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of the protein coding region of the target gene sequence. In certain aspects, said dsRNA molecule comprises a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of the 5' UTR region or the 3' UTR region of the target gene sequence. In certain aspects, said dsRNA molecule comprises a nucleic acid sequence complementary to a contiguous region comprising at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% of the length of the target gene sequence protein coding region, 5' UTR region, or 3' UTR region. In certain aspects, said dsRNA molecule comprises a nucleic acid sequence complementary to about 200 to 650 contiguous nucleotides of a target gene sequence.

[0008] Certain aspects of this disclosure are drawn to a target gene selected from the group consisting of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-Beta-1, 3-glycan-recognition protein 2 (Ms β GRP2), *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsRelF),

M. sexta-Cdc42 (MsCdc42), *M. sexta*-Dsor1 (MsDsor1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13 (MsAtg13), *M. sexta*-IAP1 (MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*-**Beta-1 tubulin (MsβTub)**, *M. sexta*-Beta fructofuranosidase 1 (MsSuc1), and orthologs thereof. In certain aspects, the target

5 gene is selected from the group consisting of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-**Beta-1, 3-glycan-recognition protein 2 (MsβGRP2)**, *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M.*

10 *sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsReIF), *M. sexta*-Cdc42 (MsCdc42), *M. sexta*-Dsor1 (MsDsor1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13

15 (MsAtg13), *M. sexta*-IAP1 (MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*-**Beta-1 tubulin (MsβTub)** and *M. sexta*-Beta fructofuranosidase 1 (MsSuc1).

[0009] Also provided herein is an isolated double stranded RNA (dsRNA) molecule comprising a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of a target gene sequence, wherein the target gene comprises a nucleic acid sequence selected

20 from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110. In certain aspects, the target gene sequence includes at least one of the protein coding region, the 5' UTR region, the 3' UTR region, and any combination thereof, of a target gene. Further, certain aspects provide that the dsRNA molecule silences the target gene when ingested by an insect.

25 **[0010]** In certain aspects disclosed herein, the target gene is sequence selected from the group consisting of: i) SEQ ID NOs: 1-9, 11, 14, 31, 39, 43, 44, and 71-75.

[0011] In certain aspects disclosed herein, the target gene is sequence selected from the group consisting of: ii) SEQ ID NOs: 3, 4, and 43. In certain aspects, the dsRNA molecule causes impeded growth, developmental progression, and/or mortality and the like of TH, DMB, and

30 FAW in an orthologous manner.

[0012] In certain aspects disclosed herein, the target gene is sequence selected from the group consisting of: iii) SEQ ID NOs: 76, 77, 80, 81, 85, 87, and 88. In certain aspects, the

dsRNA molecule causes impeded growth, developmental progression, and/or mortality and the like of DBM. Further, in certain aspects, the DBM is a Bt resistant strain.

[0013] In certain aspects disclosed herein, the target gene is sequence selected from the group consisting of: iv) SEQ ID NOs: 89, 92, 96, 101, 103, and 105. In certain aspects, the dsRNA molecule causes impeded growth, developmental progression, and/or mortality and the like of FAW.

[0014] In certain aspects disclosed herein, the target gene is sequence selected from the group consisting of: v) SEQ ID NOs: 107-110. In certain aspects, the dsRNA molecule caused impeded growth, developmental progression, and/or mortality and the like of RFB.

10 **[0015]** In certain aspects of the dsRNA molecule disclosed above, the dsRNA molecule comprises two annealed complementary RNA stands. In certain aspects, the dsRNA molecule comprises a single RNA strand comprising an inversely repeated sequence with a spacer in between and where the single RNA strand can anneal to itself to form a hairpin loop structure.

[0016] In certain of the dsRNA molecule disclosed above, the dsRNA molecule comprises a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of the protein coding region of the target gene sequence. In certain aspects, the dsRNA molecule comprises a nucleic acid sequence complementary to a contiguous region comprising at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% of the length of a sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110. In certain aspects, the dsRNA molecule comprises a nucleic acid sequence complementary to a contiguous region comprising at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% of the length of the target gene sequence protein coding region, 5' UTR region, or 3' UTR region.

[0017] In certain aspects disclosed herein the dsRNA molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 111-119, 120-126, 127-135, and 136-139. In certain aspects, the dsRNA is a fragment of at least about 200 nucleotides thereof. In certain aspects, i) the isolated dsRNA molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 110-119, or the fragment thereof, causes impeded growth, developmental progression, and/or mortality and the like of TH; ii) the isolated dsRNA molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 120-126, or the fragment thereof, causes impeded growth, developmental progression, and/or mortality and the like of DBM; iii) the isolated dsRNA molecule comprising a nucleic acid sequence selected

from the group consisting of SEQ ID NOs: 127-135, or the fragment thereof, causes impeded growth, developmental progression, and/or mortality and the like of FAW; or iv) the isolated dsRNA molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 136-139, or the fragment thereof, causes impeded growth, developmental progression, and/or mortality and the like of RFB.

[0018] In certain of any of the above aspects, the dsRNA molecule can form siRNA. Certain aspects provide for an isolated siRNA molecule derived from the processing of said dsRNA molecule.

[0019] Certain further aspects provide of an insecticidal composition comprising an isolated dsRNA molecule or an siRNA molecule disclosed anywhere herein, and a synthetic carrier or microbial conduit. In certain aspects, a microorganism has a natural capacity or is engineered to produce and/ or deliver dsRNA to increase its bioavailability and/or biostability for causing RNA interference including but not restricted to plant growth promoting organisms, normal commensal and/or symbiotic microorganisms associated with the target insect pest or parasites and/or natural enemies of the target pest or pest target host or host cultivation range etc. from an insect or parasite and/or natural enemies of the target pest engineered or identified from natural populations containing microbial conduit to produce and/or deliver dsRNA and/or drive the transmission of such microbial conduits into natural populations of insect pests as a control option. In certain aspects of an insecticidal composition disclosed herein, the dsRNA molecule is conjugated with the synthetic carrier.

[0020] Certain aspects are also drawn to a recombinant DNA construct encoding a dsRNA molecule disclose anywhere herein. In certain aspects, the recombinant DNA construct comprising a gene silencing sequence comprising about 200 to 1000 contiguous nucleotides of a target gene sequence. In certain aspects, the target gene is a MIGGS-IRTG, as defined herein, involved in gut microbe clearance and/or containment induced by microbes ingested during feeding and/or active feeding. In certain aspects, the target gene is critical for insect immune responses. In certain aspects, the target gene is abundantly expressed in the midgut. In certain aspects, said target gene sequence includes at least one of the protein coding region, the 5' UTR region, the 3' UTR region, and any combination thereof, of a target gene. In certain aspects, the target gene is a type I MIGGS RNAi target or a type 2 MIGGS RNAi target as described elsewhere herein. In certain aspects, the target gene is a pattern recognition receptor (PRR) class

gene or an insect midgut structural component gene. In certain aspects, the target gene is expressed abundantly in a midgut specific manner during active feeding.

[0021] In any of the above aspects of a recombinant DNA construct, the gene silencing sequence comprises about 200 to 1000 contiguous nucleotides of the protein coding region of the target gene sequence. In certain aspects, the gene silencing sequence comprises about 200 to 1000 contiguous nucleotides of the 5' UTR region or the 3' UTR region of the target gene sequence. In certain aspects, the gene silencing sequence comprises at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% contiguously of the length of target gene sequence protein coding region, 5' UTR region, or 3' UTR region. In certain aspects, the gene silencing sequence comprises about 200 to 650 contiguous nucleotides of the target gene sequence.

[0022] In any of the above aspects of a recombinant DNA construct, and as noted throughout this disclosure, in certain aspects, a target gene can be selected from the group consisting of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-Beta-1, 3-glycan-recognition protein 2 (MsβGRP2), *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsRelF), *M. sexta*-Cdc42 (MsCdc42), *M. sexta*-Dsr1 (MsDsr1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13 (MsAtg13), *M. sexta*-IAP1 (MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*-Beta-1 tubulin (MsβTub), *M. sexta*-Beta fructofuranosidase 1 (MsSuc1), and orthologs thereof. In certain aspects a target gene can be selected from the group consisting of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-Beta-1, 3-glycan-recognition protein 2 (MsβGRP2), *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish

F (MsReIF), *M. sexta*-Cdc42 (MsCdc42), *M. sexta*-Dsor1 (MsDsor1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13 (MsAtg13), *M. sexta*-IAP1 (MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*-Beta-1 tubulin (Ms β Tub) and *M. sexta*-Beta fructofuranosidase 1 (MsSuc1).

5 **[0023]** Further aspects provide for a recombinant DNA construct comprising a gene silencing sequence comprising about 200 to 1000 contiguous nucleotides of a target gene sequence, wherein the target gene comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110. In certain aspects, the target gene sequence includes at least one of the protein coding region, the 5' UTR
10 region, the 3' UTR region, and any combination thereof, of a target gene.

[0024] In any of the above aspects of a recombinant DNA construct, the target gene sequence is selected from the group consisting of: i) SEQ ID NOs: 1-9, 11, 14, 31, 39, 43, 44, and 71-75; ii) SEQ ID NOs: 3, 4, and 43; iii) SEQ ID NOs: 76, 77, 80, 81, 85, 87, and 88; iv) SEQ ID NOs: 89, 92, 96, 101, 103, and 105; and v) SEQ ID NOs: 107-109, and 110. In certain
15 aspects, the gene silencing sequence comprises about 200 to 1000 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110. In certain aspects, the gene silencing sequence comprises at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% contiguously of a sequence selected from the group consisting of SEQ ID Nos: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110. In
20 certain aspects, the gene silencing sequence comprises about 200 to 650 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110. In certain aspects, the gene silencing sequence is operably linked to one or more promoters for the expression of a dsRNA molecule that silences the target gene when ingested by an insect. In certain aspects, the construct is an expression vector. And, in certain
25 aspects, the expression vector can target single or multiple insect RNAi target genes or chimeric RNAi target genes.

[0025] Certain aspects of the disclosure also provide for a host cell comprising the dsRNA molecule, the siRNA molecule, a polynucleotide encoding a dsRNA molecule, and/or the construct or a dsRNA encoding segment thereof disclosed anywhere herein. In certain aspects, the
30 host cell is a bacterial or plant cell or organelle. In certain aspects, the organelle is a plastid. In certain aspects, the host cell is a transgenic and/or transplastomic plant cell. In certain aspects, the host cell expresses a dsRNA and/or produces an siRNA disclosed anywhere herein.

[0026] Certain aspects also provide for a transgenic and/or transplastomic plant comprising a dsRNA molecule, an siRNA molecule, a polynucleotide encoding the dsRNA, and/or a construct or a dsRNA encoding segment disclosed anywhere herein. In certain aspects, at least one cell of the plant expresses the dsRNA molecule and/or produces the siRNA molecule.

5 Further, certain aspects provide for a seed, part, tissue, cell, or organelle of the above transgenic and/or transplastomic plant. In certain aspects, the seed, part, tissue, cell, or organelle comprises the dsRNA molecule and/or the siRNA molecule. In certain aspects, the organelle is a plastid.

[0027] Certain aspects provide for a method of silencing: (i) an insect immune response gene and/or (ii) an insect gene encoding for structural components of the insect midgut. In certain aspects, the method comprises providing for ingesting an isolated dsRNA molecule, an siRNA molecule, an insecticidal composition, a host cell, a transgenic and/or transplastomic plant, transplastomic plant and/or a seed, part, tissue, cell, or organelle as disclosed anywhere herein, to an insect.

[0028] Certain aspects provide for a method of protecting a plant from an insect pest of the plant. In certain aspects, the method comprises topically applying to a plant an isolated dsRNA molecule, an siRNA molecule, and/or an insecticidal composition disclosed anywhere herein, and providing the plant in the diet of the insect pest. In certain aspects, the dsRNA is topically applied by expressing the dsRNA in a microbe and topically applying the microbe onto the plant.

20 **[0029]** Certain aspects provide for a method of producing a plant resistance to a pest insect of said plant. In certain aspects, the method comprises transforming a plant with a polynucleotide encoding the dsRNA molecule and/or a construct or a dsRNA encoding segment thereof as disclosed anywhere herein, wherein the plant expresses a dsRNA molecule and/or produces an siRNA molecule as disclosed anywhere herein.

25 **[0030]** Certain aspects provide for a method of improving crop yield. In certain aspects, the method comprises growing a population of crop plants transformed with a polynucleotide encoding a dsRNA molecule and/or a construct or a dsRNA encoding segment thereof wherein the plant expresses a dsRNA molecule and/or produces an siRNA molecule as disclosed anywhere herein. In certain aspects, the population of transformed plants produces higher yields in the presence of pest insect infestation than a control population of untransformed plants.

30 **[0031]** Certain aspects provide for a method for producing a plant resistant against a pest insect of said plant. In certain aspects, the method comprises: a) transforming a plant cell and/or

organelle with a polynucleotide encoding a dsRNA molecule and/or a construct or a dsRNA encoding segment thereof as disclosed anywhere herein; b) regenerating a plant from the transformed plant cell and/or organelle; and c) growing the transformed plant under conditions suitable for the expression of said double stranded RNA molecule, wherein said transformed plant of (c) is resistant to the plant pest insect compared to an untransformed plant.

[0032] In certain of any of the aforementioned aspects, the method the dsRNA is ingested by an actively feeding stage of the insect. In certain aspects, the ingestion of the dsRNA induces a melanotic response in the insect larvae. In certain aspects, the ingestion of the dsRNA results in perturbation of gut microbial homeostasis. In certain aspects, the ingestion of the dsRNA results in defective clearance of opportunistic microbes. In certain aspects, the ingestion of the dsRNA results in defective containment of gut microbes.

[0033] In certain of any of the aforementioned aspects, the silencing of the target gene results in reduced appetite and/or developmental defects resulting in incomplete development and/or mortality and/or decrease the reproductive success of the insect. In certain aspects, the reduced appetite and/or developmental defects and/or mortality and/or reduced reproductive fitness of the insect is observed after sustained feeding for at least 72 hours.

[0034] In certain of any of the aforementioned aspects, the insect is of the order Lepidoptera, Coleoptera, Hemiptera, Blattodea, or Diptera. In certain aspects, the insect is *Manduca sexta* (*M. sexta*) (tobacco hornworm), *Spodoptera frugiperda* (fall armyworm), *Ostrinia nubilalis* (European corn borer), *Plutella xylostella* (Diamondback moth), *Leptinotarsa decemlineata* Say (Colorado potato beetle), *Diabrotica spp.* (Corn rootworm complex), *Tribolium castaneum* (Red flour beetle), *Popillia japonica* (Japanese beetle), *Agrilus planipennis* (Emerald ash borer), *Diaphorina citri* (Asian citrus psyllid), *Cimex lectularius* (Bed bug), a cockroach or termite, or insect pests such as mosquitoes and flies.

[0035] In certain of any of the aforementioned aspects, the plant host is selected from the group consisting of *Zea mays L* (corn), *Sorghum bicolor* (sorghum), *Setaria italica* (fox tail millet), *Pennisetum glaucum* (Pearl millet), *Solanum tuberosum* (potato), *Oryza sativa* (rice), *Lycopersicon esculentum* (tomato), *Solanum melongena* (eggplant), cultivars of the *Brassica oleracea* family, *Citrus sinensis* (Orange), trees of the *Oleaceae* family, and crops of *Rosaceae*.

BRIEF DESCRIPTION OF THE DRAWINGS

[0036] Figure 1. Figure 1 shows schematic representation of bacterially ingestible dsRNA assay. (Kamath RS, et al. (2000) *Genome Biol.* 2: 1-10; Newmark et al. (2003) *Proc. Natl. Acad. Sci. USA* 100: 11861–11865).

5 **[0037]** Figure 2A-C. Figure 2A-C shows representative phenotypes of TH larvae. TH larvae exposed to bacterially (HT115 (DE3)) expressed dsRNA against MIGGS RNAi targets MsPGRP2 (A); MsVMP1(B); and negative control dsRNA against Cassava plant specific gene MeCAT1 (C).

10 **[0038]** Figure 3A,B. Figure 3A,B shows feeding activity of TH larvae exposed to dsRNA against negative control MeCAT1 (A) and MIGGS RNAi target MsPGRP2 (B) containing bacterial (HT115 (DE3)) plates.

[0039] Figure 4. Figure 4 shows survival rates of healthy conventionally-reared (CR) and germ-free (GF) first instar TH larvae exposed to bacterially (HT115 (DE3)) expressed dsRNA against MIGGS RNAi targets MsPGRP2; MsVMP1 and negative control dsRNA against
15 Cassava plant specific gene MeCAT1. The differences observed using 4 replicates/treatment were statistically significant across all time points at a P value between $P < 0.001$ to $P < 0.05$.

[0040] Figure 5. Figure 5 shows percentage melanotic reaction of healthy conventionally-reared (CR) and germ-free (GF) first instar TH larvae exposed to bacterially (HT115 (DE3)) expressed dsRNA against MIGGS RNAi targets MsPGRP2; MsVMP1 and
20 negative control dsRNA against Cassava plant specific gene MeCAT1. The differences observed using 4 replicates/treatment were statistically significant across all time points at a P value between $P \leq 0.001$ to $P \leq 0.05$.

[0041] Figure 6. Figure 6 shows schematic representation of dsRNA producing L4440 vector containing coding sequence of Cassava CAT1 (MeCAT1) and TH MIGGS RNAi targets
25 MsPGRP2 and MsVMP1.

[0042] Figure 7. Figure 7 shows midgut-preferred expression of two TH MIGGS RNAi target genes MsHEM and MsSPH3 in comparison to the control gene RPS3. The control cDNA libraries were derived from conventionally reared larvae and treatment cDNA libraries were derived from TH larvae injected with 75 CFU of *E. coli*. The control and treatment larvae were
30 used to isolate hemolymph fraction (HL), dissect midgut (MDG) to obtain rest of the body (RB). The HL, MDG and RB were used for RNA isolation and cDNA synthesis.

[0043] Figure 8. Figure 8 shows schematic representation of oral induction procedure for MIGGS RNAi target genes. The insect larvae were reared on induction media containing live gram-negative bacteria *E. coli* and lyophilized cell wall signatures from gram-positive bacteria and fungi, following a previously published protocol (Wang et al. (2006). *J. Biol. Chem.* 281(14): 9271–9278).

[0044] Figure 9A,B. Figure 9A,B shows expression of MIGGS RNAi target genes in TH larvae in response to feeding on induction media. Genes with immunity function (A,B) are induced (I) between 24-48 hours post larval exposure to induction media and mostly not detected in the absence of induction (UI).

[0045] Figure 9C,D. Figure 9C,D also shows expression of MIGGS RNAi target genes in TH larvae in response to feeding on induction media. Genes with immunity function (C) are induced (I) between 24-48 hours post larval exposure to induction media and mostly not detected in the absence of induction (UI). While, the genes essential for midgut structural integrity (D) are expressed under both conditions.

[0046] Figure 10A-F. Figure 10A-F shows representative phenotypes of TH larvae (initial size shown in A) exposed to bacterially expressed dsRNA against insecticidal MIGGS-RNAi target genes *MsToll2*, *MsSuc1*, and *MsβTub* in comparison to negative (B) and positive (C) control treatment. The insecticidal activity is manifested as stunted growth and development, loss of appetite and melanotic reaction (D-F) in comparison to regular growth and development observed with negative control treatment (B).

[0047] Figure 11. Figure 11 shows percentage mortality of TH larvae feeding on bacterially expressed dsRNA against insecticidal MIGGS RNAi targets *MsToll2*, *MsSuc1*, and *MsβTub*. The insecticidal MIGGS candidates confer statistically significant mortality that is comparable to positive control treatment (*MsVATPaseE*). Data is average of 3-replicates/treatment ± SEM at $p \leq 0.001$ (***).

[0048] Figure 12A-C. Figure 12A-C shows the induction of MIGGS-IRTGS in DBM larvae feeding on induction media. The genes with immunity function (A-B) are induced (I) between 24-48 hours post larval exposure to induction media and mostly not detected in the absence of induction (UI). While, the genes essential for midgut structural integrity (C) are expressed under both conditions.

[0049] Figure 13A-H. Figure 13A-H shows representative phenotypes of Bt resistant DBM larvae (initial size shown in A) exposed to bacterially expressed dsRNA against

insecticidal DBM MIGGS RNAi targets PxPGRP2 (D), PxIMD (E), PxβGRP2 (F), PxCAC (G), and PxCHS1 (H) in comparison to positive (C) and negative control (B) treatment. The insecticidal activity is manifested as stunted growth and development, loss of appetite and melanotic reaction (D-H) in comparison to regular growth and development observed with negative control treatment (B).

[0050] Figure 14. Figure 14 shows percentage mortality of DBM larvae feeding on bacterially expressed dsRNA against insecticidal MIGGS RNAi targets PxPGRP2, PxIMD, PxβGRP2, PxCAC, and PxCHS1. The insecticidal MIGGS candidates confer statistically significant mortality that is comparable to positive control treatment (MsVATPaseE). Data is average of 3-replicates/treatment $\pm$ SEM at $p \leq 0.001$ (***) $p \leq 0.01$ (**).

[0051] Figure 15A,B. Figure 15A,B illustrates a sprayable RNAi set up using dsRNA against TH MIGGS targets MsPGRP2, Ms βGRP2, MsCHS2, and MsVMP1. One cm² leaf discs from field soil grown tobacco plants (A) were drop inoculated with various concentrations of purified dsRNA against TH MIGGS RNAi targets (B). The bioassays were carried out for 5 days with 3 first instar larvae per well and leaf discs changed at the end of every 24 hours.

[0052] Figure 16. Figure 16 shows percentage mortality of TH larvae feeding on various concentrations of dsRNA against the core set of TH MIGGS RNAi targets MsPGPRP2, MsβGRP2, MsCHS2, and MsVMP1. The leaf disc coated dsRNA causes significant mortality at 8 and 16 μg of dsRNA concentration. The leaf disc coated dsRNA against three core MIGGS targets confers statistically significant mortality that is comparable to positive control treatment (MsVATPaseE). Data is average of 3-replicates/treatment $\pm$ SEM at $p \leq 0.001$ (***) $p \leq 0.01$ (**) and $p \leq 0.05$ (**).

[0053] Figure 17A-H. Figure 17A-H shows representative phenotypes of TH larvae (initial size shown in A and E) exposed to 8 and 16 μg of dsRNA against the core set of of MIGGS RNAi targets MsPGPRP2 (D), MsβGRP2 (F), MsCHS2 (G), and MsVMP1 (H). The insecticidal activity is comparable to the positive control treatment (C) and manifested as stunted growth and development, loss of appetite and melanotic reaction (D,F-G) in contrast to the regular growth and development observed with negative control treatment (B).

[0054] Figure 18A-D. Figure 18A-D shows representative phenotypes of TH larvae feeding on leaves from transplastomic plants expressing dsRNA against core MIGGS targets MsPGRP2 (PTS-28-10 and PTS-28-7-B), MsβGRP2 (PTS-26-19 and PTS-26-4-C), and dsCHS2 (PTS-27-3-1 and PTS-27-13-1-D). The TH larvae feeding on leaves expressing dsRNA against

MIGGS targets MsPGRP2 (B), Ms β GRP (C), and MsCHS2 (D) display stunted growth, development, loss of appetite and melanotic reaction in comparison to negative control PTS-27-13-2 (A).

[0055] Figure 18E. Figure 18E shows that the insecticidal activity of transplastomic lines is manifested as significant reduction in mean weights in comparison to negative control.

[0056] Figure 18F. Figure 18F shows that the transplastomic events confer significant mortality in comparison to negative control. The mortality rate was scored on a 0-3 score were 0, 1, 2 and 3 indicated ≤ 0 , 25, 50 or ≥ 50 mortality respectively. Data is average of 6 replicates/treatment (N=24) $\pm$ SEM at $p \leq 0.001$ (***); $p \leq 0.01$ (**) and $p \leq 0.05$ (*).

[0057] Figure 19. Figure 19 shows percentage mortality of Bt resistant DBM larvae feeding on various concentrations of dsRNA against the DBM orthologs of TH core MIGGS RNAi targets PxPGPRP2, Px β GRP2, Px β TUB, and PxCHS1. The leaf disc coated dsRNA causes significant mortality at 0.5-1 μ g of dsRNA concentration. The leaf disc coated dsRNA against all core MIGGS targets confers statistically significant mortality between 0.5 μ g and 1 μ g dsRNA dosage that is comparable to positive control treatment (MsVATPaseE). Data is average of 3-replicates/treatment $\pm$ SEM at $p \leq 0.01$ (**) and $p \leq 0.05$ (*).

[0058] Figure 20A-H. Figure 20A-H shows representative phenotypes of Bt resistant DBM larvae (initial size shown in A and E) exposed to 0.5-1 μ g of dsRNA against the DBM orthologs of TH core MIGGS RNAi targets PxPGPRP2(D), Px β GRP2(F), Px β TUB(G), and PxCHS1(H). The insecticidal activity is comparable to the positive control treatment (C) and manifested as stunted growth and development, loss of appetite and melanotic reaction (D,F-H) in contrast to the regular growth and development observed with negative control treatment (B).

[0059] Figure 21A-D. Figure 21A-D illustrates MIGGS-IRTG induction procedure in FAW feeding on wheat plants grown microbe rich field soil (A) and microbe depleted sterile surface (B). Ten first instar FAW larvae (C) were infested into each pot containing five wheat seedlings and contained using porous netting material (D). The larval samples were collected at various time points after infestation and used for pooled RNA-Seq approach to identify differential expressed transcripts in response to induction by the microbes in the field soil.

[0060] Figure 22A,B. Figure 22A,B shows bi-clustering comparison of differential gene expression in FAW larvae feeding on microbe-depleted plants (A) in comparison to larvae feeding on microbe rich plants (B). RNA-Seq data indicated that plants growing on field soil caused preferential up-regulation of MIGGS pathway genes in FAW. In total, 100 differential

expressed genes were identified, 30 of which were associated with MIGGS pathways. Notably, FAW orthologs of TH insecticidal targets including PGRP2, β GRP2 and IMD were captured in the data set, indicating clearly that MIGGS pathway genes are up regulated in response to insect feeding on plants exposed to soil microbiome.

5 **[0061]** Figure 23A-F. Figure 23A-F shows representative phenotypes of FAW larvae exposed to pure dsRNA against FAW orthologs of TH core MIGGS RNAi targets SFCHS2 (B), SF β GRP2 (C), SFPGRP2 (D), and two novel MIGGS RNAi targets from RNA-Seq study SFRC (un-annotated-E) and C-type lectin-6 (SFCTL-F). Leaf discs coated with dsRNA causes reduced growth, development and loss of appetite in comparison to negative control treatment (A) when
10 **supplied at 8 and 16 μ g of dsRNA concentration per leaf disc.**

[0062] Figure 23G,H. Figure 23G,H illustrates from Figure 23A-F significant weight reduction (G) and mortality (H). The rates of mortality was scored on a 0-3 scale where 0, 1, 2 and 3 indicated ≤ 0 , 25, 50 or ≥ 50 mortality respectively. The dsRNA treatments imposed caused statistically significant reduction in mean weights (G) that translated into significant rates
15 of mortality (H) in comparison to negative control. Data is average of 3 replicates/treatment $\pm$ SEM at $p \leq 0.001$ (***); $p \leq 0.01$ (**) and $p \leq 0.05$ (*).

[0063] Figure 24A,B. Figure 24 shows mean weights (A) of FAW larvae exposed to 16 μ g of pure dsRNA against newly discovered MIGGS RNAi targets from the RNA-Seq data. The rates of mortality was scored on a 0-3 score were 0, 1, 2 and 3 indicated ≤ 0 , 25, 50 or ≥ 50
20 mortality respectively. The dsRNA treatments imposed caused statistically significant reduction in mean weights (A) that also translated into significant rates of mortality (B) in comparison to negative control. Data is average of 3 replicates/treatment $\pm$ SEM at $p \leq 0.001$ (***); $p \leq 0.01$ (**) and $p \leq 0.05$ (*).

[0064] Figure 25. Figure 25 shows representative phenotypes of RFB beetles feeding on
25 rice flour mixed with 1 μ g of pure dsRNA against core MIGGS targets in RFB TcPGRP2, Ms β GRP2, dsCHS2, and a previously discovered target MDGP. The RFB beetles feeding on dsRNA against all MIGGS targets displayed significant mortalities at the end of 72 hours of feeding in comparison to negative control treatment (TE). The rates of mortality were significantly higher than negative control treatment and were comparable to the positive control
30 treatment TcvATPaseE. Mortality rate was scored on a 0-3 scale were 0, 1, 2 and 3 indicated ≤ 0 , 25, 50 or ≥ 50 mortality respectively. Data is average of 6 replicates/treatment (N=18) $\pm$ SEM at $p \leq 0.001$ (***); $p \leq 0.01$ (**) and $p \leq 0.05$ (*).

[0065] Figure 26A,B. Figure 26A,B shows imageJ analyzed RT-PCR data correlating TH larval phenotypes observed when exposed to 8-16 µg pure dsRNA against a positive control (A) and a core insecticidal MIGGS RNAi target MsβGRP2 (B). The transcript down regulation is correlated with the larval phenotypes observed in Figure 17.

- 5 [0066] Figure 26C,D. Figure 26C,D shows imageJ analyzed RT-PCR data correlating TH larval phenotypes observed when exposed to 8-16 µg pure dsRNA against core set of insecticidal MIGGS RNAi targets MsPGPRP2 (C) and MsCHS2 (D). The transcript down regulation is correlated with the larval phenotypes observed in Figure 17.

DETAILED DESCRIPTION

10 Overview

- [0067] RNAi-mediated gene-silencing offers a sustainable alternative approach to insect control. Most of the successful RNAi-based pest control strategies thus far employ homology dependent silencing of essential gene functions. Despite this, effective RNAi-based crop protection is lacking for Lepidopteran pests, due to their variable sensitivity to ingested double stranded RNA (dsRNA). (Terenius O, *et al.* (2011). *J. Insect Physiol.* 57(2): 231-245).

- [0068] Plant pests are in constant contact with, and ingest significant amount of microbes during herbivory. (Gayatri Priya N. *et al.* (2012). 7(1), *PLoS ONE*. E30768; Peñuelas and Terradas (2014). 19(5): *Trends Plant Sci.* 278 – 280; Engel and Moran (2013). *FEMS microbiol. rev.* 37(5): 699-735). This interaction between ingested microbes and insect midgut is often considered passive. Recent studies suggest, however, an active role of midgut specific immune responses in reducing variation of core microbial communities during insect herbivory through the activation of pattern recognition receptors (PRR). (Casanova-Torres and Goodrich-Blair (2013). *Insects*. 4: 320-338; Tang X, *et al.* (2012) 7(7) *PLoS ONE*:e36978; Ryu JH. *et al.* (2008). *Science*. 37(5): 777-82; Shrestha S. *et al.* (2009). *J. Asia Pac. Entomol.* 12: 277-283; Buchon, N. *et al.* (2013). *Front. Cell. Infect. Microbiol.* 11: 615–626). Further, maintenance of core gut microbial communities via active immune responses and/or their containment in the midgut is key to successful herbivory.

- [0069] Although, the core innate immune response pathways are conserved, their specific components are under strong selection for diversification. (Casanova-Torres and Goodrich-Blair (2013). *Insects*. 4: 320-338). Therefore, it is contemplated herein that these pathways provide novel and specific targets for devising sustainable pesticidal RNAi biotechnologies against insect

pests. Although gut immune responses have been studied from an immunological perspective, their active manipulation via genetic engineering for pest protection is currently lacking.

- [0070] Provided herein is the identification of “insect RNAi target genes” (IRTGs) involved in gut microbial clearance and/or containment induced by microbes ingested during feeding and/or active feeding (referred to herein as microbe-induced gut specific genes (MIGGS)) and examples of a novel biotechnology for insect protection via inter-specific silencing of MIGGS-IRTGs. In certain aspects, the MIGGS-IRTGs are Lepidoptera-specific. For example, in certain aspects detailed below, the insect is *Manduca sexta* (*M. sexta*; Lepidoptera) (tobacco hornworm (TH)). For example, in certain aspects detailed below, the insect is *Spodoptera frugiperda* (fall armyworm (FAW)). For example, in certain aspects detailed below, the insect is *Plutella xylostella* (Diamondback moth (DBM)). For example, in certain aspects detailed below, the insect is *Ostrinia nubilalis* (European corn borer). Still, it is also considered understood that successful, feeding-induced loss of appetite, developmental defects, and/or lethality has the potential to provide protection beyond the order Lepidoptera in an orthologous manner. For example, protection against coleopteran pests such as *Leptinotarsa decemlineata* (Say) (Colorado potato beetle), *Diabrotica spp.* (Corn rootworm complex), and *Tribolium castaneum* (Red Flour Beetle (RFB)). Additionally, this MIGGS-RNAi technique may allow containment of disease transmitting insect vectors and/or enable further manipulation of the plant-microbe-insect interactions for devising pesticidal RNAi for crop protection.
- [0071] In certain aspects detailed below, silencing of a target gene can result in reduced appetite and/or developmental defects and/or mortality and/or reduced fitness of the insect. In certain aspects these effects are observed after sustained feeding for at least about 24, 36, 48, or 72 hours, or any time inbetween.

25 Definitions

- [0072] To the extent necessary to provide descriptive support, the subject matter and/or text of the appended claims is incorporated herein by reference in their entirety.
- [0073] It will be understood by all readers of this written description that the exemplary embodiments described and claimed herein may be suitably practiced in the absence of any recited feature, element or step that is, or is not, specifically disclosed herein.
- [0074] It is to be noted that the term “a” or “an” entity refers to one or more of that entity; for example, “a dsRNA molecule,” is understood to represent one or more dsRNA molecules. As

such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

[0075] Furthermore, "and/or" where used herein is to be taken as specific disclosure of each of the specified features or components with or without the other. Thus, the term and/or" as
5 used in a phrase such as "A and/or B" herein is intended to include "A and B," "A or B," "A" (alone), and "B" (alone). Likewise, the term "and/or" as used in a phrase such as "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0076] It is understood that wherever aspects are described herein with the language
10 "comprising," otherwise analogous aspects described in terms of "consisting of" and/or "consisting essentially of" are also provided.

[0077] Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure is related. Numeric ranges are inclusive of the numbers defining the range. Even when not
15 explicitly identified by "and any range in between," or the like, where a list of values is recited, *e.g.*, 1, 2, 3, or 4, unless otherwise stated, the disclosure specifically includes any range in between the values, *e.g.*, 1 to 3, 1 to 4, 2 to 4, etc.

[0078] The headings provided herein are solely for ease of reference and are not limitations of the various aspects or aspects of the disclosure, which can be had by reference to
20 the specification as a whole.

[0079] As used herein, the term "non-naturally occurring" condition, substance, polypeptide, polynucleotide, composition, entity, plant, organism, individual, and/or any combination thereof, or any grammatical variants thereof and the like, is a conditional term that explicitly excludes, but only excludes, those forms that are well-understood by persons of
25 ordinary skill in the art as being "naturally-occurring," or that are, or might be at any time, determined or interpreted by a judge or an administrative or judicial body to be, "naturally-occurring."

[0080] As used herein, the term "identity," *e.g.*, "percent identity" to an amino acid sequence or to a nucleotide sequence disclosed herein refers to a relationship between two or
30 more amino acid sequences or between two or more nucleotide sequences. When a position in one sequence is occupied by the same nucleic acid base or amino acid in the corresponding position of the comparator sequence, the sequences are said to be "identical" at that position. The

percentage of “sequence identity” is calculated by determining the number of positions at which the identical nucleic acid base or amino acid occurs in both sequences to yield the number of “identical” positions. The number of “identical” positions is then divided by the total number of positions in the comparison window and multiplied by 100 to yield the percentage of “sequence identity.” Percentage of “sequence identity” is determined by comparing two optimally aligned sequences over a comparison window. In order to optimally align sequences for comparison, the portion of a nucleotide or amino acid sequence in the comparison window can comprise additions or deletions termed gaps while the reference sequence is kept constant. An optimal alignment is that alignment which, even with gaps, produces the greatest possible number of “identical” positions between the reference and comparator sequences. Percentage “sequence identity” between two sequences can be determined using, *e.g.*, the program “BLAST” which is available from the National Center for Biotechnology Information, and which program incorporates the programs BLASTN (for nucleotide sequence comparison) and BLASTP (for amino acid sequence comparison), which programs are based on the algorithm of Karlin and Altschul ((1993). *Proc. Natl. Acad. Sci. USA*. 90(12): 5873-5877).

[0081] As used herein, the term “complementary” refers to the ability of polynucleotides to form base pairs with one another. Base pairs are typically formed by hydrogen bonds between nucleotide units in antiparallel polynucleotide strands. Complementary polynucleotide strands can base pair in the Watson-Crick manner (*e.g.*, A to T, A to U, C to G), or in any other manner that allows for the formation of duplexes. When using RNA as opposed to DNA, uracil (U) rather than thymine (T) is the base that is considered to be complementary to adenosine. However, when a U is denoted in the context of the present invention, the ability to substitute a T is implied, unless otherwise stated.

[0082] As used herein, the term “polypeptide” is intended to encompass a singular “polypeptide” as well as plural “polypeptides,” and refers to a molecule composed of monomers (amino acids) linearly linked by peptide bonds (also known as amide bonds). The term “polypeptide” refers to any chain or chains of two or more amino acids, and does not refer to a specific length of the product. Thus, peptides, dipeptides, tripeptides, oligopeptides, “protein,” “amino acid chain,” or any other term used to refer to a chain or chains of two or more amino acids are included within the definition of “polypeptide,” and unless specifically stated otherwise the term “polypeptide” can be used instead of, or interchangeably with any of these terms. The term “polypeptide” is also intended to refer to the products of post-expression modifications of

the polypeptide, including without limitation glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, or modification by non-standard amino acids. A polypeptide can be derived from a natural biological source or produced by recombinant technology, but is not necessarily translated from a designated nucleic acid sequence. Thus, it can be generated in any manner, including by chemical synthesis.

[0083] As used herein, the term “protein” refers to a single polypeptide, i.e., a single amino acid chain as defined above, but can also refer to two or more polypeptides that are associated, *e.g.*, by disulfide bonds, hydrogen bonds, or hydrophobic interactions, to produce a multimeric protein.

[0084] As used herein, the term “nucleotide” refers to a ribonucleotide or a deoxyribonucleotide or modified form thereof, as well as an analog thereof. Nucleotides include species that comprise purines, *e.g.*, adenine, hypoxanthine, guanine, and their derivatives and analogs, as well as pyrimidines, *e.g.*, cytosine, uracil, thymine, and their derivatives and analogs. Further, the term nucleotide also includes those species that have a detectable label, such as for example a radioactive or fluorescent moiety, or mass label attached to the nucleotide.

[0085] As used herein, the term “polynucleotide” refers to polymers of nucleotides, and includes but is not limited to DNA, RNA, DNA/RNA hybrids including polynucleotide chains of regularly and/or irregularly alternating deoxyribosyl moieties and ribosyl moieties (i.e., wherein alternate nucleotide units have an —OH, then and —H, then an —OH, then an —H, and so on at the 2' position of a sugar moiety), and modifications of these kinds of polynucleotides, wherein the attachment of various entities or moieties to the nucleotide units at any position are included. The term “polynucleotide” is also intended to encompass a singular nucleic acid as well as plural nucleic acids, and refers to an isolated nucleic acid molecule or construct, *e.g.*, messenger RNA (mRNA) or plasmid DNA (pDNA). A polynucleotide can comprise a conventional phosphodiester bond or a non-conventional bond (*e.g.*, an amide bond, such as found in peptide nucleic acids (PNA)). A polynucleotide can be single stranded or double stranded.

[0086] As used herein, the term “nucleic acid” refers to any one or more nucleic acid segments, *e.g.*, DNA or RNA fragments, present in a polynucleotide. By “isolated” nucleic acid or polynucleotide is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, a recombinant polynucleotide encoding a polypeptide subunit contained in a vector is considered isolated as disclosed herein. Further examples of an

isolated polynucleotide include recombinant polynucleotides maintained in heterologous host cells or purified (partially or substantially) polynucleotides in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of polynucleotides. Isolated polynucleotides or nucleic acids further include such molecules produced synthetically. In addition, polynucleotide or a
5 nucleic acid can be or can include a regulatory element such as a promoter, ribosome binding site, or a transcription terminator.

[0087] As used herein, a "coding region" is a portion of nucleic acid comprising codons translatable into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is not translated into an amino acid, it can be considered to be part of a coding region, but any flanking sequences,
10 for example 5' untranslated regions (5' UTRs; also known as a leader sequence), 3' untranslated regions (3' UTRs; also known as a trailer sequence), promoters, ribosome binding sites, transcriptional terminators, introns, and the like, are not part of a coding region. Two or more coding regions can be present in a single polynucleotide construct, *e.g.*, on a single vector, or in separate polynucleotide constructs, *e.g.*, on separate (different) vectors. Furthermore, any vector
15 can contain a single coding region, or can comprise two or more coding regions, *e.g.*, a single vector can separately encode a selection marker gene and a gene of interest. In addition, a vector, polynucleotide, or nucleic acid can encode heterologous coding regions, either fused or unfused to a nucleic acid encoding a polypeptide subunit or fusion protein as provided herein. Heterologous coding regions include without limitation specialized elements or motifs, such as a
20 secretory signal peptide or a heterologous functional domain.

[0088] A variety of transcription regulatory regions are known to those skilled in the art. These include, without limitation, transcription regulatory regions that function in vertebrate cells, such as, but not limited to, promoter and enhancer segments from cytomegaloviruses (the immediate early promoter, in conjunction with intron-A), simian virus 40 (the early promoter),
25 and retroviruses (such as Rous sarcoma virus). Other transcription regulatory regions include those derived from vertebrate genes such as actin, heat shock protein, bovine growth hormone and rabbit β -globin, as well as other sequences capable of controlling gene expression in eukaryotic cells. Additional suitable transcription regulatory regions include tissue-specific promoters and enhancers.

30 **[0089]** Similarly, a variety of translation regulatory elements are known to those of ordinary skill in the art. These include, but are not limited to ribosome binding sites, translation

initiation and termination codons, and elements derived from picornaviruses (particularly an internal ribosome entry site, or IRES).

[0090] As used herein, the term "vector" is nucleic acid molecule as introduced into a host cell or organelle, thereby producing a transformed host cell or organelle. A vector can include nucleic acid sequences that permit it to replicate in a host cell, such as an origin of replication. A vector can also include one or more selectable marker gene and other genetic elements known in the art. Illustrative types of vectors include plasmids, phages, viruses and retroviruses.

[0091] As used herein, the term "transformed" cell or organelle, or a "host" cell organelle, is a cell or organelle into which a nucleic acid molecule has been introduced by molecular biology techniques. As used herein, the term transformation encompasses those techniques by which a nucleic acid molecule can be introduced into such a cell or organelle, including transfection with viral vectors, transformation with plasmid vectors, and introduction of naked DNA by electroporation, lipofection, and particle gun acceleration. A transformed cell or a host cell can be a bacterial cell or a eukaryotic cell.

[0092] As used herein, the term "expression" refers to a process by which a gene produces a biochemical, for example, a polynucleotide or a polypeptide. The process includes any manifestation of the functional presence of the gene within the cell including, without limitation, gene knockdown as well as both transient expression and stable expression. It includes without limitation transcription of the gene into messenger RNA (mRNA), and the translation of such mRNA into polypeptide(s). It also includes without limitation transcription of the gene into an RNA molecule that is not translated into a polypeptide but is capable of being processed by cellular RNAi mechanisms. If the final desired product is a biochemical, expression includes the creation of that biochemical and any precursors. Expression of a gene produces a "gene product."

As used herein, a gene product can be either a nucleic acid, *e.g.*, an RNA produced by transcription of a gene or a polypeptide that is translated from a mRNA transcript. Gene products described herein further include nucleic acids with post transcriptional modifications, *e.g.*, polyadenylation, or polypeptides with post translational modifications, *e.g.*, methylation, glycosylation, the addition of lipids, association with other protein subunits, proteolytic cleavage, and the like.

[0093] As used herein the term "engineered" includes manipulation of nucleic acid or polypeptide molecules by synthetic means (*e.g.* by recombinant techniques, *in vitro* peptide

synthesis, by enzymatic or chemical coupling of peptides or some combination of these techniques).

[0094] As used herein, the term “hpRNA” refers to hairpin RNA comprising a single-stranded loop region and a base-paired stem of an inversely repeated sequence. hpRNA can be generated from an hpRNA construct (or vector) and/or an hpRNA transgene comprising an inversely-repeated sequence of the RNAi target gene with a spacer region between the repeats. The RNA transcribed from such a sequence self-hybridizes to form a hairpin structure. The stem can be used as a substrate for the generation of siRNAs, but few or none are generated from the loop. Since a spacer region is needed for the stability of the transgene construct, but is not involved in siRNA production, an intron sequence is often used in this position. (Watson JM, et al. (2005). *FEBS Letters*. 579: 5982-8987).

[0095] As used herein, the term “siRNA” refers to small (or short) interfering RNA (or alternatively, silencing RNA) duplexes that are capable of inducing the RNA interference (RNAi) pathway. These molecules can vary in length (generally between 18-30 base pairs) and contain varying degrees of complementarity to their target mRNA in the antisense strand. Some, but not all, siRNA have unpaired overhanging bases on the 5' or 3' end of the sense strand and/or the antisense strand. The term “siRNA” includes duplexes of two separate strands, as well as single strands that can form hairpin structures comprising a duplex region.

[0096] As used herein, the phrase “duplex region” refers to the region in two complementary or substantially complementary polynucleotides that form base pairs with one another, either by Watson-Crick base pairing or any other manner that allows for a stabilized duplex between polynucleotide strands that are complementary or substantially complementary. For example, a polynucleotide strand having 21 nucleotide units can base pair with another polynucleotide of 21 nucleotide units, yet only 19 bases on each strand are complementary or substantially complementary, such that the “duplex region” has 19 base pairs. The remaining bases may, for example, exist as 5' and 3' overhangs. Further, within the duplex region, 100% complementarity is not required; substantial complementarity is allowable within a duplex region. Substantial complementarity as used herein refers to 79% or greater complementarity. For example, a mismatch in a duplex region consisting of 19 base pairs results in 94.7% complementarity, rendering the duplex region substantially complementary.

[0097] As used herein, the phrase “gene silencing” refers to a process by which the expression of a specific gene product is lessened or attenuated. Silencing of a gene does not

require that the expression or presence of the gene product is completely absent, but that in the context (e.g., comparing expression of a target gene in a plant expressing a gene silencing nucleic acid compared to a control plant or the health of an insect feeding on a gene silencing nucleic acid compared to a control insect), an observable effect in comparison to a control is observed.

- 5 While gene silencing can take place by a variety of pathways, unless specified otherwise, as used herein, gene silencing refers to decreases in gene product expression that results from RNA interference (RNAi) as understood by one of ordinary skill in the art. The level of gene silencing can be measured by a variety of means, including, but not limited to, measurement of transcript levels by Reverse transcription polymerase chain reaction (PCR), Northern Blot Analysis, B-
- 10 DNA techniques, transcription-sensitive reporter constructs, expression profiling (e.g. DNA chips), and related technologies. Alternatively, the level of silencing can be measured by assessing the level of the protein encoded by a specific gene. This can be accomplished by performing a number of studies including Western Analysis, measuring the levels of expression of a reporter protein that has e.g. fluorescent properties (e.g. GFP) or enzymatic activity (e.g.
- 15 alkaline phosphatases), or several other well-known procedures. Further, gene silencing can be assessed by its effect on a pest insect such as resulting in reduced appetite and/or developmental defects and/or mortality of an insect.

- [0098] As used herein, the term “control” is consistent with its well-established scientific use that refers to a standard of comparison recognized by one of ordinary skill in the art as having
- 20 a representative level of expression, phenotype, resistance, feeding, mortality, development, etc. Further, one of ordinary skill in the art will recognize, for example, that a statistical outlier and/or non-representative result produced by chance, abnormal environmental condition, manipulation, or other reason, that varies from a standard representation, would not be an appropriate control.

- [0099] As used herein, “microbe-induced gut specific genes (MIGGS)” refers to a gene
- 25 or group of genes expressed in the insect midgut in response to microbes ingested during normal process of insect feeding and primarily functioning to clear or respond to the ingested microbes and/ or contain the microbes to insect gut via maintenance of midgut structural integrity.

- [0100] As used herein, “actively feeding stage of the insect” refers to all feeding stages of insects with both complete and incomplete metamorphosis.

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Nucleic Acids for Gene Silencing

[0101] Provided herein are nucleic acid molecules for use in, among other things, crop protection from insect pests. In certain aspects disclosed herein, the nucleic acid molecules are isolated. The nucleic acid molecules specifically target certain insect genes (referred to herein interchangeably as “target genes,” “RNAi target genes,” “insect RNAi target genes,” and “IRTGs”), in insects for gene silencing. For example, in certain aspects, the nucleic acid molecules target certain insect microbe-induced gut gene (MIGGS) RNAi targets. In certain aspects, the silencing of a target gene occurs when a nucleic acid molecule of this disclosure is ingested by an insect. In certain aspects, the target gene is an insect gene that is implicated in insect immune responses (type 1 MIGGS RNAi target). A critical immune response gene is a genetically tractable nuclear or cytoplasmic loci that is important for providing cellular and/or humoral defense in insects against internal microorganisms, external microorganisms, and/or other insect parasites. In certain aspects, the immune response genes (type 1 MIGGS RNAi target) can also be a pattern recognition receptor (PRR) gene (Casanova-Torres and Goodrich-Blair (2013). *Insects*. 4:320-338). A PPR gene is a genetically tractable loci of an insect that encodes soluble or membrane bound proteins that recognize signatures associated with and/or released by microorganisms. PRR genes can activate or be activated by the immune response pathways to minimize microbial infection and can be co-regulated by the immune deficiency (IMD) pathway (Tang X, *et al.* (2012) 7(7) *PLoS ONE*:e36978; Ryu JH. *et al.* (2008). *Science*. 317(5): 777-82; Shrestha S. *et al.* (2009). In certain aspects the PRR type genes are co-regulated by the immune deficiency (IMD) pathway in TH were identified, these genes having been recently summarized. (Casanova-Torres and Goodrich-Blair (2013). *Insects* (4): 320-338; Zhong X, *et al.* (2012). *Insect Biochem. Mol. Biol.* 42(7): 514-524; Zhang X, *et al.* (2015). *Insect Biochem. Mol. Biol.* 62:38-50; Cao X, *et al.* (2015). *Insect Biochem. Mol. Biol.* 62:64-74; Kanost MR, *et al.* (2016). *Insect Biochem. Mol. Biol* 76:118-147). In certain aspects, the target gene is an insect gene that is necessary for structural integrity of insect organs including the mid-gut and also facilitates the containment of the ingested microbes to the insect gut. (type 2 MIGGS RNAi target). In certain aspects, the target gene is an insect midgut structural component gene (type 2) (Odman-Naresh *et al.* (2013). *PLoS ONE* 8:e82015. 10.1371/journal.pone.0082015). A midgut structural component gene is a genetically tractable loci in an insect that encodes chitin fibrils, proteins, or glycoproteins that form a protective sac-like structure called peritrophic matrix enveloping the insect food bolus/midgut also functioning to contain the ingested microbes in the

gut (Engel and Moran (2013). *FEMS Microbiol Rev.* 37 699–735). In certain aspects, the target genes (type 1 and 2 MIGGS RNAi targets) are predominantly expressed in the insect midgut, for example, abundantly and/or exclusively expressed in the larval and/or adult insect midgut in response to active feeding and/or microbial infection and/or responding to microbes ingested during feeding. In certain aspects, the target gene is induced predominantly in a midgut specific manner during active feeding (type 1 and type 2 MIGGS RNAi targets). The midgut abundance of both type 1 and 2 MIGGS RNAi target genes may mitigate problems associated with reduced amounts of bioavailability.

[0102] Representative examples of insect MIGGS RNAi target genes and their nucleic acid sequences identified from published literature are provided herein. In certain aspects, the target gene is one or more of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-Beta-1, 3-glycan-recognition protein 2 (MsβGRP2), *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsRelF), *M. sexta*-Cdc42 (MsCdc42), *M. sexta*-Dsor1 (MsDsor1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13 (MsAtg13), *M. sexta*-IAP1 (MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*-Beta fructofuranosidase 1 (MsSuc1), and orthologs thereof.

[0103] In certain aspects, the target gene is one or more of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-Beta-1, 3-glycan-recognition protein 2 (MsβGRP2), *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsRelF), *M. sexta*-Cdc42 (MsCdc42), *M. sexta*-Dsor1 (MsDsor1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-

Atg13 (MsAtg13), *M. sexta*-IAP1(MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), and *M. sexta*-Beta fructofuranosidase 1 (MsSuc1), , *M. sexta*-Sickie (MsSck), *M. sexta*-Akirin (MsAki), *M. sexta*-Cactus (MsCac), *M. sexta*- Gloverin (MsGlv) and *M. sexta*-**Beta-1-tubulin** (Ms β Tub).

[0104] In certain aspects, the target gene is an ortholog of one or more of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-**Beta-1, 3-glycan-recognition protein 2** (Ms β GRP2), *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsReIF), *M. sexta*-Cdc42 (MsCdc42), *M. sexta*-Dsr1 (MsDsr1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13 (MsAtg13), *M. sexta*-IAP1(MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*- Beta fructofuranosidase 1 (MsSuc1), and other IMD pathway or structural integrity genes.

[0105] One of ordinary skill in the art would understand that nucleic acid molecules can be, for example, deoxyribonucleic acid (DNA) or ribonucleic acid (RNA). In certain aspects of any target gene silencing nucleic acid molecule described anywhere herein, the nucleic acid molecule is a DNA molecule. In certain aspects of any target gene silencing nucleic acid molecule described anywhere herein, the nucleic acid molecule is a RNA molecule. In certain aspects of any target gene silencing nucleic acid molecule described anywhere herein, the RNA molecule is a double stranded molecule (dsRNA), for example, for use in the RNA interference (RNAi) process. As used herein, a dsRNA molecule is a RNA molecule comprising at least one annealed, double stranded region. In certain aspects, the double stranded region comprises two separate RNA strands annealed together. In certain aspects, the double stranded region comprises one RNA strand annealed to itself, for example, as can be formed when a single RNA strand contains an inversely repeated sequences with a spacer in between. One of ordinary skill in the art will understand that complementary nucleic acid sequences are able to anneal to each other but that two sequences need not be 100% complementary to anneal. The amount of complementarity needed for annealing can be influenced by the annealing conditions such as temperature, pH, and ionic condition. In certain aspects, the annealed RNA sequences are 100%

complementary across the annealed region. In certain aspects, the annealed RNA sequences are less than 100% complementary across the annealed region but have enough complementarity to anneal within their environment, such as in a host cell or the gut of an insect. In certain aspects, the annealed RNA sequences are substantial complementarity as defined elsewhere herein.

5 **[0106]** It is contemplated that the nucleic acid molecules disclosed anywhere herein for the silencing of target genes derive their specificity from comprising a nucleic acid sequence that is complementary or substantially complementary to at least a portion of a target gene sequence. Substantially complementary sequences, however, may be more likely to have reduced specificity and produce off-target effects. As referred to anywhere herein, a target gene sequence
10 can include at least the target gene protein coding region, the 5' untranslated region (5' UTR), and/or the 3' untranslated region (3' UTR) and any portion or combination thereof. For example, predicted UTR regions can be identified using previously established criteria (Siepel, et al. (2005). *Genome Res.* 15: 1034-1050) when corresponding genomic sequences are available.

[0107] In certain aspects, an isolated double stranded RNA (dsRNA) molecule comprises
15 a nucleic acid sequence complementary to about 21 to 2000 contiguous nucleotides of a target gene sequence disclosed anywhere herein. For example, in certain aspects, an isolated double stranded RNA (dsRNA) molecule comprises a nucleic acid sequence complementary to about any of 21, 22, 23, 24, 25, 30, 40, 50, 60, 100, 120, 200, 240, 300, 400, 500, 600, 650, 750, 1000 to about any of 23, 24, 25, 30, 40, 50, 100, 200, 300, 400, 500, 600, 650, 750, 1000, or 2000
20 contiguous nucleotides of a target gene sequence. For example, in certain aspects, an isolated dsRNA molecule comprises a nucleic acid sequence complementary to about 100 to 1000 or about 200 to 1000 contiguous nucleotides of a target gene sequence. For example, in certain aspects, an isolated dsRNA molecule comprises a nucleic acid sequence complementary to about 100 to 1000 or about 200 to 1000 contiguous nucleotides of the protein coding region of a target
25 gene sequence. For example, in certain aspects, an isolated dsRNA molecule comprises a nucleic acid sequence complementary to about 100 to 1000 or about 200 to 1000 contiguous nucleotides of the 5' UTR region or the 3' UTR region of a target gene sequence. In certain aspects, the isolated dsRNA molecule comprises a nucleic acid sequence complementary to a contiguous region comprising at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% of the
30 length of the target gene sequence protein coding region, the target gene sequence 5' UTR region, the target gene 3' UTR region, and/or any combination thereof. For example, if a target gene sequence protein coding region is determined to be 200 nucleotides long, then an isolated

dsRNA molecule comprising a nucleic acid sequence complementary to a contiguous region comprising 95% of the length of the target gene sequence protein coding region would be complementary to a contiguous region 190 nucleotides long.

[0108] In certain aspects of any target gene silencing nucleic acid molecule described anywhere herein, including dsRNA molecules for RNAi, the target gene comprises one or more of the nucleic acid sequence of SEQ ID NO: 1-14, 16-29, 31-69, 70-75, 76-88, 89-105, and 106-110. In certain aspects, the target gene comprises the nucleic acid sequence of SEQ ID NO: 3 or 14. Thus, in certain aspects, the isolated dsRNA molecule comprises a nucleic acid sequence complementary to about any of 21, 22, 23, 24, 25, 30, 40, 50, 100, 200, 300, 400, 500, 600, 650, 750, 1000 to about any of 23, 24, 25, 30, 40, 50, 100, 200, 300, 400, 500, 600, 650, 750, 1000, or 2000 contiguous nucleotides of a target gene sequence comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-69, 70-75, 76-88, 89-105, and 106-110. For example, in certain aspects, the isolated dsRNA molecule comprises a nucleic acid sequence complementary to about 100 to 1000 or about 200 to 1000 contiguous nucleotides of a target gene sequence comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-69, 70-75, 76-88, 89-105, and 106-110. In certain aspects, the isolated dsRNA comprises a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of the protein coding region of a target gene sequence comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-69, 70-75, 76-88, 89-105, and 106-110. In certain aspects, the isolated dsRNA molecule comprises a nucleic acid sequence complementary to a contiguous region comprising at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% of the length of the target gene sequence protein coding region, the target gene 5' UTR region, and/or the target gene 3' UTR region. In certain aspects, the isolated dsRNA molecule comprises a nucleic acid sequence complementary to a contiguous region comprising at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% of the length of a sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-69, 70-75, 76-88, 89-105, and 106-110.

[0109] In certain aspects of any target gene silencing nucleic acid molecule described anywhere herein, the nucleic acid molecule can form siRNA. Thus, certain aspects provide for an siRNA molecule derived from the processing of a dsRNA molecule for silencing a target gene disclosed herein.

Insecticidal Compositions

[0110] Certain aspects of the disclosure provide for an insecticidal composition comprising a nucleic acid molecule disclosed anywhere herein for silencing a target gene, including long dsRNA, hpRNA, and siRNA. In certain aspects, the insecticidal composition also
5 comprises a synthetic carrier or a microbial conduit. For example, a microbial conduit can be a microorganism that has a natural capacity or is engineered to produce and/ or deliver dsRNA to increase its bioavailability and/or biostability for causing RNA interference. Representative examples include plant growth promoting organisms, normal commensal and/or symbiotic microorganisms associated with the target insect pest or pest target host or host cultivation range
10 etc. from an insect engineered or identified from natural populations to produce and/or deliver dsRNA. In certain aspects a microbial conduit can be used as a direct topical application on a whole plant or coated onto a seed or mixed with growth media or transmitted through fertilizer or irrigation, etc. In certain aspects, the nucleic acid molecule of the insecticidal composition is conjugated to the synthetic carrier. For example, a synthetic carrier can be an inert chemical
15 compound with a natural or engineered affinity to bind (conjugate) a dsRNA molecule to increase its biostability and/or bioavailability for causing RNA interference. In certain aspects, a synthetic carrier comprises a combination of inert chemicals or nanoparticles that upon combining and/or individually have a net positive charge or general affinity to bind to negatively charged dsRNA. Representative examples include chitosan, liposomes, carbon quantum dots,
20 biodegradable particles of plant (e.g. coconut coir or grain flour, etc.) or soil (e.g. calcified clay) origin etc. In certain aspects, the dsRNA conjugated with a synthetic carrier can be used as a direct topical application directly and/or after aerosolization on a whole plant or coated onto a seed or mixed with growth media or transmitted through fertilizer or irrigation, etc. In certain aspects, dsRNA or a composition comprising dsRNA can be used as a direct topical spray on
25 application to whole plant, coated onto a seed or mixed with growth media or transmitted through fertilizer or irrigation or combined with plant growth promoting microbes etc.

Recombinant Constructs

[0111] Certain aspects of this disclosure provide for a recombinant nucleic acid construct,
30 such as a DNA vector, comprising and/or encoding a nucleic acid molecule disclosed anywhere herein for silencing a target gene, including long dsRNA, hpRNA, and siRNA. Certain aspects provide for recombinant nucleic acid constructs comprising and/or encoding an RNAi precursor

of a nucleic acid molecule disclosed anywhere herein for silencing a target gene, including long dsRNA, hpRNA, and siRNA.

[0112] Certain aspects of this disclosure provide for a recombinant nucleic acid construct, such as a DNA vector, comprising a target gene silencing sequence for silencing a target gene described anywhere herein. In certain aspects, a recombinant DNA construct comprises a gene silencing sequence comprising about any of 21, 22, 23, 24, 25, 30, 40, 50, 60, 100, 120, 200, 240, 300, 400, 500, 600, 650, 750, 1000 to about any of 23, 24, 25, 30, 40, 50, 100, 200, 300, 400, 500, 600, 650, 750, 1000, or 2000 contiguous nucleotides of a target gene sequence disclosed anywhere herein. In certain aspects, a recombinant DNA construct comprises a gene silencing sequence comprising about 100 to 1000 or about 200 to 1000 contiguous nucleotides of a target gene sequence. In certain aspects, the gene silencing sequence comprises about 100 to 1000 or about 200 to 1000 contiguous nucleotides of the protein coding region of the target gene sequence. In certain aspects, the gene silencing sequence comprises about 100 to 1000 or about 200 to 1000 contiguous nucleotides of the 5' UTR region or the 3' UTR region of the target gene sequence. In certain aspects, the gene silencing sequence comprises at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% contiguously of the length of target gene sequence protein coding region, the target gene sequence 5' UTR region, target gene sequence 3' UTR region and/or any combination thereof.

[0113] In certain aspects, the target gene comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-69, 70-75, 76-88, 89-105, and 106-110. In certain aspects, the gene silencing sequence comprises about 100 to 1000 or about 200 to 1000 contiguous nucleotides of a sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-69, 70-75, 76-88, 89-105, and 106-110. In certain aspects, the gene silencing sequence comprises at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% contiguously of the length of a sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-69, 70-75, 76-88, 89-105, and 106-110.

[0114] In certain aspects, the recombinant DNA construct has a gene silencing sequence operably linked to one or more promoters for the expression of a dsRNA molecule that silences the target gene when ingested by an insect. Thus, in certain aspects, the construct is an expression vector. Representative promoters for use in expressing a dsRNA molecule include, but are not limited to, CaMV35S or ZmUbi1 promoters etc. In certain aspects, the expression vector can target single or multiple insect RNAi target genes, for example, the vector could comprise one or

more gene silencing sequences or could employ multiple vectors to target multiple insect RNAi target genes or chimeric dsRNA molecules.

Host Cells and Plants

5 [0115] Provided herein are host cells, plants, and plants parts comprising, expressing, processing, and the like a dsRNA as described anywhere herein for inducing RNAi in an insect. In certain aspects, a host cell comprises a dsRNA molecule, siRNA molecule, a polynucleotide encoding a dsRNA molecule, and/or a construct or a dsRNA encoding segment thereof described anywhere herein. Representative examples of host cells include bacterial cells, fungal cells, yeast
10 cells, plant cells, plant organelles (e.g., including plastids), and mammalian cells. In certain aspects, the host cell is a bacterial or plant cell. In certain aspects, the host cell is a transgenic and/or transplastomic plant cell. One of ordinary skill will understand that there are many well-known methods for introducing a nucleic acid, such as a vector, into a host cell including well-known methods for generating transgenic and/or transplastomic plant cells. In certain aspects, the
15 host cell expresses a dsRNA molecules and/or produces siRNA to silence a target gene. In certain aspects, a transgenic and/or transplastomic plant can comprise a dsRNA molecule, siRNA, a polynucleotide encoding a dsRNA, and/or a construct or a dsRNA encoding segment thereof. In certain aspects, at least one cell of a transgenic and/or transplastomic plant expresses a dsRNA molecule and/or produces a siRNA for silencing a target gene. Certain aspects provide
20 for a seed, part, tissue, cell, or organelle of a plant described herein, wherein said seed, part, tissue, cell, or organelle comprises a dsRNA molecule and/or the siRNA for silencing a target gene.

Methods of Insect Control

25 [0116] Also provided for herein are various methods of using a dsRNA molecule or vector encoding such dsRNA described anywhere herein for inducing RNAi in an insect and/or silencing a target gene. In certain aspects, this provides for control of insect pests.

[0117] Certain aspects provide for a method of silencing an insect immune response gene and/or an insect gene encoding for structural components of the insect midgut. In certain aspects,
30 a method provides for the silencing an insect MIGGS-IRTG. Such method comprises providing for ingestion through spray, drenches, granules, seed coating or plant-incorporated protectant, or the like, to an insect an isolated dsRNA (pure or crude extract), siRNA, insecticidal composition,

host cell, transgenic and/or transplastomic plant, and/or the seed, part, tissue, cell, or organelle thereof described anywhere herein.

[0118] Certain aspects provide for a method of silencing an insect immune response gene and/or an insect gene encoding for structural components of the insect midgut. In certain aspects, a method provides for the silencing an insect MIGGS-IRTG. Such method comprises providing for ingestion through spray, drenches, granules, seed coating or plant-incorporated protectant, or the like, to an insect an isolated dsRNA, siRNA, insecticidal composition, host cell, transgenic and/or transplastomic plant, and/or the seed, part, tissue, cell, or organelle thereof described anywhere herein.

[0119] Certain aspects provide for protecting a plant, such as a crop plant, from an insect pest including but not limited to pests of the order Lepidoptera like *Manduca sexta* (tobacco hornworm), *Spodoptera frugiperda* (fall armyworm), *Ostrinia nubilalis* (European corn borer), *Plutella xylostella* (Diamondback moth) or pests of the order Coleoptera like *Leptinotarsa decemlineata* Say (Colorado potato beetle), *Diabrotica spp.* (Corn rootworm complex), *Tribolium castaneum* (Red flour beetle), *Popillia japonica* (Japanese beetle), *Agilus planipennis* (Emerald ash borer) or pests of the order Hemiptera like *Diaphorina citri* (Asian citrus psyllid), *Cimex lectularius* (Bed bug) or pests of the order Blattodea like all species of cockroaches and termites or insect pests of the order Diptera like all species of Mosquitoes and flies etc. Representative examples of plant hosts include, but are not restricted to, *Zea mays* L (corn), *Sorghum bicolor* (sorghum), *Setaria italica* (fox tail millet), *Pennisetum glaucum* (Pearl millet), *Solanum tuberosum* (potato), *Oryza sativa* (rice), *Lycopersicon esculentum* (tomato), *Solanum melongena* (eggplant), all cultivars of *Brassica oleracea* family, *Citrus sinensis* (Orange), trees of Oleaceae family and crops of *Rosaceae* etc. Such methods comprise, for example, topically applying to the plant the isolated dsRNA (pure or crude extract), the siRNA, and/or the insecticidal composition described anywhere herein, and providing the plant in the diet of the insect pest. In certain aspects the dsRNA molecule is topically applied by expressing the dsRNA in a microbe followed by topically applying the microbe onto the plant and/or seed.

[0120] Certain aspects provide for producing a plant resistance to a pest insect of said plant. Such methods comprises transforming the plant with a polynucleotide encoding a dsRNA and/or a construct or a dsRNA encoding segment describe anywhere herein, wherein the plant expresses a dsRNA and/or siRNA and/or the plant comprises a dsRNA and/or siRNA containing insecticidal compositions described anywhere herein, for silencing a target gene. In certain

aspects, the transformed plant is more resistant to a pest insect of said plant than untransformed plants.

[0121] Certain aspects provide for improving crop yield. Such methods comprise growing a population of crop plants transformed with a polynucleotide encoding a dsRNA and/or the construct or a dsRNA encoding segment thereof described anywhere herein, wherein the plant expresses a dsRNA and/or siRNA and/or the plant comprises a dsRNA and/or siRNA containing insecticidal compositions described anywhere herein, for silencing a target gene. In certain aspects, a population of transformed plants produces higher yields in the presence of pest insect infestation than a control population of untransformed plants.

[0122] Certain aspects of the disclosure provide for an insecticidal composition comprising a nucleic acid molecule disclosed anywhere herein for silencing a target gene, including long dsRNA, hpRNA, and siRNA. In certain aspects, the insecticidal composition also comprises a synthetic carrier or a microbial conduit. For example, a microbial conduit can be a microorganism that has a natural capacity or is engineered to produce and/ or deliver dsRNA to increase its bioavailability and/or biostability for causing RNA interference. Representative examples include plant growth promoting organisms, normal commensal and/or symbiotic microorganisms associated with the target insect pest or parasites and/or natural enemies of the target pest or pest target host or host cultivation range etc. from an insect or parasite and/or natural enemies of the target pest engineered or identified from natural populations containing microbial conduit to produce and/or deliver dsRNA and/or drive the transmission of such microbial conduits into natural populations of insect pests as a control option. In certain aspects a microbial conduit can be used as a direct topical application on a whole plant or coated onto a seed or mixed with growth media or transmitted through fertilizer or irrigation, etc. In certain aspects, the nucleic acid molecule of the insecticidal composition is conjugated to the synthetic carrier. For example, a synthetic carrier can be an inert chemical compound with a natural or engineered affinity to bind (conjugate) a dsRNA molecule to increase its biostability and/or bioavailability for causing RNA interference. In certain aspects, a synthetic carrier comprises a combination of inert chemicals or nanoparticles that upon combining and/or individually have a net positive charge or general affinity to bind to negatively charged dsRNA. Representative examples include chitosan, liposomes, carbon quantum dots, biodegradable particles of plant (e.g. coconut coir or grain flour, etc.) or soil (e.g. calcified clay) origin etc. In certain aspects, the dsRNA conjugated with a synthetic carrier can be used as a direct topical application directly

and/or after aerosolization on a whole plant or coated onto a seed or mixed with growth media or transmitted through fertilizer or irrigation, etc. In certain aspects dsRNA or composition comprising the dsRNA can be used as a direct topical spray on application to whole plant, coated onto a seed or mixed with growth media or transmitted through fertilizer or irrigation or
5 combined with plant growth promoting microbes etc.

[0123] Certain aspects provide for producing a plant resistant against a pest insect of said plant. Such methods comprise first transforming a plant cell with a polynucleotide encoding the dsRNA and/or the construct or a dsRNA encoding segment described anywhere herein. Next, a plant is regenerated from the transformed plant cell. The plant is then grown under conditions
10 suitable for the expression of the dsRNA. In certain aspects, the transformed plant confers genetically tractable (maternal and/or paternal inherited) gain of function phenotypically manifested as an ability to impair the normal feeding and/or growth and/or development and/or reproductive success of the target plant pest and is consequently resistant to the plant pest insect compared to a control untransformed plant.

[0124] In certain aspects of any of the aforementioned methods, the insect larvae ingest the dsRNA. In certain aspects of any of the aforementioned methods, ingestion of the dsRNA induces a melanotic response in the insect larvae. In certain aspects of any of the aforementioned methods, ingestion of the dsRNA results in perturbation of gut microbial homeostasis. In certain aspects of any of the aforementioned methods, ingestion of the dsRNA results in defective
20 clearance of opportunistic microbes. In certain aspects of any of the aforementioned methods, ingestion of the dsRNA results in defective containment of gut microbes.

[0125] One of ordinary skill in the art will recognize that, the inventors have demonstrated midgut specific expression of a representative number of MIGGS-IRTGS in TH in response to their feeding on a lab strain of *Escherichia coli* (*E. coli*) bacteria. For example, a set
25 of 20 MIGGS-IRTGS (SEQ ID NOs: 1-9, 11, 14, 31, 39, 43, 44, 71-75) that are induced in TH larvae feeding on an induction medium (Wang et al. (2006). J. Biol. Chem. 281(14): 9271–9278) is disclosed herein. It was previously reported that these twenty genes are expressed abundantly in the gut (Table 1). The gut specific expression of 2/20 genes were tested and validated the same (Figure 7).

[0126] Orthologs of the representative TH MIGGS-IRTG (SEQ ID NOs: 76-88) set were identified from transcriptomic resources of an economically important Bt. resistant lepidopteran pest DBM using a combination of reciprocal best Blast analysis (Ward et al. (2014). PLoS ONE

9(7): e101850) and literature curation. Most of these MIGGS-IRTGS were induced in response to the feeding of DBM larvae on induction medium (Wang et al. (2006). J. Biol. Chem. 281(14): 9271–9278), similar to observations with TH larvae.

[0127] It was also demonstrated that most of the MIGGS-IRTGS were induced in another economically important lepidopteran pest, FAW, feeding on plants grown on representative field soil, using a RNA-Seq approach.

[0128] The RNA-Seq approach also identified additional RNAi candidates (SEQ ID NOs: 89-105) belonging to the MIGGS category. Further, orthologs of the expanded representative TH MIGGS-IRTG set (SEQ ID NO: 106-110) were identified from transcriptomic resources of an economically important Coleopteran pest RFB. It was demonstrated that most of the MIGGS-IRTGS were induced in response to the feeding of RFB beetles on induction medium (Wang et al. (2006). J. Biol. Chem. 281(14): 9271–9278), similar to observations with the order lepidoptera.

[0129] It was demonstrated that the targeted silencing of 9 out of 20 MIGGS-IRTGS employing bacterially expressed dsRNA protocol (Timmons L. et al. (2001). Gene. 263:103-112.) is insecticidal to TH larvae. Insecticidal activity against TH larvae correlated with the down regulation of target transcripts. It was demonstrated that the targeted silencing of 7 out of 14 MIGGS-IRTGS using bacterially expressed dsRNA protocol (Timmons L. et al. (2001). Gene. 263:103-112.) is insecticidal to DBM larvae. It was demonstrated that targeted silencing of 9 MIGGS-IRTGS are insecticidal to FAW larvae using bacterially expressed dsRNA protocol (Timmons L. et al. (2001). Gene. 263:103-112.). A core set of three MIGGS-IRTGS (SEQ ID NO: 3, 4, and 43) was identified that are efficacious against all three lepidopteran pests TH, DBM and FAW in an orthologous manner and that leaf discs coated with dsRNA against the core MIGGS-IRTGS are insecticidal against TH, DBM and FAW larvae. Further, plastidial expressed dsRNA against the core MIGGS-IRTGS impacted larval growth and survival.

[0130] The following examples are included to demonstrate certain embodiments of the disclosure. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventor to function well in the practice of the disclosure. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are

disclosed and still obtain a like or similar result without departing from the spirit and scope of the disclosure.

EXAMPLES

[0131] In certain aspects, work was performed towards the identification, induction,
5 isolation and cloning of the selected *M. sexta* (tobacco hornworm (TH)) MIGGS-IRTGS into a bacterial expression system capable of enabling the cloned genes to produce dsRNA (Timmons L. et al. (2001). *Gene*. **263**:103-112.). Upon ingestion by *M. sexta* larvae, the bacterially expressed dsRNA is intended to silence, or at least knock-down, reduce, and the like the corresponding MIGGS-IRTG in order to curtail the feeding behavior and/or cause lethal effects
10 in the insect pests. Based upon these results, additional testing was done on other representative insect species to demonstrate and establish for purposes of support wide applicability of the compositions and approaches of the disclosure.

[0132] For MIGGS-IRTG selection, PRR type genes co-regulated by the immune deficiency (IMD) pathway in TH were identified, these genes having been recently summarized
15 (Casanova-Torres and Goodrich-Blair (2013). *Insects* (4): 320-338; Zhong X, et al. (2012). *Insect Biochem. Mol. Biol.* 42(7): 514-524); Zhang X, et al. (2015). *Insect Biochem. Mol. Biol.* 62:38-50; Cao X, et al. (2015). *Insect Biochem. Mol. Biol.* 62:64-74; Kanost MR, et al. (2016). *Insect Biochem. Mol. Biol.* 76:118-147). Notably, most of the PRR genes selected for this study are abundantly induced or predicted to express in a midgut specific manner (Pauchet Y, et al. (2010).
20 *Insect. Mol. Biol.* 19: 61-75; Kim and Lee (2014). *Front. Cell. Infect. Microbiol.* 3: 116; Lee and Hase (2014). *Nat. Chem. Biol.*, 10: 416-424).

[0133] The TH-Transferrin, Arylphorin β subunit, chymotrypsinogen-like protein 1 and few other immunity related genes do not belong to the conventional PRR type immune responsive genes. However, these genes were included as they potentially contribute to the
25 midgut microbial homeostasis through IMD co-regulation (Pauchet Y, et al. (2010). *Insect. Mol. Biol.* 19: 61-75). Additionally identified were a TH gene indicated to be a valine rich midgut protein critical for the formation of midgut peritrophic matrix and related genes critical for maintaining the structural integrity of the midgut, which are possibly involved, in the gut microbial containment. (Odman-Naresh et al. (2013). *PLoS ONE* 8:e82015.
30 10.1371/journal.pone.0082015; Engel and Moran (2013). *FEMS Microbiol Rev.* 37 699-735). A

non-insect gene that encodes for catalase 1 from cassava (*Manihot esculanta*) was used as a control.

Materials and Methods

- 5 [0134] TH larvae required for isolation of IRTG genes and subsequent bioassays were reared as follows: Eggs were procured from Carolina Biological Sciences (Burlington, NC, USA). The eggs were not surface sterilized and used directly for conventional rearing (CR). The larval colony establishment and maintenance was performed employing a Phytatray II (Sigma, MO, USA) unit containing Gypsy Moth diet. (Gunaratna RT and Jiang H (2013). *Dev. Comp. Immunol.* 39: 388-398).
- 10 [0135] *Bt.*-resistant DBM eggs were procured from Benzon Research (Carlisle, PA, USA) and reared conventionally, as described above.
- [0136] FAW eggs were procured from Benzon Research (Carlisle, PA, USA) and reared conventionally, as described above.
- 15 [0137] For germ free (GF) rearing procedure, all eggs were surface sterilized with a solution of Tween-80 (polyoxyethylene sorbitan monooleate), bleach, and distilled water as described previously. (Broderick NA, et al. (2009). *Environ. Entomol.* 29:101-107). The surface sterilized eggs were transferred to Phytatray II (Sigma, MO, USA) unit containing Gypsy Moth diet augmented with antibiotics (500 mg/l each of penicillin, gentamicin, rifampicin, streptomycin). (Broderick NA, et al. (2009). *Environ. Entomol.* 29:101-107; Gregory R. Richards (2008). *Journal of Bacteriology.* 190, 4870-4879).
- 20 [0138] Both CR and GF larvae were reared in an environmental chamber with a 16:8 hours (light:dark) photoperiod at 25 °C, until use. For the induction of a representative set of MIGGS-IRTGS of PRR category, 75 colony forming units (CFU) of DH5 α competent cells (Invitrogen, CA, USA) re-suspended in PBS buffer were injected into healthy 2-3 instar *M. sexta* larvae. The larvae were snap frozen in liquid nitrogen and processed for RNA isolation and cDNA synthesis described herein.
- 25 [0139] For testing the up-regulation of MIGGS-IRTGS by oral feeding on induction media, first instar larvae were reared on Luria broth agar media plated with a mixture of live *E. coli* (3 x 10⁷ cells), *M. luteus* (30 μ g), and curdlan (30 μ g) in 50 μ l of H₂O (Wang et al. (2006). *J. Biol. Chem.* 281(14): 9271–9278).
- 30

[0140] Total RNA was isolated using RNeasy Mini Kit reagent (QIAGEN, NY, USA) and treated with TURBO DNase (Ambion-Life Technologies, NY, USA) using manufacturer's protocols. One µg of DNase treated RNA was used for cDNA synthesis using iScript cDNA synthesis kit (Bio-Rad, CA, USA). The cDNA was used as a template for amplifying near full-length transcripts of the IRTG. Similarly, a control gene from cassava was also amplified. For tissue specific cDNA synthesis the control and treatment larvae were squeezed to isolate hemolymph fraction (HL), dissect midgut (MDG) to obtain rest of the body as described in Pauchet et al. (2010). *Insect. Mol. Biol.* 19: 61-75). The cDNA template was used for RT-PCR reactions were appropriate using the SuperScript III One-Step RT-PCR system following manufacturers protocol (Thermo Scientific; USA).

[0141] Transcripts of TH, DBM, and FAW MIGGS-IRTGS and non-insect control genes were PCR amplified using PrimeSTAR GXL DNA Polymerase (Clontech Laboratories, CA, USA). The PCR reactions were conducted using the following conditions: denaturation at 98 °C for 30 s, annealing at 55/60 °C for 30 s and elongation at 72 °C for 45 s, for 35 cycles. The PCR products were resolved by agarose gel electrophoresis and stained with ethidium bromide. The transcripts were gel eluted using QIAquick gel extraction kit (QIAGEN, NY, USA).

[0142] Sequence confirmed transcripts were cloned into pCR8/GW vector (Invitrogen, CA, USA) using manufacturer's protocol. The sequence confirmed recombinant pCR8 clones were cloned into L4440gtwy using LR clonase enzyme (Invitrogen, CA, USA). The L4440gtwy is a modified version of Timmons and Fire feeding Vector and was a kind gift from Guy Caldwell (Addgene plasmid # 11344). (Timmons & Fire (1998). *Nature*, 395: 854).

[0143] For ingestible RNAi bioassays, sequence confirmed MIGGS-IRTG were cloned into an L4440 feeding vector between two T7 promoters in inverted orientation and transformed into an *E. coli* bacterial strain carrying IPTG-inducible expression of T7 polymerase, HT115 (DE3). (Timmons & Fire (1998). *Nature*, 395: 854). Modification of IRTG in this manner was previously demonstrated to induce the expression of dsRNA. (Timmons L, et al. (2001). *Gene*, 263, 103-112; Kamath RS, et al. (2000). *Genome Biol.* 2: 1-10.).

[0144] The HT115 (DE3) strain is an RNase III-deficient *E. coli* strain whose T7 polymerase activity is IPTG-inducible. The HT115 (DE3) genotype is as follows: F-, mcrA, mcrB, IN (rrnD-rrnE) 1, lambda -, mcl4::Tn10 (DE3 lysogen: lavUV5 promoter -T7 polymerase) (IPTG-inducible T7 polymerase) (RNase III minus), with tetracycline as a selectable

marker. (Kamath RS, *et al.* (2000). *Genome Biol.* 2:1-10). The standard heat shock protocol for transformation of L4440::IRTG and control construct was used.

5 **[0145]** Single colonies of HT115 bacteria containing cloned L4440 plasmids were picked and grown in a 5 mL LB culture with 50 mg/ml ampicillin (Amp). One mL of the liquid culture was saved for plasmid isolation followed by sequence confirmation of the L4440::IRTG clone. The recombinant bacterial clones were grown for 8 hours in liquid culture and were seeded directly on LB plates containing 1 mM IPTG and 50 mg/ml Amp for inducing the dsRNA. (Kamath RS, *et al.* (2000). *Genome Biol.* 2: 1-10). Seeded plates were allowed to dry under laminar airflow chamber and incubated at 37 °C temperature overnight.

10 **[0146]** For larval bioassay three to five 1-2-instar TH, DBM, and FAW larvae were placed on induced plates containing HT115 (DE3) cells containing the desired L4440::IRTG. Bioassays were conducted testing the TH larvae against MIGGS-IRTGS and controls listed in Table 1.

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Table 1. List of total MIGGS-IRTGS from TH tested.

<i>Manduca sexta</i> MIGGS RNAi Target Genes	NCBI Accession Number	Insect Biological Function	Midgut Expression	Insecticidal Activity
Ms_PGRP2 (SEQ ID NO: 3)	GQ293365.1	Immunity	Yes*	Yes
Ms_IMD (SEQ ID NO: 31)	Msex2.05477-RA	Immunity	Yes^	No
Ms_Toll2 (SEQ ID NO: 8)	EF442782.1	Immunity	Yes^	Yes
Ms_Sck (SEQ ID NO: 71)	Msex2.03324-RA	Immunity	Yes^	No
Ms_Akl (SEQ ID NO: 72)	Msex2.12479-RA	Immunity	Yes^^	No
Ms_Rel2A (SEQ ID NO: 5)	HM363513.1	Immunity	Yes^	Yes
Ms_Spz1A (SEQ ID NO: 47)	GQ249944.1	Immunity	Yes^	Yes
Ms_Cac (SEQ ID NO: 73)	Msex2.02793-RA	Immunity	Yes^	No
Ms_Dorsal (SEQ ID NO: 6)	HM363515.1	Immunity	Yes^^	No
Ms_Cad1 (SEQ ID NO: 39)	Msex2.04570-RA	Immunity	Yes^	No
Ms_Hemolin1 (SEQ ID NO: 1)	M64346.1	Immunity	Yes++	No
Ms_SPH3 (SEQ ID NO: 2)	AF413067.1	Immunity	DNA	No
Ms_Transferrin1 (SEQ ID NO: 11)	M62802.1	Immunity	Yes+++	No
Ms_Gloverin1 (SEQ ID NO: 74)	GH110649240	Immunity	Yes^^^	No
Ms_HPA18 (SEQ ID NO: 9)	AY672794.1	Immunity	No	No
Ms_βGRP2 (SEQ ID NO: 4)	AY135522.1	Immunity	Yes*	Yes
Ms_CHS2 (SEQ ID NO: 43)	AY821560.1	Structural Integrity	Yes*	Yes
Ms_βTub (SEQ ID NO: 75)	AF030547	Structural Integrity	Yes+	Yes
Ms_Suc1 (SEQ ID N: 44)	GQ293363.1	Structural Integrity	Yes*	Yes
Ms_VMP1 (SEQ ID NO: 14)	NA	Structural Integrity	Yes+	Yes
Ms_vATPaseE (Positive Control)	X67131	ATP Hydrolysis	Yes	Yes
Me_Catalase 1 (Negative Control)	AF170272	None	No	No

[0147] Phenotypic differences in the larval development on L4440::IRTG containing HT115 (DE3) plates were documented and compared with the larval growth on negative and positive controls containing HT115 (DE3) plates. The larval phenotypes for a given treatment with appropriate controls were only considered true and documented if they were reproducibly observed in 2/3 or 4/5 larvae, in at least two independent feeding experiments.

[0148] For sprayable RNAi, a 24-well plate-based bioassay system was developed using a modified cetyl trimethylammonium bromide method of MEGAscript RNAi kit following manufacturer's protocol (Thermo Scientific, USA) for large-scale purification of dsRNA against a given MIGGS-IRTG. Integrity of the dsRNA was determined by electrophoresis on 1% agarose gel and its concentration determined using NanoDrop UV-VIS spectrometer. Leaf discs of 1 cm² diameter were detached from *Nicotiana benthamiana* (for TH) or *Arabidopsis Col-WT* (for DBM) or wheat cultivar Bobwhite (for FAW) plants grown on field soil were drop inoculated with 0, 4, 8 or 16 µg of purified dsRNA in TE buffer. Air-dried dsRNA coated leaf discs were placed in the bioassay plate containing 1 mL of 1% Murashige and Skoog agar medium per well. Each well contained one leaf disc and was infested with conventionally reared three first instar TH or DBM or FAW larvae. dsRNA coated leaf discs were replaced once every 24 hours and insecticidal activity of each dsRNA measured as a function of larval mortality after five days continuous feeding. The RFB bioassays were conducted using a previously published flour disc assay protocol (Cao et al. (2018). *Int. J. Mol. Sci.* 19, 1079) with adult beetles.

[0149] For RNA-Seq analysis to test if the MIGGS pathway genes are induced by soil microbiome in FAW, wheat (*Triticum aestivum*) seeds were surface sterilized and planted in 4.5'' pots containing field soil or filled with 4:1 sterile turface:sand mix. Seedlings were grown a growth chamber at for 20 days and infested with ten first-instar FAW larvae per pot. Vigorous larval feeding activity was confirmed and larval samples collected for RNA-Seq analysis. A "pooled RNA-Seq" approach (Rajkumar et al. (2015). *BMC Genomics*. 16(1): 548) was used to obtain a snap shot of differential FAW gene expression in response to feeding on plants grown on microbe rich (field soil) and microbe depleted (sterile surface) substrate.

[0150] In order to demonstrate additional dsRNA delivery methods a plastidal dsRNA expression system was employed. Since high concentrations of long dsRNAs can be stably produced in plastids (Zhang et al. (2015). *Science*. 347(6225): 991-994), three of the most potent insecticidal TH MIGGS-IRTGS (SEQ ID NO: 3, 4, and 43) dsRNAs (dsMsPGRP2; dsMsβGRP2 and dsMsCHS2) were expressed by plastid transformation in tobacco plants in collaboration with

Plastomics Inc. following a previously published protocol (Zhang et al. (2015). *Science*. 347(6225): 991-994). Detached leaves of stable transplastomic lines expressing dsRNA against MIGGS targets were fed to TH larvae and assessed for insecticidal activity.

5 Results

[0151] Bioassays (Figure 1) indicated that the oral feeding activity of TH larvae on L4440::MsPGRP2 and L4440::MsVMP1 containing HT115 (DE3) plates resulted in growth impediment and/or mortality. Contrawise, the larvae growing on L4440::MeCAT1 containing HT115 (DE3) plates developed normally without any aberrant phenotypes.

10 **[0152]** The representative phenotypes of TH larvae at 192 hours post exposure (HPE) to larvae exposed to bacterially (HT115 (DE3)) expressed dsRNA against MIGGS RNAi targets MsPGRP2 (Figure 2A); MsVMP1 (Figure 2B) and negative control dsRNA against Cassava plant specific gene MeCAT1 (Figure 2C). The phenotypic effects leading to larval mortality were usually associated with the development of melanotic reaction, reduced appetite, growth and
15 development (Figure 2A and B).

[0153] Consistent with above, the TH larvae exposed to bacterially expressed negative control MeCAT1 dsRNA displayed vigorous feeding (area between the arrowheads Figure 3A). In contrast, the TH larvae exposed to bacterially expressed dsRNA against the MIGGS RNAi target MsPGRP2 displayed a curtailed feeding (representative picture, area between arrowheads
20 Figure 3B).

[0154] In general, melanization is a highly conserved immune response and is often associated with microbial infection of insects. (Kim SR, *et al.* (2005). *Insect molecular biology*, 14(2): 185-194. doi:10.1111/j.1365-2583.2004.00547). The intensification of melanotic response in TH larvae upon continued exposure to bacterially expressed dsRNA against the MIGGS RNAi
25 targets MsPGRP2 and MsVMP1 containing HT115 (DE3) plates strongly indicates an infection, possibly due to the defective clearance of opportunistic microbes ingested during feeding. Such defective clearance has been previously associated with the perturbation of gut microbial homeostasis. (Packey and Sartor (2009). *Curr. Opin. Infect. Dis.* 22(3): 292-301).

[0155] Closer observation indicated that the CR larvae feeding on bacterially expressed
30 dsRNA against the MIGGS RNAi targets MsPGRP2 and MsVMP1 displayed discernable mortality starting at day 5, reaching up to 100% and 80% mortality respectively, by day 8 (Figure 4).

[0156] To test if both the incidence and intensity of the observed phenotype could be delayed by clearing gut microbiotas, a GF set of TH larvae were also subjected to the above treatment with appropriate controls, in parallel. Interestingly, that the incidence of larval mortality was not only delayed, but also lower in GF larvae in comparison to CR larvae (Figure 4) was observed.

[0157] The incidence of larval mortality on bacterially expressed dsRNA against MIGGS RNAi targets MsPGRP2 and MsVMP1 plates also correlated with the development of melanotic reaction (Figure 5). Most notably, there was a concomitant delay in the development of melanotic reaction in GF larvae in comparison to CR larvae (Figure 5). All the phenotypes observed were statistically significant at a p-value between 0.001 and 0.05. No significant development of mortality or melanotic reaction was observed in larvae exposed to the bacterially expressed negative control MeCAT1 dsRNA (Figures 4 and 5).

[0158] Although MsVMP1 is not directly involved in immune responses, down regulation may abrogate microbial containment, resulting in an infectious phenotype (Figure 2B). Alternatively or in addition, down regulation of MsVMP1 may have resulted in wounding of the peritrophic matrix (the protective lining of the larval midgut) that also may have contributed to a sepsis mediated infectious phenotype (Figure 2B); this is further substantiated by delayed onset of infectious symptoms in the larvae (CR or GF) exposed to dsRNA against MsVMP1 in comparison with larvae exposed to dsRNA against MsPGRP2 (Figures 4 and 5). Both defective clearance and defective containment of opportunistic microbes have been previously associated with lethal phenotypes. (Packey and Sartor (2009). *Curr. Opin. Infect. Dis.* 22(3): 292-301). The schematic representation of dsRNA delivery vectors used for above study is indicated in Figure 6.

[0159] Most of the TH MIGGS RNAi targets disclosed herein (e.g., Table 1) are inducible and have been identified from open access midgut specific immunotranscriptome and/or other datasets (Pauchet Y, et al. (2010) *Insect. Mol. Biol.* 19:61-75; Odman-Naresh et al. (2013) PLoS ONE 8:e82015; Kanost MR, et al. (2016) *Insect Biochem. Mol. Biol.* 76:118-147; Brummett et al. (2017) *Insect Biochem Mol Biol.* 81: 1-9; Cao X, et al. (2015) *Insect Biochem. Mol. Biol.* 62:64-74; Zhong X, et al. (2012) *Insect Biochem. Mol. Biol.* 42(7): 514-524; Xia Xu et al (2012). *Dev Comp Immunol.* 38(2): 275-284). A validation study targeting two MIGGS RNAi targets MsHEM and MsSPH3 confirmed their preferential midgut specific manner (Figure

7) when injected with 75 CFU of gram negative *E. coli*. Further, literature curation confirmed the abundant expression of these MIGGS targets in the insects gut (Table 1).

[0160] Oral feeding of TH larvae on induction media containing a mixture of live *E. coli* and lyophilized cell wall signatures from gram positive bacteria and fungi (Figure 8) successfully induced (Figure 9) the MIGGS RNAi target genes listed in Table 1. The genes with immunity related function were induced between 24-48 hours post larval exposure to induction media and mostly not detected in the absence of induction (Figure 9A-C). While, the genes essential for midgut structural integrity are expressed under both conditions (Figure 9D). This, clearly suggests that the MIGGS RNAi targets are induced in response to microbes ingested during feeding.

[0161] High-throughput screening of microbe induced MIGGS RNAi targets (Figure 9) using bacterially delivered dsRNA screen identified 3 insecticidal candidates (Figure 10). These MIGGS RNAi targets include Toll receptor (MsToll2), Beta fructofuranosidase 1 (MsSuc1) and Beta tubulin (Ms β Tub) genes (Figure 10D-F). The insecticidal activity was manifested as stunted growth and development, loss of appetite and melanotic reaction (Figure 10D-F) as observed with the positive control MsVATPaseE treatment (Figure 10C) in comparison to the negative control treatment (Figure 10B). The developmental defects due to the bacterially expressed dsRNA exposure resulted in lethality ranging from 60-70% (Figure 11), with MsSuc1 being the most effective target for killing TH larvae. Mortality rates were statistically significant and comparable to the MsVATPaseE positive control.

[0162] Additionally, a combination of reciprocal best BLAST analysis and literature curation was used to identify the orthologs of TH MIGGS RNAi targets from the DBM transcriptomic resources (Table 2).

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Table 2. List of MIGGS-IRTGS identified from DBM transcriptome resources.

<i>Manduca sexta</i> MIGGS RNAi Target Genes	Insect Biological Function	Putative <i>Plutella</i> <i>Xylostella</i> Orthologs	Midgut Expression in <i>Plutella</i> <i>Xylostella</i>	Insecticidal Activity in <i>Plutella</i> <i>Xylostella</i>
Ms_PGRP2	Immunity	Px_PGRP2 (SEQ ID NO: 76)	Yes*	Yes
Ms_IMD	Immunity	Px_IMD (SEQ ID NO: 77)	Yes*	Yes
Ms_Rel2A	Immunity	Px_Rel (SEQ ID NO: 78)	Yes*	No
Ms_Tol2	Immunity	Px_Tol2 (SEQ ID NO: 79)	Yes*	No
Ms_Cac	Immunity	Px_Cac (SEQ ID NO: 80)	Yes*	Yes
Ms_Dorsal	Immunity	Px_Dorsal (SEQ ID NO: 81)	Yes*	Yes
Ms_Hemolin1	Immunity	Px_Hemolin1 (SEQ ID NO: 82)	Yes*	No
Ms_SPH3	Immunity	Px_SPH3 (SEQ ID NO: 83)	DNA*	No
Ms_Transferrin1	Immunity	Px_Transferrin1 (SEQ ID NO: 84)	Yes*	No
Ms_βGRP2	Immunity	Px_βGRP2 (SEQ ID NO: 85)	Yes*	Yes
Ms_Gloverin1	Immunity	Px_Gloverin (SEQ ID NO: 86)	Yes*	No
Ms_CHS2	Structural Integrity	Px_CHS1 (SEQ ID NO: 87)	Yes*	Yes
Ms_βTub	Structural Integrity	Px_βTUB (SEQ ID NO: 88)	Yes*	Yes
Ms_vATPaseE (Positive Control)	ATP Hydrolysis	Px_vATPaseE	Yes*	Yes
Me_Catalase 1 (Negative Control)	None	Ne_Catalase 1	No*	No

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Table 2 Cont. List of MIGGS-IR TGS identified from DBM transcriptome resources.

<i>Manduca sexta</i> MIGGS RNAi Target Genes	NCBI Accession Number	Putative <i>Plutella</i> Xylostella Orthologs	NCBI Accession Number
Ms_PGRP2	GQ293365.1	Px_PGRP2 (SEQ ID NO: 76)	AFV15800.1
Ms_IMD	Msex2.05477-RA	Px_IMD (SEQ ID NO: 77)	Px103008
Ms_Rel2A	HM363511.1	Px_Rel (SEQ ID NO: 78)	Px102858
Ms_Tol2	EF442782.1	Px_Tol2 (SEQ ID NO: 79)	Px106338
Ms_Cac	Msex2.02793-RA	Px_Cac (SEQ ID NO: 80)	Px116565
Ms_Dorsal	HM363515.1	Px_Dorsal (SEQ ID NO: 81)	Px100110
Ms_Hemolin1	M64346.1	Px_Hemolin1 (SEQ ID NO: 82)	ACN53154.1
Ms_SPH3	AF413067.1	Px_SPH3 (SEQ ID NO: 83)	XP_004322155.1
Ms_Transferrin1	M62802.1	Px_Transferrin1 (SEQ ID NO: 84)	BAF36818.1
Ms_βGRP2	AY135522.1	Px_βGRP2 (SEQ ID NO: 85)	QβVJ95.1
Ms_Gloverin1	GI110649240	Px_Gloverin (SEQ ID NO: 86)	ACN69342.1
Ms_CHS2	AY821560.1	Px_CHS1 (SEQ ID NO: 87)	KX420588.1
Ms_βTub	AF030547	Px_βTUB (SEQ ID NO: 88)	EUIZ7912.2
Ms_vATPaseE (Positive Control)	X67131	Px_vATPaseE	ABI89032
Me_Catalase 1 (Negative Control)	AF170272	Ne_Catalase 1	AF170272

[0163] It was demonstrated that 14 MIGGS RNAi target genes identified could also be induced in Bt resistant strain of DBM feeding on the induction media (Figure 12), thus suggesting that oral induction of microbe associated cell wall signatures could induce the MIGGS RNAi target genes in economically important DBM.

5 [0164] High throughput screening of microbe induced DBM MIGGS RNAi target genes (Figure 12) using bacterially delivered dsRNA screen indicated that 7/15 MIGGS RNAi targets tested showed insecticidal activity against a Bt resistant strain of DBM (Figure 13). The DBM insecticidal targets included PxPGRP2 (SEQ ID NO. 76), Px β GRP2 (SEQ ID NO. 85), PxCHS2 (SEQ ID NO. 87), PxCAC (SEQ ID No. 80), PxIMD1 (SEQ ID No. 77), PxDor (SEQ ID No. 81)
10 and Px β Tub (SEQ ID NO. 88). The insecticidal activity was manifested as stunted growth and development, loss of appetite and melanotic reaction (Figure 13D-H) as observed with the positive control MsVATPaseE treatment (Figure 13C) in comparison to the negative control treatment (Figure 13B). The developmental defects due to the bacterially expressed dsRNA exposure resulted in lethality ranging from 53-70% (Figure 14), with PxPGRP2 the most
15 effective target for killing DBM larvae (Figure 14). Mortality rates were statistically significant and comparable to the PxVATPaseE positive control (Figure 14).

[0165] In order to test if our MIGGS RNAi technology could work using multiple dsRNA delivery platforms we tested if dsRNA against the four TH MIGGS insecticidal targets could work in a sprayable format. We used dsRNA against MsPGRP2, Ms β GRP2, MsCHS2 and
20 MsVMP1 for sprayable RNAi assays (Figure 15) at a concentration of 0, 4, 8 or 16 μ g of purified dsRNA in TE buffer. Most efficacious leaf disc coated dsRNA was 16 μ g of dsRNA against MsCHS2 that caused 58% mortality. Similar, but slightly reduced, mortality was observed when insects were fed 8 μ g of leaf disc coated dsRNA against the same MIGGS targets. Observed mortality rates were statistically significant and comparable to those observed in TH larvae
25 exposed to dsRNA against a known positive control target MsVATPaseE (Figure 16). No statistically significant larvae death was observed when feeding on 4 μ g dsRNA (Figure 16), indicating that 8-16 μ g dsRNA per leaf disc was required to cause mortality in this assay. In addition to death, TH larvae feeding on dsRNA were characterized by developmental defects, loss of appetite, melanotic reaction and reduced growth compared to negative controls, indicating
30 significant detrimental impact of MIGGs targeting on insect health (Figure 17). The insecticidal TH MIGGS targets MsPGRP2, Ms β GRP2 and MsCHS2 will be henceforth referred to as core set.

[0166] Similarly, in order to test an additional delivery platform, the core insecticidal MIGGS RNAi targets MsPGRP2; MsβGRP2 and MsCHS2 were expressed by plastid transformation in tobacco plants in collaboration with Plastomics Inc. Detached leaves of stable transplastomic lines (Figure 18) expressing dsRNA against MIGGS targets indicated that the TH larvae feeding on leaves expressing dsRNA against MIGGS targets MsPGRP2 (B); MsβGRP (C) and MsCHS2 (D) display stunted growth, development, loss of appetite and melanotic reaction in comparison to negative control (A). The insecticidal activity is manifested as significant reduction in mean weights in comparison to negative control (E). The mortality rate was scored on a 0-3 score were 0, 1, 2 and 3 indicated ≤ 0 , 25, 50 or ≥ 50 mortality respectively. The transplastomic events confer significant mortality in comparison to negative control (F). Data is average of 6 replicates/treatment (N=24) $\pm$ SEM at $p \leq 0.001$ (***); $p \leq 0.01$ (**) and $p \leq 0.05$ (*). Clearly suggesting that the stably expressed dsRNA against the core MIGGS RNAi targets also impacts larval growth and development.

[0167] Next, we tested if our MIGGS RNAi technology can also work in a sprayable format against Bt resistant strain of DBM. We used the DBM orthologs of insecticidal TH MIGGS core set (PxPGRP2, PxβGRP2 and PxCHS2) and two newly discovered insecticidal DBM MIGGS targets (PxCAC and PxIMD1) for sprayable RNAi assays at a concentration of 0.1, 0.5 and 0.25 μ g. We observed lethality ranging from 53-67%, with PxPGRP2 being the most effective target for killing DBM larvae (Figure 19). Mortality rates were statistically significant and comparable to the PxVATPaseE positive control (Figure 19). In a manner similar to that seen for sprayable dsRNA against TH, in addition to death, DBM larvae exposed dsRNA treatments were characterized by developmental defects, loss of appetite, melanotic reaction and arrested growth (Figure 20). Clearly suggesting that dsRNA against the insecticidal MIGGS RNAi targets identified herein when used in sprayable format is also effective against Bt resistant strain of DBM.

[0168] Most of our MIGGS RNAi target gene induction procedures thus far relied upon either direct injection or oral feeding of extraneously supplied microbial signatures. To determine if our MIGGS RNAi target genes are induced under field conditions, we exposed the larvae of economically important lepidopteran pest FAW to wheat seedlings grown on microbe rich and microbe depleted plants (Figure 21). Pooled RNA-Seq analysis indicated that plants growing on field soil caused preferential up-regulation of MIGGS pathway genes in FAW. In total, 100

differential expressed genes were identified, thirty of which were MIGGS pathway related genes (Figure 22).

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Table 3. List of MIGGS-IRTGS identified from using RNA-Seq approach in FAW.

<i>Spodoptera frugiperda</i> MIGGS RNAI Target Genes	Query_Contigs_ID*	Putative Insect Biological Function	Midgut Expression*	Insecticidal Activity
Sf_PGRP1 (SEQ ID NO: 89)	rep_c7951	Immunity	Yes	Yes
Sf_Attacin (SEQ ID NO: 90)	rep_c9395	Immunity	Yes	Yes
Sf_Ctypelectin15 (SEQ ID NO: 91)	joint2_rep_c488	Immunity	Yes	No
Sf_Galectin4 (SEQ ID NO: 92)	rep_c25253	Immunity	Yes	No
Sf_Lysozyme (SEQ ID NO: 93)	rep_c18992	Immunity	Yes	No
Sf_Hemolymph proteinase 10 (SEQ ID NO: 94)	c12881	Immunity	No	Yes
Sf_Trypsin like Serine protease (SEQ ID NO: 95)	rep_c48453	Immunity	Yes	Yes
Sf-C type Lectin 6 (SEQ ID NO: 96)	joint2_rep_c448	Immunity	Yes	Yes
Sf_Serine protease 13 (SEQ ID NO: 97)	rep_c1904	Immunity	Yes	No
Sf_Cecropin (SEQ ID NO: 98)	rep_c42380	Immunity	Yes	Yes
Sf_Relish (SEQ ID NO: 99)	c13122	Immunity	Yes	No
Sf_Toll2 (SEQ ID NO: 100)	joint2_c3284	Immunity	Yes	No
Ms_βGRP2 (SEQ ID NO: 101)	EF641300	Immunity	Yes	Yes
Sf_c20042 (SEQ ID NO: 102)	c20042	Immunity	Yes	No
Sf_rc16438 (SEQ ID NO: 103)	rc16438	Immunity	Yes	Yes
Sf_L2rC2367 (SEQ ID NO: 104)	joint2_rep_C2367	Immunity	Yes	No
Sf_CHSB(SEQ ID NO: 105)	AY525599	Structural Integrity	Yes	Yes

[0169] Most notably, FAW orthologs of TH insecticidal targets including PGRP2, β GRP2 and IMD were captured in the data set. This discovery indicated that MIGGS pathway genes are up regulated in response to insect feeding on plants exposed to microbes in the field soil.

5 [0170] Preliminary experiments were performed to screen the insecticidal activity of 17 FAW MIGGS RNAi targets discovered during RNA-Seq (Table 3, above) in which dsRNA against the FAW orthologs of insecticidal TH MIGGS core set (SfPGRP2 (SEQ ID NO. 89), Sf β GRP2 (SEQ ID NO. 101) and SfCHS2 (SEQ ID NO. 105) and three newly discovered MIGGS targets SfCTL (SEQ ID NO. 96), SfRC (SEQ ID NO. 103) and SfGAL (SEQ ID NO. 92)

10 from RNA-Seq were fed to FAW larvae at 0, 4, 8 or 16 μ g-purified dsRNA in TE buffer. FAW 1st instar larvae were allowed to feed on dsRNA coated leaves following the bioassay described for TH above. Data indicated that FAW larvae (Figure 23) exposed to pure dsRNA against SFCHS2 (B); SF β GRP2 (C); SFPGRP2 (D), SFRC (E), and SFCTL (F) causes reduced growth, development and loss of appetite in comparison to negative control treatment (A) resulting in

15 significant weight reduction (G) and mortality (H) at 8 and 16 μ g of dsRNA concentration. The rates of mortality was scored on a 0-3 score were 0, 1, 2 and 3 indicated ≤ 0 , 25, 50 or ≥ 50 mortality respectively. The dsRNA treatments imposed caused statistically significant reduction in mean weights (G) that also translated into significant rates of mortality (H) in comparison to negative control (Figure 23). Screening of insecticidal activity of additional MIGGS RNAi target

20 genes identified from the RNA-Seq dataset indicated that 16 μ g of leaf disc coated dsRNA against MIGGS RNAi targets SfTSP (SEQ ID NO. 95), SfAtta (SEQ ID NO. 90), SfCec (SEQ ID NO. 98) and SfHp10 (SEQ ID NO. 94) caused statistically significant reduction (Figure 24) in mean weights (A) that also translated into significant rates of mortality (B) in comparison to negative control. Data is average of 3 replicates/treatment $\pm$ SEM at $p \leq 0.001$ (***); $p \leq 0.01$ (**) and $p \leq 0.05$ (*).

25

[0171] Experiments with an economically important coleopteran pest RFB were also conducted to test if MIGGS-IRTGS targets identified by a combination of reciprocal best BLAST analysis and literature curation (Table 4) are insecticidal against the order coleoptera.

[0172] Preliminary feeding trails with 1 μ g of purified indicated that dsRNA against RFB

30 MIGG RNAi targets TcPGRP2 (SEQ ID NO. 107), Tc β GRP2 (SEQ ID NO. 108), TcMDGP (SEQ ID NO. 109) and TcCHS2 (SEQ ID NO. 110) is insecticidal to the adult RFB beetles. Significant rates of RFB mortalities were observed (Figure. 25) when scored on a 0-3 scale were

0, 1, 2 and 3 indicated ≤ 0 , 25, 50 or ≥ 50 mortality respectively in comparison to the negative control treatment. Data is average of 3 replicates/treatment $\pm$ SEM at $p \leq 0.001$ (***); $p \leq 0.01$ (**) and $p \leq 0.05$ (*).

5 Table 4. List of MIGGS-IRTGS identified from RFB transcriptome resources.

Spodoptera frugiperda MIGG RNAi Target Genes (SEQ ID NO)	Query_Contigs _ID	Putative Insect Biological Function	Midgut Expression	Insecti- cidal Activity
TcPGRPL0 (SEQ ID NO: 106)	DT786101.1	Immunity	Yes*	No
TcPGRP2 (SEQ ID NO: 107)	XM_965754.3	Immunity	Yes*	Yes
TcβGRP2 (SEQ ID NO: 108)	XM_966587.4	Immunity	DNA	Yes
TcMDGP (SEQ ID NO: 109)	XM_971351	Structural Integrity	Yes**	Yes
TcCHS2 (SEQ ID NO: 110)	EFA 10719.1	Structural Integrity	Yes***	Yes

[0173] One possible reason for larval mortality could involve down regulation of MIGGS-IRTGS transcripts upon feeding on exogenously supplied dsRNA against the target genes. Preliminary RT-PCR data indicated that the larval phenotypes (Figure 17) also correlated with down regulation of target transcripts (Figure 26).

[0174] Importantly RNA-Seq analysis indicated that the MIGGS-IRTG pathway targets are induced by soil microbiome indicating that our novel RNAi approach could be effective even under field conditions.

[0175] Given the ease of identification, high specificity, and applicability to diverse pests and delivery platforms, RNAi silencing of the MIGGS-IRTG pathway genes identified, this approach offers an unprecedented potential as a novel pesticidal strategy.

[0176] The translation of these preliminary findings into a pesticidal RNAi technology against economically important pests might lead to sustainable alternatives including but not restricted to the methods described anywhere herein.

[0177] Additionally, the proposed approach will shed more light into understanding the tri-trophic interaction between plants-microbe-insect interactions as it pertains to sustainable insect pest protection.

5 Sequences

[0178] SEQ ID NOs: 1-14 and 31-44 are representative examples of *M. sexta*-RNAi target gene sequences.

[0179] SEQ ID NO: 15 is non-insect gene sequence that encodes for catalase 1 from cassava (*Manihot esculanta*).

10 [0180] SEQ ID NOs: 16-29 are coding region sequences of representative *M. sexta*-RNAi target genes.

[0181] SEQ ID NO: 30 is the coding region sequence of catalase 1 from cassava (*Manihot esculanta*).

15 [0182] SEQ ID NOs: 45-70 are 5'UTR and 3'UTR region sequences of representative *M. sexta*-RNAi target genes.

[0183] SEQ ID NOs: 71-75 are the coding region sequences of additional representative *M. sexta*-RNAi target genes.

[0184] SEQ ID NOs: 76-88 are the coding region sequences of representative *P. xylostella*-RNAi target genes.

20 [0185] SEQ ID NOs: 89-105 are the coding region sequences of representative *S. frugiperda*-RNAi target genes.

[0186] SEQ ID NOs: 106-110 are the coding region sequences of representative *T. castaneum*-RNAi target genes.

25 [0187] SEQ ID NOs: 111-119 are representative examples of *Manduca sexta* insecticidal dsRNA sequences.

[0188] SEQ ID NOs: 120-126 are representative examples of *Plutella xylostella* insecticidal dsRNA sequences.

[0189] SEQ ID NOs: 127-135 are representative examples of *Spodoptera frugiperda* insecticidal dsRNA sequences.

30 [0190] SEQ ID NOs: 136-139 are representative examples of *Tribolium castaneum* insecticidal dsRNA sequences.

[0191] > *M. sexta*-Hemolin (MsHEM); M64346.1 (SEQ ID NO: 1)

ATGGTTTCAAAAAGTATCGTCGCTTTGGCTGCGTGCGTCGCAATGTGCGTAGCCCAGCCA
GTGGAGAAGATGCCTGTGCTGAAGGACCAACCCGCTGAAGTCCTCTTCCGGGAGTCTCAG
GCCACCGTTCTCGAATGTGTTACCGAGAATGGCGATAAAGATGTCAAATATTCTTGCGAA
5 AAAGACGGCAAAGAATTCAAATGGCAGGAACACAATATCGCCCAGCGCAAAGACGAAGGC
AGCCTGGTCTTCTCAAGCCCCGAGGCTAAAGATGAAGGCCAATACAGATGTTTCGCTGAG
TCGGCCCGCGGAGTCGCCACCTCCACATCATCTCCTTTAGAAGGACCTACATGGTCGTA
CCTACTACTTTTTAAGACTGTAGAAAAGAAACCGGTAGAAGGGTCATGGCTCAAACCTTGAG
TGCAGCATCCCCGAAGGTTATCCTAAACCTACTATTGTATGGAGAAAGCAGCTTGGTGAA
10 GACGAAAGTATAGCAGATTCTATACTGGCACGTCGTATTACACAATCTCCAGAGGGGAGAC
CTGTACTTCACGAGCGTCGAGAAAAGAAGACGTAAGCGAAAGCTATAAATACGTTTGCGCT
GCTAAGTCACCGGCTATTGATGGGGATGTCCCTCTTGTTGGATACACTATTAAGGCTTA
GAAAAGAATACAAATCAGAAAAACGGTGAGCTGGTCCCGATGTACGTCAGTAATGATATG
ATAGCTAAGGCCGGAGACGTTACTATGATCTACTGCATGTATGGTGGAGTCCCAATGGCT
15 TACCCCAACTGGTTCAAAGACGGTAAGGACGTGAACGGCAAACCGAGCGACCGCATCACC
CGCCACAACAGAACCTCCGGCAAAAGACTGTTTCATCAAGGAGACGCTGCTCGAAGATCAG
GGCACTTTTACTTGCGACGTGAACAACGAAGTCGGCAAGCCACAGAAACATTCCGTCAAA
CTTACCGTAGTCAGTGGACCCAGATTTACGAAGAAACCAGAAAAGCAAGTCATCGCTAAG
CAGGGCCAGGACTTTGTAATCCCCTGTGAAGTATCCGCCTTACCGGCCGCCCTGTCTCC
20 TGGACGTTCAACGCCAAGCCCATCAGCGGCAGCCGCTGGTAGCCAGCCGAGCGGACTG
ACCATCAAGGGCATCCAGAAGTCTGACAAGGGTTATTATGGCTGCCAGGCCCAACGAG
CACGGAGATGCCTACGCTGAGACGCTCGTGATTGTTGCTTAA

[0192] > *M. sexta*-Serine proteinase homolog 3 (MsSPH-3); AF413067.1 (SEQ ID NO: 2)

ATGTTGTTGCTTCTGTATTGTCTTGTGGCGCCTCCGCGCCGTTCTTTATTGCAGCGGAC
CAAGGCAGCCCTGACCTGCCTTTAGCTACCGAACCACCAACAGAATGCGGAACAATAGCA
CCTGATGATAGCTTAGTATTAGATGGGTCCGTTGGTAAAAGTGACAAATTACCTTGGTAT
GCTATTATCTACACAACCACCACCCGGCCATACAAGCAGATCGGTGGAGGAACCCTCATC
30 ACTCCTTCAGTAGTAATCTCAGCCGCTCACTGTTTCTGGCGCAATGGTGAGGTTCCATCT
AAGGATAATTACGCCGTGGCGCTCGGCAAGACCCATAGTGCTTGGAATAGCCATGCCGAT
GTAAACGCTCACAAGTCTGATGTAAAAGAAATACACATACCACCGCAGTTTAAGGGAAGG
AACACTAATTATCGGAATGATATAGCAATCGTGGTCATGTCAGACCCTGTGACCTACAAA

GTGGACATCCGCCCTATCTGTTTGAAC TTCGATGTACAATTTGAAAGACTGCAATTAAAA
 GACGGCATTATGGGGAAGATCGGCACATGGAATGTAAGTCGTGAGACACTGAAACTATCG
 AAAACATTAAAAAGTGGTGGAGAATCCATACATTGACGCAGCGACTTGTATTAGTGAGTCT
 CCGGCAAGCTTCAGAAATTCCATCACTGCGGACAAAATATGCATCGGATACGTTAACGGC
 5 ACCGGGCTATGTAGAGGTGATGGCGGCGCTGGGGTGGCTTCCCTAGCCAGGAACAAGGA
 GTGCAACGTTACTACCTCAGAGGTGTTATATCTACAGCCCATACCAGCGATGATGGCAAC
 TTATGTGCAGATGGATTTGTAAGTCCACTGCTATAGGCCATCACGAACATTTTATCAAA
 CAGTTTATAAGCGTTTAG

10 [0193] > *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2);
 GQ293365.1 (SEQ ID NO: 3)

ATGGCGAGCTTCGCTTTAATAGTTATCCTTAGCGTAATTGGCTTTATATCGGCCTATCCT
 AGTCCTGAAGGTTACAGTTCTGCCTTCAACTTTCCATTTCGTAACCAAGGAGCAGTGGGGC
 GGCAGGGAGGCACGCACGTCGACGCCACTCAACCACCCAGTGCAGTTTCGTGGTGATCCAC
 15 CACAGTTACATTCCCGGCGTGTGCCTCAGCCGGGACGAGTGC GCGCGCAGCATGCGCTCC
 ATGCAGAACTTCCACATGAACAGTAACGGGTGGAGTGATATTGGATACAACTTCGCTGTC
 GGCGGTGAAGGGTCGGTGTACGAGGGCCGCGGCTGGGACGCGGTGCGCGCACACGCAGCT
 GGCTATAACAGTAACAGTATCGGCATCGTGCTCATCGGCGATTTTGTTCAAACCTCCCG
 CCGGCGGTGCAAATGCAAACCACACAAGAATTGATCGCAGCGGGCGTGCGACTCGGTTAC
 20 ATCAGGCCCAACTACATGCTCATCGGGCATCGTCAGGTCTCCGCCACTGAGTGCCAGGA
 ACCAGACTCTTCAACGAAATCACCAACTGGAACAACTTCGTGAGGATATGA

[0194] > *M. sexta*-Beta-1, 3-glucan-recognition protein 2 (MsβGRP2);
 AY135522.1 (SEQ ID NO: 4)

25 ATGTGGATCAAGAGCGTCTGTTTGTTCGCAACCATTGCGGGCTGCTTGGGCCAGCGAGGG
 GGTCCATACAAGGTGCCTGATGCGAAACTCGAAGCTATCTACCCCAAAGGCTTGAGAGTC
 TCTGTGCCAGATGATGGCTACTCCCTATTTGCCTTCCACGGCAAGCTCAATGAGGAGATG
 GAAGGTTTAGAGGCTGGCCATTGGTCCAGAGACATCACCAAAGCGAAGCAGGGCAGATGG
 ATATTTCAGAGATAGGAATGCTGAGCTGAAGCTTGAGACAAAATTTACTTCTGGACTTAC
 30 GTTATTAAGGATGGATTGGGATACAGGCAGGACAATGGAGAATGGACTGTTACAGAATTC
 GTCAATGAGAACGGTACAGTGGTGGACACTAGTACAGCGCCGCCACCAGTAGCACCCGCC
 GTTTCAGAGGAAGATCAATCGCCAGGTCCTCAGTGGAGACCTTGCGAAAGATCCCTGACT
 GAGTCCTTGGCCCGCGAACGCGTTTGCAAAGGCAGCCTTGTCTTTAGCGAGGACTTTGAT

GGTTCCAGTTTGGCCGACTTGGGCAATTGGACCGCTGAAGTCAGATTCCCTGGCGAACCG
GACTACCCGTACAACCTTGTACACTACGGACGGCACTGTGGGATTTCGAAAGTGGGTCTCTG
GTGGTGAGACCCGTCATGACCGAGTCCAAATACCACGAGGGCATCATATACGACCGCCTC
GACCTTGAGAGATGTACAGGACAGCTGGGTACGCTGGAATGCAGGCGAGAGAGCAGCGGC
5 GGTCAGATTGTACCACCTGTGATGACAGCTAAACTGGCCACTCGACGCAGCTTCGCGTTC
AAGTTTCGGCAGGATCGATATAAAGGCGAAGATGCCGCGCGGGGACTGGTTGATACCAGAA
CTCAACCTCGAACCTTTAGATAACATATACGGCAACCAGCGATACGCTTCGGGTCTCATG
CGGGTCGCGTTCGTGAGAGGAAACGATGTATACGCCAAGAAGCTCTACGGAGGTCCGATA
ATGTCCGACGCGGACCCGTTTCAGGTCCATGCTGTTGAAGGACAAGCAAGGGTTGGCCAAC
10 TGGAAATAATGATTACCACGTCTACTCGCTGCTGTGGAAGCCTAACGGTTTAGAGCTGATG
GTGGACGGTGAAGTGTACGGCACCATCGACGCTGGCGATGGCTTCTACCAGATTGCGAAG
AACAACCTCGTGAGCCACGCCTCGCAGTGGCTCAAGGGCACCGTCATGGCGCCGTTTGAT
GAAAAGTTCTTCATCACTCTGGGTCTTCGCGTGGCGGGTATCCACGACTTCACGGACGGT
CCGGGCAAACCTTGGGAGAACAAAGGCGACCAAGGCCATGATCAACTTCTGGAACAATCGG
15 TTCCGCTGGTTCCCCACGTGGCACGACACCAGTCTTAAAGTCGACTACGTCAGAGTCTAT
GCTCTTTAG

[0195] > *M. sexta*-Relish family protein 2A (MsREL2A); HM363513.1 (SEQ ID
NO: 5)

20 ATGTCCCTCTTGTTCCAAGCGACTATGATCCCAGTGAATCGTCCAAATCTCCACAAAAGTATT
TGGGAGTCAGGAGGATACAGTTTCCGTCGCAACAAGTTCCTCAATTGACTTCTAACTTA
ACAGAAATTGTCTGTTGATCACAGCTATAGATACAATGGAAATGGACCATATCTACAGATC
ACAGAGCAACCACAGAAATACTTTCGGTTCCGTTATGTTAGCGAGATGGTGGGAACACAT
GGATGTTTGCTTGGCAAATCTTATACAACAAACAAAGTTAAAACTCATCCGACAGTTGAA
25 CTCGTGAATTACACCGGTGAGCCCTGATAAAGTGCCAACTATCGCAAAACAAGAGCGAA
GACGAACACCCGCACAAACTGCTCGATGAACAAGACAGAGACATGAGCCACCACGTTCCC
GAGCACGGCAGTTATAGAGTGGTATTTGCTGGTATGGGTATAATTCATGCTGCCAAAAAG
GAAGTTGCGGGGTGGCTCTATAGAAAATATATACAGCAGAACAAGAATGAAAAGTTTAAT
AAGAAAGAGCTCGAAGCGCATTGTGAGAGGATGTCCAAAGAGATCGATTTAAATATAGTT
30 AGACTGAAGTTTAGCGCTCACGATATTGACACTGGCATTGAAATTTGCCGGCCAGTGTTT
TCTGAACCCATTTATAATTTGAAGTGTGCGTCTACGAATGATTTGAAAATATGCCGCATA
AGCCGTTGTTACGGTAGACCGAGAGGCGGCGAAGATATCTTCATATTTGTGAAAAGGTC
AACAAGAAAAACATCCAAGTTCGGTTCTTTAGACTGGAAAACGGGGAGCGCACCTGGTCA

GCGATGGCGAACTTTCTGCTAAGCGATGTTACCACCAATACGCTATCGCTTTTAGAACG
 CCACCGTACGTCAATCACCAAATTTCTGAAGACGTGCAAGTTTTTATAGAACTCGTACGC
 CCTTCAGACGGTAGGACGAGCGCTCCCATGGAGTTCACATACAAGGCTGAGCAAATCTAT
 AAACAGAACAAGAAACGTAAAACTACTTCGTCTGCTACTCGTCGCTCGACAGCTCCTCAGGT
 5 TCGGCCGGTTCAATTAAAAGCATCAGCGAACTGCCCCGCGCCGTTGTTTTTGTGAAAAAC
 GTAAGTTTTTTCTATGACACATTACTCATTCTTCAACCCATGACGAATCTATAA

[0196] > M.sexta-Dorsal (MsDor); HM363515.1 (SEQ ID NO: 6)

ATGCTTGTGACGTTATGCGGCGGGAACATAGTGGATTGTCGTTAACAAAACTAATCAT
 10 TATATGTCACCAAAATCATATGTGCCAGGAAATGGTTATGACGCCGCCGTAATCCTAGGT
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 CACACGCAGCCCCAGCCGCTGCAAATGCCGTACGTGGTCGTCGTGCAGCAGCCCGCCAGC
 AAAGCGCTCAGATTTTCGATATGAGTGCGAGGGCAGATCAGCCGGTTCGATTCCCGGCGCG
 15 TCGAGCACGCCCCGAGAACCGAACCTTCCCCGCCATCAAGATAATCGGCTACACCGGCACC
 GTCTCCATCGTAGTGTCGTGTGTCACCAAAGATGAGCCTTGCAGGCCGCACCCACACAAC
 CTGGTCGGGCGCGACCACTGCGACCGCGGCGTGTTCTCCGTCCGCATCGAGATCACCGAC
 GAGAATAACGAATACCAGTTTCGGAACCTGGGCATACAGTGCGTCAAGCGGCGCGACATC
 GGCGAGGCGCTGCGGATCCGAGAGGACCTGCGCGTCGATCCGTTCAAAACCGGCTTCACC
 20 CACCGGAACCACCCGCAAGGCATCGATCTGAATGCAGTGCGGCTCGCGTTCCAAGTGTTT
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 TACGACAAGAAGGCCATGAGCGACCTGCTCATCGTGCGCGCGAGCCACTGCGCCGGCCCCG
 GCGCGCGGCGGCACGCAGGTCTGCTCTGTGAAAAGGTGACTCGCGAGGACACCGTG
 GTGGTGTTCTACCAGGAGGACAACAACCGCGTGCTGTGGGAGGAGATGGCGATCATCATC
 25 GTGGTGACAAACAGTATGCCATAGCGTTTCGAGACGCCGCCATACAAGAACCCAAACATT
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 TCAGAAAAGAAATCCCCAATCGCAGCCAATTACGCACAAGGTAACGGTGGAGGACTTTGAA
 TCGACAACATAAAGATATTTTACGCGAAGCACTGACAACAGTAATTACGGTTGGGATGCG
 30 GTTCCGGTCACGTACAATGGAAGAAAGAAGTTTGCTATTGCCCCAAGAGGAGCTAA

[0197] > *M. sexta*-Spätzle (MsSPZ1A); GQ249944.1 (SEQ ID NO: 7)

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CAACCTGACAGACGGATAGCGGGACGGTCAGCACAAATACGAACATTTAAGAACAAACGAG
5 AGGTCTCTCCCGGTCTACAGCGAGACCCAGAGGATACAAGCAGAAGAGAGAAGAAGACAC
AGTTCGAGACTAGAAGAACCGAGACAACGTGCTGAGAATGGTTCATATAAGATATTGAAT
AACCCCTCCGAAACCCTGTATTACTAATAGGAGAAGTCAAATTGATTTCGTGCAATGATAGG
GTAGTGTTCCCCGGTCCGACTTCAGAAAGGTTCGTACGTACCCGAAGTGCCAGAGGAATGC
AAGAAAAATCGGCATATGCGACAGTATACCGAATTACCCAGAAGAACACGTAGCTAATATT
10 ATATCTCGACTTGGAGACAAAGGAAAAGTATTACAAATAGACGAACTGGACGTATCAGAC
ACTCCAGATATCGCCAGAGGTTGGGTCCGCAGGAGGACAACATGGAACATATGTAGCTTT
AGAGAAAAGATTTTTTACCCCAAGGCAGCGCCAGACAAAGATGGAAATTGGTTCTTCGTT
GTGAATTCAAAGAAAACCCAGTACAGGGTTATAAAGTTGAAATTTGCGACCGTCAGCAA
TTACCATGCGCGGAGTTCGCGAGCTTCCAACAGGGATATGAAGCGAGGTGCATCCAGAAA
15 TACGTTCGCCGGACCATGTTGGCGTTGGATCCCAAGGGTCAGATGACCGACATGCCCTT
AAAGTGCCCGAGCTGTTGCTCATGCGTGGCCAAATTGACAATCATATGA

[0198] > *M. sexta*-Toll receptor (MsTOLL); EF442782.1 (SEQ ID NO: 8)

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20 GTCAGTGGACACTTACCGCGTCCCGAGTGC GCGCCAGCCGCAGATTGCCAACTTATACGA
GACAACATAATCGATGGATATGCACAATTCTACTTCAACGTATCAGGACATGAAGTGAAA
TTTGAACATTACATCGGAAACGACTTCGATGTGCAATTGTCATGCAATTACATCGCCATG
GACAACGCAATGCTGCCGCGGTCTCAACGACCTTTTCAGTCAACGTAATAGTGGTTAAA
GAATGTGCTTTGCCAAGAAGTGGGTCAATCGATGCCGCTGTCGCTGCACTTAATATCAAC
25 GTTTTGACGGAGCTGACTCTGGACAAATTCCTAGAGCCGGCGGTGATCACGCGGCACAT
CTTACCAGTTTACAACGACTAGAGAGGCTGGAGCTACACGGTAACTCAAACACAAGCCTC
GCCCCGGCGCACTGGCCGCGCTCTCCGCCGCGTCCGCACTGAAATGTCTTGTATTGCAT
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30 TTCGTAATCGATACACATTATCCTGTCGTCGTGAATGTGAGCAACGCCGTTGCGCTCAGA
GACTTGCACATAAATACCCCAAGTACTGTGTTGACCGAAGACGTGCTCCCGTCGTCACTC
AACTCACTTGAAC TAGAGGGGTGGAACGAAACGCATCCGGTGCCTAAGACACGTGTGTGTA
CTACTTAAGGAAC TTAATGTAATCGGCACCGACAATGATGCCTATCCGGTGA CTCTCCC

GACGAGTGGCTGTCCAACCTGCGGACAGCTGAGGGATCTTGAAATGATCTCCGTGCCGATT
AGCGCCGTACTTCCGGCGCGGATGCTGGCTAACGCAATTAGGCTTGAAACGATTACTATC
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ACACTCGACTTGTCCAACAATCAACTTGCATCGTTGCCCAGAAAATTATTTGAGCACACG
5 AAGTTACTACGCAGTCTCATACTATCGAACAATCAGCTGACGAGCGAGGTAGTGTGGACG
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TTATGTTCCACGACTCAGTGTGAGCAGGTCCCTCACCCTGAGTTCACTGACGGGGCTA
AACTATCTCCATCTGAGCAACACAGGAGTATCACACGTGTGCTCCGACTGGCGAGAAAAG
CTAACCTACCTCAGCAATCTCAACTTAAGGGACAACCCCATCACTCTCTACAATTTGGCG
10 GATCTACAGTTTCGTGCAATCTGGGTGGACGCTCGTGTGTATTTAGGACATTTCAAGCAG
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15 ACGTGCCGTATCCGCGACGACATTCAGTACAAACAAGTGGTCGTTGTGCACTGCACCGGA
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AACAACATATCATACCTCGCCGCGGCCGACGTATCGCCGAACATCGTGGAACCTCGATCTA
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20 CTGCTCAAACCTGACTCAAAGCTGCTTGACAGAAAGGACGTGAAATGTGAGAACGACGCG
CAGATTACCTTGGCGATGCTGAAATTATGTACTAAGTCATCCAATGGGCTGATGTACTTG
CTGTTCCCTGTTGCTGTTACTCGCATTTGTGCTAACCGGACTGCTCGCACGAACCGCAATT
CGCCTGCGCATCAAATGATCCTCATGAGACTGGGTGGATGTCGAGACTACTGGAGCCC
GCGGACGACGATCGCCCGTACGACGCGTTTGTGTCTTTCGCACACGAGGATGAGGAGCTG
25 GTGATGGAGCAGCTGGCGGCACGGCTCGAGAGCGGCTCGCGGCCGTACCGACTGTGTCTG
CACTACCGCGATTGGGCGCCAGGCGAGTGGATCCCGGCGCAAATAGCGGCTTCGGTGCGG
GCCTCTCGGCGCACGGTGGCGGTTGTGTCGGCGCACTACTTACAGTCGGGCTGGGCGCTT
GCCGAGATCCGGGAGGCGACCGCAGCCTCGCTGCAGGAAGGCATGCCACGTCTCATCATC
GTGCTGCTCGACGAGACCGACCGGTTGATGCTCGATATAGACCCTGAGTTGCACGCCTAT
30 GTGCGCAACAATACCTACGTGCGCTGGCATGATCCATGGTTTTGGGAGAAGCTGAAGCAG
GCGCTGCCTCCACCGCGGGAACAACGGTCGCCAATAGCTCCGTCGCTACCAGCGCTGGCG
CTGTCCCATGACAGCCTAACTCTGCGCACGTACTCTCCAGAGAAAGTGACCCAGCGCCC

GCTGCTAAGCCGGCGCACACTCCGCACGAGACGGACGAGCCAGCGCCGGGCGCGAGTCCT
TGCTACAAATGA

[0199] > *M. sexta*-Scolexin A (MsSCA1); AF087004.1 (SEQ ID NO: 9)

5 CGGCAGTCGGTTGTGTTGGCAGTGGCGGCGGTGCTCTTCGGGTGCGCGTGCGCAGCGCCC
AATCCTGGGCGCCAACGACATACAACCTTAATCAAAAATTAAGTATCGAAGCTAAGGGGGCA
AAGCAGCCAATTGATACGAGGGCAGTGAAGGAACGGTATCCATACGCAGTTCGGAGTTTC
GGAGGCTTCTGCGGAGGAACCATTTATCAGTCCCACCTGGATCCTGACCGCCGGCCACTGC
TCGATACTCTATGCGGGGAGCGGCCTACCGGCCGGCACCAACATTACCGAGGTATCTAGC
10 TTGTACCGCTTCCCCAAGCGGCTCGTCATACACCCGCTCTTCTCCATAGGACCCGTCTGG
CTCAACGCTACGGAGTTCAACCTCAAACAGGCGGCTGCACGATGGGACTTCTTGTGATA
GAACTGGAGGAACCGCTGCCGTTGGACGGCAAGATCCTGGCGGCTGCGAAGCTCGACGAC
CAGCCCGACCTCCCCGCAGGCCTCGACGTGGGCTATCCGAGCTACAGCACCGACACCTAC
GAGGCTAAGATACAAAGCGAGATGCACGGAAAGAAGCTTTCGGTTCAATCTAACGAGGTG
15 TGCTCGAAGCTAGAGCAGTTCAAGGCGGAGGACATGTTGTGCGCCAAGGGACGTCCACCG
CGATACGACTTCGTCTGCTTCAGCGACAGTGGCAGTGGGCTAGTAGACAACAATGGTCGC
CTAGTCGGCGTGGTGTCTGTTGGGCCGAGAACAACGCTTTCGAGTGCCGCAACGGCAACCTG
GCGGTCTTCTCGCGAGTGTCCAGCGTACGCGAGTGGATCCGACAAGTCACCAACATATAA

20 [0200] > *M. sexta*-Hemolymph proteinase 18 (MsHP18); AY672794.1 (SEQ ID
NO: 10)

ATGGTTTATATTTTAATAATTTTAGTGATTTGCAATTTTAGTTGTATTAGTTGTCAGTCC
GGGACAGTGGAAAGCAGGATTCATTTTAAAGATGAAGGGCCGGAATGTTATGATGCAAAT
AAAAAGGGCACCTGTGTTAGTGCTCACAGATGCCTTGATGTAGTTAGAAAACCTTAAAGAC
25 GGAGAGAAACCCACGATATGTGGCTACCAAGGCACGGAACCAATGGTGTGTTGCACAGAC
TGTA CTCTGGTTGATAATATTAGTAATTTGGTCGTAAGTTCCATATCCGGGTACCTGTGG
AAGGATGGTCAGAAAGCGTGGGACAAATGTCTGGAATACGTTGACAAGCTGTCTGTAACCA
TGCGCTTCAACCTACTCCCACTACCTCAGCTCCGTTTGGGAGAAAGATAAGGAGTGCAGT
ATGGTT CAGTTTGTGTTGGCGTGAGGCGATTTCGCTCGTATAACGGACAACCGGCGAAACGG
30 AACGAGTACCCTCACATGGCTCTGCTCGGCTACGGCGACGACCAGGAGACGGCGCAGTGG
CTCTGCGGCGGCTCAGTGATCAGTGATCAATTCATCCTCACGGCTGCACACTGCATCTTT
ACAAATCTATTGGGTCCAGTACGTTTCGCAGCGCTAGGAATACTGCAGCGATCGGATCCA
GTAGAGTTATGGCAAGTTTACAAGATCGGCGGCATAGTCCCCATCCGCAGTATAAGTCA

CCTATCAAGTACCACGACATTGCTCTCCTGAAGACTGAAAACAAAATAAAGTTTAATGAG
AACGTGCTGCCAGCGTGTTTGTTCATAGAGGGCAGAGTGGGTGGGAGTGAGCAGGCTAAA
GCGACCGGTTGGGGCGCGCTTGGACATAAACAGACGGCAGCTGACGTACTGCAAGTGTT
GACCTTCAAAAGTTTCAGTGACGAAGAGTGCGGAAGTACCTACCGTCCTTACCGGCATTTG
5 CCTCAAGGCTACGACAGCGCCACGCAGATGTGCTACGGCGACAAGGGAAAACCTGAATATG
GACACCTGTGAGGGCGACAGCGGGCGGTCTCTACAGTTCCAAAACCTCCTCGCTCCTCTGC
ATACACATAGTAGCGGGAGTGACGTCATTTCGGCGACGCGTGCGGGTTTTCGGGGCGGGCGCC
GGGATGTACACACGAGTGTCGTACTATATTCCCTGGATCGAGAGCGTTGTATGGCCGTGA

10 [0201] > *M. sexta*-Transferrin (MsTRN); M62802.1 (SEQ ID NO: 11)

ATGGCTTTGAAACTTTTAACTTTGATAGCCCTGACTTGTGCGGCTGCGAATGCAGCTAAA
TCTTCATACAACTATGCGTGCCAGCAGCATACATGAAGGACTGCGAGCAGATGCTTGAA
GTACCCACGAAGTCTAAAGTGGCCTTGGAAATGTGTACCGGCTAGAGACAGGGTGGAAATGC
CTCAGCTTTGTTTCAGCAGCGACAGGGCGGACTTCGTCCCCGTGACCCCTGAGGACATGTAC
15 GTGGCCTCCAAGATCCCCAACCAGGACTTCGTCTGTTCCAGGAGTACAGGACTGATGAA
GAGCCTGATGCGCCATTCCGTTATGAAGCCGTTATTGTGGTTCACAAAGACCTACCCATC
AACAACCTGGATCAGCTGAAGGGACTGAGGTCTTGCCACACCGGAGTCAATCGTAACGTC
GGGTACAAGATCCCATAACGATGTTGATGAAACGTGCCGTGTTCCCGAAAATGAACGAC
CACAGCATTTCCGCCGAAAGAGAACGAACTGAAAGCGCTATCGACGTTCTTCGCAAAGTCG
20 TGCATCGTCGGCAAATGGTCGCCTGACCCCAAAACCAACTCGGCTTGGAATCACAATAC
AGCCATTTGTGTTCAATGTGCGAACACCCGGAGCGTTGTGACTATCCCGACAATTACAGC
GGGTACGAGGGCGCGTTGAGATGCCTCGCCACAACAACGGGGAGGTCGCGTTACCCAAA
GTCATATTCACACGTAAATTCTTTGGGCTTCCAGTAGGTACCACTCCAGCGAGTCCATCA
AACGAAAATCCCGAAGAGTTCAGATATCTCTGCGTGGACGGATCTAAAGCCCCCATCACT
25 GGCAAGGCTTGTTTCATGGGCTGCCAGACCTTGCAAGGACTGATCGGTACCAATGACGTA
CTTGCCAAACTCGCTCCGCTCAGAGAGAAGGTTAAGCAACTTGCTGATTCTGGTGCAGCT
GACAAACCGGAGTGGTTCACCAAAGTCCTTGGTCTATCAGAGAAGATCCACCATGTGCGCT
GACAATATCCCAATCAAGCCCATCGACTACCTGAACAAGGCTAACTACACGGAGGTCATT
GAAAGAGGACATGGAGCTCCCGAGCTGGTCGTCAGGCTATGTGTGACGTCAAACGTGGCA
30 TTATCTAAGTGCCGGGCTATGTCCGTGTTTCGATTTCAGTAGAGACATCAGGCCGATCCTA
GACTGTGTTCAAGAAAACAGCGAAGATGCCTGTCTTAAGAGCGTCCAAGACAACGGTTCA
GATCTTGCTCAGTAGACGATATGAGAGTAGCTGCAGCGGCTAAGAAGTACAACCTTACAT
CCAGTTTTCCACGAAGTGTATGGAGAGCTAAAGACGCCCAACTACGCAGTGGCTGTTGTC

AAGAAGGGCACTGCCTACAACAAGATCGACGACTTAAGGGGAAAGAAATCTTGCCACAGC
 TCTTACAGTACTTTCAGCGGTCTGCACGCGCCTCTCTTCTACCTTATTAACAAGAGGGCC
 ATTC AATCTGACCACTGCGTGAAGAACTTGGGAGAATTCTTCTCAGGCGGATCTTGCTTG
 CCTGGTGTGACAAACCCGAAAACAACCCAAGCGGTGATGATGTGTCTAAATTGAAGAAG
 5 CAATGTGGATCCGACAGCAGCGCTTGGAAGTGCTTGGAAGAGGACAGAGGAGACGTCGCA
 TTTGTTTCAAGTGCCGATCTGTCCCACCTTCGACGCCAACCAATACGAGCTGCTCTGCCTG
 AACCGCGACGCTGGCGGTAGAGATGTTCTCTCCAGTTTCGCCACCTTGCAACGTCGCCATG
 GCCCCGTCCAGGACCTGGGTGGCTGCGAAGGACTTCCTGTCTGACGTATCTATCGCCCAC
 ACACCATTGAGCCTCGCCCCAAATGCTCGCTACGAGACCTGACCTCTTCAACATTTACGGA
 10 GAGTTCTTGAAGAACAACAATGTTATTTTCAATAATGCCGCTAAAGGCTTAGCAACAAC
 GAGAACTTGACTTCGAGAAGTTCAAGACCATCCACGACGTCATCTCTTCATGTGGTCTC
 GCCTAA

[0202] > *M. sexta*-Arylphorin β subunit (MsARP); M28397.1 (SEQ ID NO: 12)

15 ATGAAGACTGTCATAATCCTAGCGGGGTTGGTGGCCCTGGCCCTCGGCAGCGAAGTGCCT
 GTCAAGCACTCCTTCAAAGTTAAGGATGTTGATGCGGCTTTCGTGCAACGTCAAAAGAAG
 GTCTTAGATCTTTTCCAAGATGTCGACCAAGTAAATCCTAACGATGAGTACTACAAGATT
 GGCAAGGAATACAACATCGAGGCTAACATCGACAATTACTCGAACAAGAAGGCCGTCGAA
 GAATTCTTGCAAGTTATACAGGACAGGTTTCTTGCCCTAAGTACTATGAATTTTACCCCTTC
 20 TATGACAGACTAAGGGACGAGGCCATTGGTGTCTTCCACCTCTTTTACTACGCTAAAGAT
 TTTGATACGTTCTACAAATCTGCCGCATGGGCGCGTGTGTACCTCAACGAAGGACAGTTC
 TTATACGCCTACTACATTGCTGTGATTACAGCGTAAAGATACTCAGGGCTTCGTTGTACCA
 GCACCGTATGAAGTCTACCCTCAATTCTTCGAAACTTGAACACTATGCTCAAAGTCTAC
 CGTACCAAAAATGCAGGATGGAGTTGTTAGTGCCGATTTAGCTGCACAACACGGCATCGTA
 25 AAGGAGAAAACTACTACGTATACTATGCCAATTACTCCAATCATTAGTGTAACAAC
 GAGGAACAGAGACTGTCGTACTTCACTGAGGACATCGGCTTGAATTCGTACTACTACTAC
 TTCCACTCTCACTTGCCCTTCTGGTGGAAATTCTGAGAGATACGGAGCACTAAAATCGCGC
 CGTGGTGAAATCTACTATTACTTCTATCAGCAATTAATTGCACGTTATTACTTTGAACGT
 CTCTCGAACGGCCTGGGTGACATTCCCGAATTCTCATGGTACTCACCAGTCAAGTCTGGC
 30 TACTATCCACTGATGTCTTCTTATTACTACCCCTTCGCTCAAAGGCCCACTACTGGAAC
 GTGCACAGCGAAGAAAACCTACGAGAAAGTACGATTCTTGACACGTATGAAATGTCATTC
 CTTCAAGTTCTCCAAAACGGACACTTCAAAGCGTTTGACCAGAAGATTGACTTCCACGAT
 TTCAAAGCTATCAACTTTGTTGGAAACTACTGGCAAGATAATGCTGACCTGTACGGTGAG

GAAGTTACTAAGGACTACCAACGTTTCATATGAAATTATAGCCCGCCAAGTGCTTGGTGCT
 GCACCTAAACCATTTCGACAAGTACACATTCATGCCCAGCGCTTTAGACTTCTACCAGACG
 TCTCTGCGTGACCCAATGTTCTACCAACTTTACAACAGAATTCTGAAGTACATATATGAG
 TACAAGCAGTACCTGCAACCGTACTCTTCAGAAAACTGGCATTCAAGGGTGTCAAGGTG
 5 GTCGATGTTGTAGTAGACAACTGGTTACCTTCTTCGAGTACTACGACTTTGATGCGTCC
 AACAGCGTTTTTCTGGAGCAAAGAGGAGGTTAAATCTAGCTACCCCCATGATTTCAAGATC
 CGTCAGCCACGCCTTAACCACAAGCCATTCTCTGTCTCTATCGACATCAAATCTGAAGCT
 GCCGTTGATGCCGTTGTCAAGATATTCATGGCACCTAAATACGACGATAATGGATTCCCT
 CTGAAATTAGAAAACAACCTGGAACAAATTCTTCGAGCTGGACTGGTTACATACAAATTT
 10 GTTGCTGGTGACAACAAAATCGTGAGGAACTCAAACGACTTCTTGATCTTCAAGGACGAC
 TCTGTTCCCATGACTGAGTTGTACAAATTATTAGAACAAAATAAGGTTCCACACGACATG
 TCCGAGGATTACGGCTACCTGCCTAAAAGACTGATGCTGCCAAGAGGTACTGAGGGTGGT
 TTCCCATTTCCAGTTCTTCGTTTTTCGTATATCCATTCAACGCTGACAGCAAAGATCTTGCA
 CCGTTTCGAGGCCTTCATCCAGGACAACAAACCTTTGGGCTATCCATTCGACCGTCCCGTT
 15 GTTGACGCTTACTTCAAGCAACACAACATGTTCTTCAAGGACGTCTTCGTATACCATGAC
 GGCGAGTACTTCCCGTACAAGTTCAATGTTCTTCCCATGTGATGCACTCAAACGTTGTT
 CCTAAACACTGA

[0203] > *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1); AM419170.1
 20 (SEQ ID NO: 13)

ATGTACGTGAAAGTAGCACTTCTGTTGGTAGCCCTCATTGCTGGGAGCTGGGCCTTCCCA
 AAGCTCGAAGATGAGCAGGACATGTCCATCTTCTTCACGCAGCTCGATTGAGCGCGCGT
 ATCGTGGGTGGTACCCAGGCCCCCAGCGGAAGTCACCCTCACATGGTGGCGATGACCACC
 GGTACCTTCATCAGGAGCTTCAGCTGTGGAGGCTCAGTTGTCGGTAGACGTTCCGTTCTG
 25 ACTGCGGCTCATTGCATCGCTGCTGTTTTTCAGTTTTCGGTTCCCTCGCCAGTACCCCTCCGC
 TTGACGGTCGGCACCAACTTCTGGAACCAGGAGGCACCATGTACACCGTCGCTCGCAAC
 ATAACCCACCCCCACTACGTCTCTGCGACCATCAAGAACGACATCGGTCTGTTCACTACT
 CACAACAACATCATCGACACGACTGTCGTCCGCAGCATCCCTCTTAACCTTTGACTATGTG
 CCCGGTGGTGTCTCACTAGAGTCGCCGGATGGGGCAGGATCAGGACCGGCGGTGCCATC
 30 TCTCCCTCTCTGCTGGAGATCATTTGTGCCTACTATCAGTGGAAGCGCATGCGTAGCCAGT
 GCAATCCAAGCTGGCATCGATCTGAACATGAGACCACCTCCCGTCGAGCCTCACATCGAG
 CTGTGCACCTTCCACGGTCCTAACGTAGGCACTTGTAATGGTGACTCCGGCAGCGCTCTT
 GCCCCCTAGACAACGGCCAGCAGATCGGTGTGGTATCGTGGGGCTTCCCGTGCGCACGC

GGCGGTCCCGACATGTTTCGTCAGGGTCAGCGCCTACCAATCCTGGCTGCAGCAGAGCATC
GTATAA

[0204] > *M. sexta*-Valine Rich Midgut Protein (MsVMP1); NCBI accession
5 number not assigned as yet (SEQ ID NO: 14)

ATCATTGACGGACCTTCCGTTGGACCNCCATCATCGGCGCTGGAGACATCGCTGTCGGC
CCTGCTATCGTCGACTTCCCTTTCCCCGACGGCGGTGCCGTGTCTGCCCCCGTTGAGCCT
TCCCCCATCGCCATCGGACCCGCTATCGTCGGTGAATCCCCTATCTCCGTCGGACCTGCC
ATCGTTGAGGCCGAGACATCGCTGTTGGACCCGCTATCATCGACTTCCCCCTTCCCGAC
10 GGTGGCGCCGTGTCCGCCCCCGTTGAGGTTTCTCCCGTCGACTCCGTCGTCTCGGCCCT
GCCGCCGGCTCTCAGAGCTCTCCCCCTCGTCCAGATCATCATCAACGTTAAGGCCCCCGCT
GGTGCCGGCCCCGTTGTTCGATGCCGTCTGACAAGCCCATGGACATCATTGATGTTATG
CCCGTCGTGACCCTGCTGATTTTCGTGGACCTCACCCCCGTTGTAGAGCCTGTAGAAGTC
GTCGACATTGTTCGATGTCATGCCCGTGGTTGACCCCATCAACATCATCGATGTTATGCCT
15 GTTGTTAAGCCCGTAAACCCCCTTGCCCGTTCTTAAGGG

[0205] > *M. esculanta*-Catalase 1 (MeCAT1); AF170272 (SEQ ID NO: 15)
ATGGATCCTTGCAAGTTCCGTCCATCAAGCTCAAACAATACCCCCTTCTGGACCACCGAT
GCTGGTGCTCCAGTATGGAACAACAATTCTCCATGACTGTTGGAACCAGAGGTCCAATC
20 CTTTTGGAGGACTATCATATGATAGAGAACTTGCCAACTTTACCAGAGAGAGGATTCCA
GAGCGTGTCGTCCATGCTAGGGGAATGAGTGCAAAGGGCTTCTTTGAAGTCACCCACGAT
GTCTCTCACCTTACTTGTGCTGATTTCTTCGAGCCCCCTGGAGTTCAAACCCCTGTCATC
GTCCGTTTCTCCACTGTTATCCACGAGCGTGGCAGCCCTGAAACACTCAGGGATCCTCGA
GGTTTTGCGACTAAGTTCTACACCAGAGAGGGCAACTTTGATATTGTGGGAAACAAC TTC
25 CCTGTCTTCTTCATCCGTGATGGAATAAAATTCCCAGATGTGATACACGCTTTTAAGCCC
AATCCCAAGTCTCACATCCAAGAATACTGGAGGATCTTTGACTTCTTATCACACCATCCT
GAGAGCTTGAGCACCTTCGCCTGGTTCTTCGATGATGTTGGAATTCCTCAAGATTACAGA
CACATGGAAGGTTTCGGTGTTTACACCTTTACTTTTCATCAACAAGGCTGGAAAAGTAACC
TACGTGAAATTTCACTGGAAACCCACTTGCGGGGTCAAGTGTGTTGATGGATGATGAGGCA
30 CTTAAGATCGGAGGTGCCAACCACAGCCATGCTACGCAGGATTTATACGACTCCATTGCC
GCTGGCAACTATCCTGAGTGGAGACTCTTCATCCAGACAATGGATCCAGCTGATGAAGAC
AAATTCGACTTTGATCCACTTGATATGACCAAGATCTGGCCTGAGGATATTTTTCTCTA
CAGCAAATTGGCCGTTTGGTCTTGAACAGGAACATCGATAACTGGTTTGCTGAGAATGAA

ATGCTCGCATTTCGACCCTGGTCATATTGTTCTGGCATTCACTATTCAAACGACAAGTTG
TTTCAGCTCAGAACCTTTGCATATGCTGACACTCAGAGGCACCGTCTCGGACCCAACTAT
AAGATGCTCCCTGTTAATGCTCCCAAGTGTGCTTATCACACAATCATTACGATGGTTTC
ATGAATTTTCATGCACAGGGATGAGGAGGTGGATTACTTCCCATCCAGGTATGATCCAGTT
5 CGCCATGCTGAGAGAAGCCCCATTCTAACGCTATCTGTAGTGGAAGGCGTGAAAAGTGC
GTCATTGAAAAGGAGAACAAATTTCAAGCAACCTGGAGAGAGATATCGATCCTGGGCACCT
GATAGACAAGAAAGATTCTGTGCAGATTGGTTAACGCCTTATCAGAGCCACGTATCACC
TTTGAGATTTCGAGTATCTGGGTCTCTTACTGGTCTAAGTGCGACGCGTCTCTGGGTCAA
AAGCTGGCTTCTCGTCTCAACGTGAGGCCAAATATATGA

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[0206] > *M. sexta*-Hemolin (MsHEM); M64346.1 (SEQ ID NO: 16)

GGCAAAGAATTCAAATGGCAGGAACACAATATCGCCCGCGCAAAGACGAAGGCAGCCTG
GTCTTCCTCAAGCCCGAGGCTAAAGATGAAGGCCAATACAGATGTTTCGCTGAGTCGGCC
GCCGGAGTCGCCACCTCCCACATCATCTCTTTTGAAGGACCTACATGGTCGTACCTACT
15 ACTTTTAAGACTGTAGAAAAGAAACCGGTAGAAAGGGTCATGGCTCAAACCTTGAGTGCAGC
ATCCCCGAAGGTTATCCTAAACCTACTATTGTATGGAGAAAGCAGCTTGGTGAAGACGAA
AGTATAGCAGATTCTATACTGGCACGTCGTATTACACAATCTCCAGAGGGAGACCTGTAC
TTCACGAGCGTCGAGAAAGAAGACGTAAGCGAAAGCTATAAATACGTTTGCGCTGCTAAG
TCACCGGCTATTGATGGGGATGTCCCTCTTGTTGGATACACTATTAAGCTTAGAAAAG
20 AATACAAATCAGAAAAACGGTGAGCTGGTCCCGATGTACGTCAGTAATGATATGATAGCT
AAGGCCGGAGACGTTACTATGATCTACTGCATGTATGGTGGAGTCCCAATGGCTTACCC
AACTGGTTCAA

[0207] > *M. sexta*- Serine Proteinase homolog 3 (MsSPH-3); AF413067.1
25 (SEQ ID NO: 17)

ATGTTGTTGCTTCTGTATTGTCTTGTGGCGGCCTCCGCGCCGTTCTTTATTGCAGCGGAC
CAAGGCAGCCCTGACCTGCCTTTAGCTACCGAACCACCAACAGAATGCGGAACAATAGCA
CCTGATGATAGCTTAGTATTAGATGGGTCCGTTGGTAAAAGTGACAAATTACCTTGGTAT
GCTATTATCTACACAACCACCACCCGGCCATACAAGCAGATCGGTGGAGGAACCTCATC
30 ACTCCTTCAGTAGTAATCTCAGCCGCTCACTGTTTCTGGCGCAATGGTGAGGTTCCATCT
AAGGATAATTACGCCGTGGCGCTCGGCAAGACCCATAGTGCTTGGAATAGCCATGCCGAT
GTAAACGCTCACAAGTCTGATGTAAAAGAAATACACATACCACCGCAGTTTAAGGGAAGG
AACACTAATTATCGGAATGATATAGCAATCGTGGTCATGTCAGACCCTGTGACCTACAAA

GTGGACATCCGCCCTATCTGTTTGAACCTTCGATGTACAATTTGAAAGACTGCAATTAAAA
 GACGGCATTATGGGGAAGATCGGCACATGGAATGTAAGTCGTGAGACACTGAAACTATCG
 AAAACATTAAAAAGTGGTGGAGAATCCATACATTGACGCAGCGACT

5 [0208] > *M. sexta*- Peptidoglycan recognition protein 2 (MsPGRP2);
 GQ293365.1 (SEQ ID NO: 18)

ATGGCGAGCTTCGCTTTAATAGTTATCCTTAGCGTAATTGGCTTTATATCGGCCTATCCT
 AGTCCTGAAGGTTACAGTTCTGCCTTCAACTTTCCATTTCGTAACCAAGGAGCAGTGGGGC
 GGCAGGGAGGCACGCACGTCGACGCCACTCAACCACCCAGTGCAGTTCGTGGTGATCCAC
 10 CACAGTTACATTCCCGGCGTGTGCCTCAGCCGGGACGAGTGC GCGCGCAGCATGCGCTCC
 ATGCAGAACTTCCACATGAACAGTAACGGGTGGAGTGATATTGGATACAACTTCGCTGTC
 GGCGGTGAAGGGTCGGTGTACGAGGGCCGCGGCTGGGACGCGGTGCGCGCACACGCAGCT
 GGCTATAACAGTAACAGTATCGGCATCGTGCTCATCGGCGATTTTGTTCAAACCTCCCG
 CCGGCGGTGCAAATGCAAACCACACAAGAATTGATCGCAGCGGGCGTGCGACTCGGTTAC
 15 ATCAGGCCCACTACATGCTCATCGGGCATCGTCAGGTCTCCGCCACTGAGTGCCCAGGA
 ACCAGACTCTTCAACGAAATCACCAACTGGAACAACTTCGTGAG

[0209] > *M. sexta*- Beta-1, 3-glucan-recognition protein 2 (MsβGRP2);
 AY135522.1 (SEQ ID NO: 19)

20 GCGTCTGTTTGTTCGCAACCATTGCGGGCTGCTTGGGCCAGCGAGGGGGTCCATACAAGG
 TGCTTGATGCGAAACTCGAAGCTATCTACCCCAAAGGCTTGAGAGTCTCTGTGCCAGATG
 ATGGCTACTCCCTATTTGCCTTCCACGGCAAGCTCAATGAGGAGATGGAAGGTTTAGAGG
 CTGGCCATTGGTCCAGAGACATCACCAAAGCGAAGCAGGGCAGATGGATATTAGAGATA
 GGAATGCTGAGCTGAAGCTTGAGACAAAATTTACTTCTGGACTTACGTTATTAAGGATG
 25 GATTGGGATACAGGCAGGACAATGGAGAATGGACTGTTACAGAATTCGTCAATGAGAACG
 GTACAGTGGTGGACACTAGTACAGCGCCGCCACCAGTAGCACCCGCCGTTTCAGAGGAAG
 ATCAATCGCCAGGTCCTCAGTGGAGACCTTGCGAAAGATCCCTGACTGAGTCCCTGGCCC
 GCGAACGCGTTTGCAAAGGCAGCCTTGTCTTTAGCGAGGACTTTGATGGTTCCAGTTTGG
 CCGACTTGGGCAATTGGACCGCTGAAGTCAGATTCCCTGGCGAACCGGACTACCCGTACA
 30 ACTTGTA CACTACGGACGGCACTGTGGGATTGCAAAGTGGGTCTCTGGTGGTGAGACCCG
 TCATGACCGAGTCCAAATACCACGAGGGCATCATATACGACCGCCTCGACCTTGAGAGAT
 GTACAGGACAGCTGGGTACGCTGGAATGCAGGCGAGAGAGCAGCGCGGTGAGATTGTAC
 CACCTGTGATGACAGCTAAACTGGCCACTCGACGCAGCTTCGCGTTCAAGTTCGGCAGGA

TCGATATAAAGGCGAAGATGCCGCGCGGGGACTGGTTGATACCAGAACTCAACCTCGAAC
 CTTTAGATAACATATACGGCAACCAGCGATACGCTTCGGGTCTCATGCGGGTCGCGTTCTG
 TGAGAGGAAACGATGTATACGCCAAGAAGCTCTACGGAGGTCCGATAATGTCCGACGCGG
 ACCCGTTTCAGGTCCATGCTGTTGAAGGACAAGCAAGGGTTGGCCAACTGGAATAATGATT
 5 ACCACGTCTACTCGCTGCTGTGGAAGCCTAACGGTTTAGAGCTGATGGTGGACGGTGAAG
 TGTACGGCACCATCGACGCTGGCGATGGCTTCTACCAGATTGCGAAGAACAACCTCGTGA
 GCCACGCCCTCGCAGTGGCTCAAGGGCACCGTCATGGCGCCGTTTGATGAAAAGTTCTTCA
 TCACTCTGGGTCTTCGCGTGGCGGGTATCCACGACTTCACGGACGGTCCGGGCCAAACCTT
 GGGAGAACAAGGGC

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[0210] > *M. sexta*-Relish family protein 2A (MsREL2A); HM363513.1 (SEQ ID
 NO: 20)

AGTGTGCGTCTACGAATGATTTGAAAATATGCCGCATAAGCCGTTGTTACGGTAGACCGA
 GAGGCGGCGAAGATATCTTCATATTTGTGCGAAAAGGTCAACAAGAAAAACATCCAAGTTC
 15 GGTTCCTTTAGACTGGAACCGGGGAGCGCACCTGGTCAGCGATGGCGAACTTTCTGCTAA
 GCGATGTTACACCACCAATACGCTATCGCTTTTAGAACGCCACCGTACGTCAATCACCAAA
 TTTCTGAAGACGTGCAAGTTTTTATAGAAGTTCGTACGCCCTTCAGACGGTAGGACGAGCG
 CTCCCATGGAGTTCACATACAAGGCTGAGCAAATCTATAAACAGAACAGAAACGTAAAA
 CTACTTCGTCTGCTCGTCTGACAGCTCCTCAGGTTTCGGCCGGTTCAATTAAAAGCA
 20 TCAGCGAACTGCCCCGCGCCCGTTGTTTTTGCTGAAAACGTAAGTTTTTCTATGACACAT
 TACTCATTTCTCAACCCATGACGAATCTATAA

[0211] > *M. sexta*-Dorsal (MsDor); HM363515.1 (SEQ ID NO: 21)

ATGCTTGTGACGTTATGCGGCGGGAACATAGTGGATTGTCGTTAACAAAACTAATCAT
 25 TATATGTCACCAAAATCATATGTGCCAGGAAATGGTTATGACGCCGCCGTAATCCTAGGT
 ACCACGGAGCAGAATGACAGCGAACCCTCAAACCTGAATATTAGTGATGTTTTTGAAGCC
 ATCACGCTCGCTGATCCGTCGTTTCGGCGCGGGCGTGCCGTCGGTAGAGGAGACGATGGCG
 CACACGCAGCCCCAGCCGCTGCAAATGCCGTACGTGGTTCGTCGTGCAGCAGCCCCGCCAGC
 AAAGCGCTCAGATTTTCGATATGAGTGCAGGGGCAGATCAGCCGGTTTCGATTCCCGGCGCG
 30 TCGAGCACGCCCCGAGAACCGAACCTTCCCCGCCATCAAGATAATCGGCTACACCGGCACC
 GTCTCCATCGTAGTGTGTCGTGTGTCACCAAAGATGAGCCTTGCAGGCCGCACCCACACAAC
 CTGGTTCGGGCGCGACCACTGCGACCGCGGCGTGTCTCCGTCCGCATCGAGATCACCGAC
 GAGAATAACGAATACCAGTTTCGGAACCTGGGCATACAGTGCGTCAAGCGGCGCGACATC

GGCGAGGCGCTGCGGATCCGAGAGGACCTGCGCGTCGATCCGTTCAAACCGGCTTCACC
CACCGGAACCAACCCGCAAGGCATCGATCTGAATGCAGTGC GGCTCGCGTTCCAAGTGTTCC
CTGCCGCACTCCAGCGGCAAGATGCGGCGCACGCTCGCGCCCGTCGTGTCCGACGTCATC
TACGACAAG

5

[0212] > *M. sexta*-Spätzle (MsSPZ1A); GQ249944.1 (SEQ ID NO: 22)

CGAACAACCTGACAGACGGATAGCGGGACGGTCAGCACAAATACGAACATTTAAGAACAAA
CGAGAGGTCTCTCCCGGTCTACAGCGAGACCCAGAGGATACAAGCAGAAGAGAGAAGAAG
ACACAGTTCGAGACTAGAAGAACCGAGACAACGTGCTGAGAATGGTTCATATAAGATATT
10 GAATAACCCTCCGAAACCCTGTATTACTAATAGGAGAAAGTCAAATTGATTTCGTCGAATGA
TAGGGTAGTGTTCCCCGGTCCGACTTCAGAAAGGTTCGTACGTACCCGAAGTGCCAGAGGA
ATGCAAGAAAATCGGCATATGCGACAGTATACCGAATTACCCAGAAGAACACGTAGCTAA
TATTATATCTCGACTTGGAGACAAAGGAAAAGTATTACAAATAGACGAACTGGACGTATC
AGACACTCCAGATATCGCCAGAGGTTGGGTCCGCAGGAGGACAACATGGAACATATGTAG
15 CTTTAGAGAAAAGATTTTTTACCCCAAGGCAGCGCCAGACAAAGATGGAAATTGGTTCTT
CGTTGTGAATTCAAAGAAAACCCAGTACAGGGTTATAAAGTTGAAATTTGCGACCGTCA
GCAATTACCATGCGCGGAGTTCGCGAGCTTCCAACAGGGATATGAAGCGAGGTGCATCCA
GAAATACGTTCCCGGACCATGTTGGCGTTGGATCCCAAGGGTCAGATGACCGACATGCC
CCTTAAAGTGCCCAGCTGTTGCT

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[0213] > *M. sexta*-Toll receptor (MsTOLL); EF442782.1 (SEQ ID NO: 23)

CAAGTGGTCGTTGTGCACTGCACCGGACTCGCCGAGTTCCCGCGCCTGCCACTAACCACG
GACAAGTGGATCCTGCACCTGCCCCACAACAACATATCATACCTCGCCGCGGCCGACGTA
TCGCCGAACATCGTGGAACCTCGATCTAAGAAACAATTCAATCAAGAATATCGACGTACAG
25 GCATCAGCAAACTAGCCTTCGTCCGGCTGCAATTGGGTGGTAACCCGATCGAGTGTGAC
TGCGAGGCGTTGAAGCTGCTGGCGCCGCTGCTCAAACCTGACTCAAAGCTGCTTGACAGA
AAGGACGTGAAATGTGAGAACGACGCGCAGATTACCTTGGCGATGCTGAAATTATGTACT
AAGTCATCCAATGGGCTGATGTACTTGCTGTTCTGTTGCTGTTACTCGCATTTGTCGTA
ACCGGACTGCTCGCACGAACCGCAATTGCCTGCGCATCAAATGATCCTCATGAGACTG
30 GGTTGGATGTGCGAGACTACTGGAGCCCGCGGACGACGATCGCCCGTACGACGCGTTTGTG
TCTTTCGCACACGAGGATGAGGAGCTGGTGATGGAGCAGCTGGCGGCACGGCTCGAGAGC
GGCTCGCGGCCGTACCGACTGTGTCTGCACTACCGCGATTGGGCGCCAGGCGAGTGGATC
CCGGCGCAAATAGCGGCTTCGGTGCGGGCCTCTCGGCGCACGGTGGCGGTTGTGTGGCG

CACTACTTACAGTCGGGCTGGGCGCTTGCCGAGATCCGGGAGGCGACCGCAGCCTCGCTG
CAGGAAGGCATGCCACGTCTCATCATCGTGCTGCTCGACGAGACCGACCGGTTGATGCTC
GATATAGACCCTGAGTTGCACGCCTATGTGCGCAACAATACCTACGTGCG

5 [0214] > *M. sexta*-Scolexin A (MsSCA1); AF087004.1 (SEQ ID NO: 24)

TCGAAGCTAAGGGGGCAAAGCAGCCAATTGATACGAGGGCAGTGAAGGAACGGTATCCAT
ACGCAGTTCGGAGTTTCGGAGGCTTCTGCGGAGGAACCATATCAGTCCCACCTGGATCC
TGACCGCCGGCCACTGCTCGATACTCTATGCGGGGAGCGGCCTACCGGCCGGCACCACA
TTACCGAGGTATCTAGCTTGTACCGCTTCCCCAAGCGGCTCGTCATACACCCGCTCTTCT
10 CCATAGGACCCGTCTGGCTCAACGCTACGGAGTTCAACCTCAAACAGGCGGCTGCACGAT
GGGACTTCTTGTGATAGAACTGGAGGAACCGCTGCCGTTGGACGGCAAGATCCTGGCGG
CTGCGAAGCTCGACGACCAGCCCCGACCTCCCCGCGAGGCCTCGACGTGGGCTATCCGAGCT
ACAGCACCGACACCTACGAGGCTAAGATACAAAGCGAGATGCACGGAAAGAAGCTTTCGG
TTCAATCTAACGAGGTGTGCTCGAAGCTAGAGCAGTTCAAGGCGGAGGACATGTTGTGCG
15 CCAAGGGACGTCCACCGCGATACGACTTCGTCTGCTTCAGCGACAGTGGCAGTGGGCTAG
TAGACAACAATGGTCGCCTAGTCGGCGTGTTGTCGTGGGCCGAGAACAACGCTTTCGAGT
GCCGCAACGGCAACCTGGCGGTCTTCTCGCGAGTGTCCAGCGTACGCGAGTGGATCCGAC
AAGTC

20 [0215] > *M. sexta*-Hemolymph proteinase 18 (MsHP18); AY672794.1 (SEQ ID NO: 25)

GATGGTCAGAAAGCGTGGGACAAATGTCTGGAATACGTTGACAAGCTGTCTGATCCCATGC
GCTTCAACCTACTCCCACTACCTCAGCTCCGTTTGGGAGAAAGATAAGGAGTGCAGTATG
GTTCAAGTTTGTGGCGTGAGGCGATTTCGCCTCGTATAACGGACAACCGGCGAAACGGAAC
25 GAGTACCCTCACATGGCTCTGCTCGGCTACGGCGACGACCAGGAGACGGCGCAGTGGCTC
TGCGGCGGCTCAGTGATCAGTGATCAATTCATCCTCACGGCTGCACACTGCATCTTTACA
AATCTATTGGGTCCAGTACGTTTCGCAGCGCTAGGAATACTGCAGCGATCGGATCCAGTA
GAGTTATGGCAAGTTTACAAGATCGGCGGCATAGTTCCCCATCCGAGTATAAGTCACCT
ATCAAGTACCACGACATTGCTCTCCTGAAGACTGAAAACAAAATAAAGTTTAAATGAGAAC
30 GTGCTGCCAGCGTGTTTGTTCATAGAGGGCAGAGTGGGTGGGAGTGAGCAGGCTAAAGCG
ACCGGTTGGGGCGCGCTTGGACATAAACAGACGGCAGCTGACGTACTGCAAGTGGTTGAC
CTTCAAAAGTTCAGTGACGAAGAGTGCGGAAGTACCTACCGTCCTTACCGGCATTTGCCT

CAAGGCTACGACAGCGCCACGCAGATGTGCTACGGCGACAAGGGAAAACCTGAATATGGAC
ACCTGTGAGGGCGACAGCGGCGGTCTCTACAGTTCCAAAACCTCTCGCTCCTCTGC

[0216] > *M. sexta*-Transferrin (MsTRN); M62802.1 (SEQ ID NO: 26)

5 ATGGCTTTGAACTTTTAACTTTGATAGCCCTGACTTGTGCGGCTGCGAATGCAGCTAAA
TCTTCATACAACTATGCGTGCCAGCAGCATACATGAAGGACTGCGAGCAGATGCTTGAA
GTACCCACGAAGTCTAAAGTGGCCTTGAATGTGTACCGGCTAGAGACAGGGTGAATGC
CTCAGCTTTGTTTCAGCAGCGACAGGCGGACTTCGTCCCCGTGACCCCTGAGGACATGTAC
GTGGCCTCCAAGATCCCCAACCAGGACTTCGTGCTCTTCCAGGAGTACAGGACTGATGAA
10 GAGCCTGATGCGCCATTCCGTTATGAAGCCGTTATTGTGGTTCACAAAGACCTACCCATC
AACAACCTGGATCAGCTGAAGGGACTGAGGTCTTGCCACACCGGAGTCAATCGTAACGTC
GGGTACAAGATCCCACTAACGATGTTGATGAAACGTGCCGTGTTCCCGAAAATGAACGAC
CACAGCATTTTCGCCGAAAGAGAACGAACGAAAGCGCTATCGACGTTCTTCGCAAAGTCG
TGCATCGTCGGCAAATGGTCGCCTGACCCCAAAACCAACTCGGCTTGGAATCACAAATAC
15 AGCCATTTGTGTTCAATGTGCGAACACCCGAGCGTTGTGACTATCCCGACAATTACAGC
GGGTACGAGGGCGCGTTGAGATGCCTCGCCACAACAACGGGGAGGTCGCGTTCACCAAA
GTCATATTCACACGTAAATTCTTTGGGCTTCCAGTAGGTACCACTCCAGCGAGTCCATCA
AACGAAAATCCCGAAGAGTTCAGATATCTCTGCGTGGACGGATCTAAAGCCCCCATCACT
GGCAAGGCTTGTTTCATGGGCTGCCAGACCTTGGAAGGACTGATCGGTACAAATGACGTA
20 CTTGCCAAACTCGCTCCGCTCAGAGAGAAGGTTAAGCAACTTGCTGATTCTGGTGCAGCT
GACAAACCGGAGTGGTTACCAAAAGTCCTTGGTCTATCAGAGAAGATCCACCATGTCGCT
GACAATATCCCAATCAAGCCCATCGACTACCTGAACAAGGCTAACTACACGGAGGTCATT
GAAAGAGGACATGGAGCTCCCGAGCTGGTCGTGAGGCTATGTGTGACGTCAAACGTGGCA
TTATCTAAGTGCCGGGCTATGTCCGTGTTTCGATTTCAGTAGAGACATCAGGCCGATCCTA
25 GACTGTGTTCAAGAAAACAGCGAAGATGCCTGTCTTAAGAGCGTCCAAGACAACGGTTCA
GATCTTGCCCTCAGTAGACGATATGAGAGTAGCTGCAGC

[0217] > *M. sexta*-Arylphorin β subunit (MsARP); M28397.1 (SEQ ID NO: 27)

CTGTCATAATCCTAGCGGGGTTGGTGGCCCTGGCCCTCGGCAGCGAAGTGCCTGTCAAGC
30 ACTCCTTCAAAGTTAAGGATGTTGATGCGGCTTTTCGTGGAACGTCAAAGAAGGTCTTAG
ATCTTTTCCAAGATGTGACCAAGTAAATCCTAACGATGAGTACTACAAGATTGGCAAGG
AATACAACATCGAGGCTAACATCGACAATTACTCGAACAAGAAGGCCGTGGAAGAATTCT
TGCAGTTATACAGGACAGGTTTCTTGCCTAAGTACTATGAATTTTCACCCTTCTATGACA

GACTAAGGGACGAGGCCATTGGTGTTCCTCCTTTTACTACGCTAAAGATTTTGATA
CGTTCTACAAATCTGCCGCATGGGCGCGTGTGTACCTCAACGAAGGACAGTTCTTATACG
CCTACTACATTGCTGTGATTGAGCGTAAAGATACTCAGGGCTTCGTTGTACCAGCACCGT
ATGAAGTCTACCCTCAATTCTTCGAAACTTGAACACTATGCTCAAAGTCTACCGTACCA
5 AAATGCAGGATGGAGTTGTTAGTGCCGATTTAGCTGCACAACACGGCATCGTAAAGGAGA
AAAATACTACTAGTATACTATGCCAATTACTCCAACCTCATTAGTGTACAACAACGAGGAAC
AGAGACTGTCGTACTTCACTGAGGACATCGGCTTGAATTCGTACTACTACTTCCACT
CTCACTTGCCTTTCTGGTGGAATTCTGAGAGATACGGAGCACTAAAATCGCGCCGTGGTG
AAATCTACTATTACTTCTATCAGCAATTAATTGCACGTTATTACTTTGAACGTCTCTCGA
10 ACGGCCTGGGTGACATTCCCGAATTCTCATGGTACTCACCAGTCAAGTCTGGCTACTATC
CACTGATGTCTTCTTATTACTACCCCTTCGCTCAAAGGCCCACTACTGGAACGTGCACA
GCGAAGAAAACGAGAAAGTACGATTCTTGGACACGTATGAAATGTCATTCCCTCAGT
TCCTCCAAAACGGACACTTCAAAGCGTTTGACCAGAAGATTGACTTCCACGATTTCAAAG
CTATCAACTTTGTTGGAACTACTGGCAAGATAATGCTGACCTGTACGGTGAGGAAGTTA
15 CTAAGGACTACCAACGTTTCATATGAAATTATAGCCCGCCAAGTGCTTGGTGCTGCACCTA
AACCATTGACAAAGTACACATTCATGCCCAGCGCTTTAGACTTCTACCAGACGTCTCTGC
GTGACCCAATGTTCTACCAACTTTACAACAGAATTCTGAAGTACATATATGAGTACAAGC
AGTACCTGCAACCGTACTCTTCAGAAAACTGGCATTCAAGGGTGTCAAGG

20 [0218] > *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1); AM419170.1
(SEQ ID NO: 28)

ATGTACGTGAAAGTAGCACTTCTGTTGGTAGCCCTCATTGCTGGGAGCTGGGCCTTCCCA
AAGCTCGAAGATGAGCAGGACATGTCCATCTTCTTCACGCAGCTCGATTGAGCGCGCGT
ATCGTGGGTGGTACCCAGGCCCCCAGCGGAAGTCACCCTCACATGGTGGCGATGACCACC
25 GGTACCTTCATCAGGAGCTTCAGCTGTGGAGGCTCAGTTGTCGGTAGACGTTCCGTTCTG
ACTGCGGCTCATTGCATCGCTGCTGTTTTAGTTTCGGTTCCCTCGCCAGTACCCCTCCGC
TTGACGGTCGGCACCAACTTCTGGAACCAGGAGGCACCATGTACACCGTCGCTCGCAAC
ATAACCCACCCCCACTACGTCTCTGCGACCATCAAGAACGACATCGGTCTGTTCACTACT
CACAACAACATCATCGACACGACTGTCGTCCGACGATCCCTCTTAACCTTTGACTATGTG
30 CCCGGTGGTGTTCTCACTAGAGTCGCCGGATGGGGCAGGATCAGGACCGGCGGTGCCATC
TCTCCCTCTCTGCTGGAGATCATTTGTGCCTACTATCAGTGGAAGCGCATGCGTAGCCAGT
GCAATCCAAGCTGGCATCGATCTGAACATGAGACCACCTCCCGTCGAGCCTCACATCGAG
CTGTGCACCTTCCACGGTCCTAACGTAGGCACTTGTAATGGTGACTCCGGCAGCGCTCTT

GCCCCCCTAGACAACGGCCAGCAGATCGGTGTGGTATCGTGGGGCTTCCCGTGCGCACGC
GGCGGTCCCACATGTTTCGTCAGGGTCAGCGCCTACCAATCCTGGCTGCAG

[0219] > *M. sexta*- Valine Rich Midgut Protein (MsVMP1); NCBI accession
5 number not assigned as yet (SEQ ID NO: 29)

ATCATTGACGGACCTTCCGTTGGACCNCCATCATCGGCGCTGGAGACATCGCTGTCGGC
CCTGCTATCGTCGACTTCCCTTTCCCCGACGGCGGTGCCGTGTCTGCCCCCGTTGAGCCT
TCCCCCATCGCCATCGGACCCGCTATCGTCGGTGAATCCCCTATCTCCGTCGGACCTGCC
ATCGTTGAGGCCGGAGACATCGCTGTTGGACCCGCTATCATCGACTTCCCCCTTCCCGAC
10 GGTGGCGCCGTGTCCGCCCCCGTTGAGGTTTCTCCCGTCGACTCCGTCGTGTCGGCCCT
GCCGCCGGCTCTCAGAGCTCTCCCCTCGTCCAGATCATCATCAACGTTAAGGCCCCCGCT
GGTGCCGGCCCCGTTGTGCGATGCCGTGCTGACAAGCCCATGGACATCATTGATGTTATG
CCCGTCGTGACCCTGCTGATTTTCGTGGACCTCACCCCCGTTGTAGAGCCTGTAGAAGTC
GTCGACATTGTGCGATGTCATGCCCGTGGTTGACCCCATCAACATCATCGATGTTATGCCT
15 GTTGTTAAGCCCGTAAACCCCCCTTGCCCGTT

[0220] > *M. esculanta*- Catalase 1 (MsCAT1) AF170272 (SEQ ID NO: 30)
ATGGATCCTTGCAAGTTCCGTCCATCAAGCTCAAACAATACCCCCTTCTGGACCACCGAT
GCTGGTGCTCCAGTATGGAACAACAATTCTCCATGACTGTTGGAACCAGAGGTCCAATC
20 CTTTTGGAGGACTATCATATGATAGAGAACTTGCCAACTTTACCAGAGAGAGGATTCCA
GAGCGTGTCGTCCATGCTAGGGGAATGAGTGCAAAGGGCTTCTTTGAAGTCACCCACGAT
GTCTCTCACCTTACTTGTGCTGATTTCTTCGAGCCCCCTGGAGTTCAAACCCCTGTCATC
GTCCGTTTCTCCACTGTTATCCACGAGCGTGGCAGCCCTGAAACACTCAGGGATCCTCGA
GGTTTTGCGACTAAGTTCTACACCAGAGAGGGCAACTTTGATATTGTGGGAAACAAC TTC
25 CCTGTCTTCTTCATCCGTGATGGAATAAAATTCCCAGATGTGATACACGCTTTTAAGCCC
AATCCCAAGTCTCACATCCAAGAATACTGGAGGATCTTTGACTTCTTATCACACCATCCT
GAGAGCTTGAGCACCTTCGCCTGGTTCTTCGATGATGTTGGAATCCCCAAGATTACAGA
CACATGGAAGGTTTCGGTGTTACACCTTTACTTTTCATCAACAAGGCTGGAAAAGTAACC
TACGTGAAATTTCACTGGAACCCACTTGCGGGGTCAAAGTGTGTTGATGGA
30

[0221] > *M. sexta*-IMD (MsIMD); Msex2.05477-RA (SEQ ID NO: 31)
ATGACTTCTTTGAAAAGCAAATTAGCAGAATTCTTGAAGGGGTAAAATCAGATGCAACC
CCAAGCCCCGAGGCCATCGACAGAACCCAGGGTAAATCCACAACTGAGCAATGAAAATG

ACGCACCCCTCGGATAGTGAACCTGAAGAAATCATTATAGAAGATATGACGATACGAAGAA
AAAGAAAAAGGCAAGTTACAAGAAACCGTTCTTTAGCTCCAAACCTGGTGCATTCCCCGA
AAAGAAAAAGACAAGAATACCAAAGACGATTACAGCAACTTTGTGAATACTCAAGCCAC
TGGTGATGTCATCAATATTGTAGGCTGTAACAATTTCCGCTGGGGTAATAATTATTATTT
5 GGGAAATACCAAGAAACAGGCTCCTCCTAAGAAATATTTCCAAGAAGAGGAAGACAGTGA
ACCAGAAGATGATATTCAGAAATGCAACTTAATCAAACCTGCTATTTGAAGCTGAAAATAA
GCCAGAACATGAGTACCTGGACTACATTTCCCAGAACATGAATGAAAAGTGGCACAGATT
CTTTGTGAACTAGGTTTTACACCAGGAAGGATCAAAACATCCATCATAGATAATGCCAG
TTATGGTATTTTCAGAGGCTCGATACGCATTGCTACTTGAGTGGGTGAATAAAAAACGGGA
10 CTCTAATCTTGGACAGCTATCGAATTTATTGTGGAAACACGGCGAGAGGCGAATTGTCAA
AGAATTAGCCATTATGTACTCTGCAAGCAAGGCCAAATCTGATGATGAATAG

[0222] > *M. sexta*-FADD (MsFADD); Msex2.03129-RB (SEQ ID NO: 32)

ATGACTCTATCGGAATCAAAATTTAAACAATTAAAAGAACAAATTATTTTACATGCAAGT
15 GCAACTGAAAGACATGCTCAAATTTTGAAGTCAATTAAGGATTTGTTTAAAGAAGATATT
AATTCTGTTCTGAAGATTTGAACAAATCAGCAATATAGCACAAATTATTAAGGTTTGTAGAA
ATAAGAGATGTGTTGTCAGAGGATGATGTTGCTCCTTTGAAAGATGTGGCACGCCAACTA
CCAAATAGCTCAGAAATGCTGCGGAAAATTGCTGAATATGAAGAAAATCACAAAGTGTGGA
GAGTTTATTTCTGTTCTAAGTCACCTCCAAAACAAAAAGAACATAGTCATTCTGGATGG
20 GATATTAACAGCATAACAGAATTCTGAATATTCTGTAAAAAAGGAAAGGATATTTGAAGTT
ATTTCTGAAGAAATTGGCACCCATTGGAGAAATCTAGCGAGATATTTGAAAACAAGGGAA
TGTACAATAATTGAAATTGACAGTAAAAACATAACCACTTTCAAGTAAAGCTATGGAGATT
TTGAAATTGCATTGTAAAAAGCAAATCCACAAAAGTGGTTTTTTGACTTGTGTAATGCA
TTGGACAAAGTGCATAGGACTGACATAGTGTTATCACTGCAAGAAATTATGTCTATGAAT
25 ATTTAG

[0223] > *M. sexta*-Dredd (MsDRD); Msex2.04297-RC (SEQ ID NO: 33)

ATGTTGTCTTCCGATGCCAGAAAGTTCCCTAAATTCCAAGAGTGATAATGAAACGTTTATA
TTAAACTTGGATTTCGATTTCAAAGATTGAAAAACAATTACAAGATAATCCTTATGATATG
30 ATCTCTTTAGTGTTTCTGTTGTACGACGTGCCGGATACGGCGCTGCAGAGATTGATGGTG
TATCAACGAGTGACGAGTGACGTCAGTGGAAACAAATATTAATTTGTTGCAAGAATGGTAC
TGTCACGCCAGCAGTCGCCCTGACTGGCAACATGAATTATTAGAAGCATTAAATGATATGC
CAATTGAACTCCATTGTGAAGAGCCTTGGTTTTCCATATACCCACTATGAGAGTATTTTAC

CAATCAAATGATCCCTTCAGCAGCAAGTACATAAATCCCGTAAAGAAAGTCCTTTATCAT
GCCTGTGAAAATATAAACTCAACTAATCTTTTGAAATTAAAAAATCACTTCTTTTCATAT
GATATAAATGTAATGGAATATACAACCTTGTGAGCTTATATTTTTAGAGCTCCTGTCCAAT
AAATTTATTACTATTAATAATATTGGCCAAAAGATTAAAACAAACCAGAACTGCATATGT
5 AATGTAGAAAACCTTGTGAAGATCTTAGACAACCTTAAATGGATTGAAAAAGTGGCTATG
AATTTGAGATATTTTCAAAGTAAATTCATGATGAAGAGGTGGATTTCATTCGCGTCTGTC
AATGGAAGCAGCTCACCATCACTTCCAGTGCCTCCTCTTGATGGTACAAAATTAAAGCAA
GATGACAAGAATTATGGAGCTGAAGATTTCTCAGAGCTATTTCGACATAATAAATAATATG
CCAGAACCGCTTGAAAACAATTTTAAATCTGATACAATGTCAACTAAACAGAATAGATAT
10 GAGATAAAAAATCCGGAACAACCTAGGTGTTTGCATAGTTATAAACCAAGAGAATTTTAT
CCATCCAAAAATAGTATTGAAGACCACCAAATTGTTCCATTAGAAGAGAGAAAAGGATCT
AGTGTGGATAAAAGGACTTTGGAAAGAACCATGACATCATTAATTTTCAAGTTCACAGT
TGCTCTGATTTAGATCATGATGAAATGATAGAATTCATCAAAAAGAAAATTAATAAACAT
GTTACATCAAATGACAGTATTTTTATGTTGTGTATACTGTCACATGGTGTAAGGGACCAT
15 GTGTATGCTGCTGACTCTGTGAAAATTAAAGTAGAGTCTATACAAAATCTGTTGGATTCA
GATGAAATGAGCCACTTGAGAGGCATACCGAAGGTGTTTATTATACAAGCTTGCCAAGTT
GAGGATACACCTCATCTACATTTGCTGCTGACAATGTCCAAACAAATTACTACTTGGGA
AAATTAGACTTCCTTATTTACTGGGCCACTGCACCTGAATATGAAGCCTTCAGACATGAG
CAGACGGGGTCAATTATTCATTCAAGCTCTTTGTAACTGTTGCGTCAAAGAGCTAAACAT
20 GATCACTTACATGAAATCTTTACACAAGTAAATAACAATGTTACCAATCTGTGCACTAAG
TTGCAGCGTGCACAAGTACCTCTCTTCAAAGTACTCTGAGGAAAAATTTATATTTACAA
GTGCCAGAATAA

[0224] > *M. sexta*-Relish F (MsRelF); Msex2.08004-RE (SEQ ID NO: 34)

25 ATGTCCTCTTGTCCAAGCGACTATGATCCCAGTGAATCGTCCAAATCTCCACAAAAGTATT
TGGGAGTCAGGAGGATACAGTTCTCCGTCGCAACAAGTTCCTCAATTGACTTCTAACTTA
ACAGAAATTGTCTGTTGATCACAGCTATAGATACAATGGAAATGGACCATATCTACAGATC
ACAGAGCAACCACAGAAATACTTTTCGGTTCCGTTATGTTAGCGAGATGGTGGGAACACAT
GGATGTTTGCTTGCAAATCTTATACAACAAACAAAGTTAAACTCATCCGACAGTTGAA
30 CTCGTGAATTACACCGGTGCGAGCCCTGATAAAGTGCCAACTGTCGCAAAACAAGAGCGAA
GACGAACACCCGCACAACTGCTCGATGAACAAGACAGAGACATGAGCCACCACGTTCCC
GAGCACGGCAGTTATAGAGTGGTATTTGCCGGTATGGGTATAATTCATACTGCCAAAAAG
GAAGTTGCAGGGTGGCTCTATAGAAAATATATACAGCAGAACAAGAATGAAAAGTTTAAT

AAGAAAGAGCTCGAAGCGCATTGTGAGAGGATGTCCAAAGAGATCGATTTAAACATAGTT
AGACTGAAGTTTACGCTCACGATATTGACACTGGCATTGAAATTTGCCGGCCAGTGTTT
TCTGAACCCATTTATAATTTGAAGTGTGCGTCTACGAATGATTTGAAAATATGCCGCATA
AGCCGTTGTTACGGTAGGCCGAGAGGCGGCGAAGATATCTTCATATTTGTGCGAAAAGGTC
5 AACAAGAAAAACATCCAAGTTCGGTTCCTTTAGACTGGAAAACGGGGAGCGCACCTGGTCA
GCGATGGCGAACTTTCTGCTAAGCGATGTTACCACCAATACGCTATCGCTTTTAGAACG
CCACCGTACGTCAATCACCAAATTTCTGAAGACGTGCAAGTTTTTATAGAACTCGTACGC
CCTTCAGACGGTAGGACGAGCGCTCCCATGGAGTTCACATACAAGGCTGAGCAAACTCTAT
AAACAGAACAAGAAACGTAAAACTACTTCGTCTGCTACTCGTCGCTCGACAGCTCCTCAGGT
10 TCGGCCGGTTCAATTAAAAGCATCAGCGAACTGCCCCGACCCGTTGTTTTTGTGAAAAC
TTACCTGAAAACAATGAGCGTATTATAGATATACCCGTACAACAGAATATGCTGTACCAG
GTTCTGCCAAGTCAATGTGATTTAGCCGACGCGTTCATGGAGGTGGACAGCAAGGGAAGT
CCGGCCAGCGTCGTGGACCCGATGTGGGCCGGCGCCGACGTCGGGCTGCAGATGGCGTCG
AGCCTGCCCCGCATCAAACCTCGGCTCCACCGAACTAGAGAGCTTGGCGCACCCGACGCCG
15 GACGGAGTGCCCATGGACAAAGAATTCCTTGACAATTATCTCAGCTCTCTCAACTCGCTT
GGTGAACCTTAACGACGATGATGAGATCAATCATATGCAATATGTGCGCTCGTTACAGATG
GTCCACGCCGACTCGGCACGACGAAAGGCTGAACCGCAACCCAAAGACACTGTAACCAA
CCGACTCAATCTTCCCCGAAGGACACAGACTATGGCGCCCAGTCGGGACGCCCCACTGAA
TATTCTGCTTATTATAAAATGGAAGACGGCGTGGAAGTCAAAAACTGGTGAAAGAATTG
20 TGTAGTATCATAACAGAACAAAGCGGGATATAAAAAACAAGAAGTGAGAAACAAATTGGAG
AGGCTGTTACCTACCGTCTGTCCAACGGAGATACATTCCCTTCATATGACATTGTGCAGC
AATCAAAGTAGTTTTGAATACATCGTCAAATCATAACATAGCGTGAAAATGACACATCTA
TTGGACTATTGTAATAATAACAGCAAACCATATTACACATGGCTATTGTAAACGACCTG
CCTCGAATGGTCTCTTTACTTATTGCAAAGGTTGCAATCCAATGAATAAAGACAGCGAG
25 GGCGACAATGCGGTGCACTACGCTGTGAGGAGCGAATGTTGTTTAGAAGCATTATTGGAC
GCCATCAAAAATAACAATGTTTCGGTGCGATTTGAACGACTGCAATAACGAGAAGCAGACG
GCGCTGCACCTGTCGACGAGCGGCGCGAGCGCGCGGACGCTGGCGGCGCGCGGCGCCGAC
CCGCGCGTGCGCGACGCGCAGGGCCGCACGCCGCTGCACCTCGCCGCCTACGACGACAAC
TGCGACGTCGTGAGGGCGCTGCTCGAGTTCGTGTCGCCCTCGGAAATAGACGTTGTGGAC
30 GGCTGTGGCAACACTGCGTTACAGATCGTCTGCGGCGGCTCCGTTAAGAAGAACACTTTG
GAAATAGTAAACTGTTGCTCCAAAAAAGGCTGATCCGTTGAAGCAAGATGGGCACAAC
ATATCGGCGTGGAAGATGGCGCGGAACACTCCGAAATACGGGACGCGATGAAGGACTAT
GTCCCCGCCGCCGCTACGAGGAGGACACCAAGTCGGAAATGGACGATGAGTTCGAATCC

5 GCTGATGAGGAGGACTACCGGATGGGTTCGGATCGGGCGCTGTGAGTCTGCCGGAGCTG
GGCGCATACGTGGAGGCGCTGAGCGCGGCGCTGGAGGCGCGGCGCGTGGCGCGCGCTC
GCGCACCGCCTCGGCCTCGCCGCCGCGCTCGACTGGTGCGCGCGACAGCACGCGCCCGCG
CGCACGCTGCTGCTGCACCTCAAGGAATGCAGAAACGACATATCCTCGAAAACGTTGGCT
GTAATTCTAGAAGATATGGGAGAATTAGAGGCTGCTTCAATTATAAGGAGACACATAGAG
TGA

[0225] > *M. sexta*-Cdc42 (MsCdc42); Msex2.04668-RA (SEQ ID NO: 35)

10 ATGCAGGCGATCAAGTGTGTCTGTCGTCGGAGACGGTGCCGTGCGTAAACATGTCTGCTC
ATCAGCTACACGACAAATGCCTTCCCCGGAGAATACATACCTACAGTATTGACAATTAT
TCAGCGAATGTGATGGTGGACGGGAAGCCGATCAACCTGGGCCTGTGGGATACGGCGGGG
CAGGAGGACTACGACCGGCTGCGGCCGCTGTCCTACCCACAGACCGACGTGTTCCCTTATA
TGCTTCTCGCTCGTCAACCCGGCTTCGTTTCGAGAACGTTTCGGGCTAAGTGGTACCCAGAA
GTGCGGCATCACTGCCCCTCGACGCCCATCATCCTCGTCGGTACCAAGCTGGACTTGCGC
15 GAAGACAAAGACACCATAGAGAACTTAAGGACAAGAAGCTCGCGCCTATCACTTACACA
CAGGGTCTGGGCATGTCTGAAGGAGATCAACGCGGTGAAGTACCTCGAGTGTCTGCGCTG
ACGCAGAAGGTCTGAAGACGGTGTTTCGACGAGGCCATCCGCGCCGTGCTGTGTCCCCTG
CCGCCCCCAAACAGAGCCGGAAGTGCACGCTGCTGTAA

20 [0226] > *M. sexta*-DSor1 (MsDSor1); Msex2.00725-RB (SEQ ID NO: 36)

ATGAGTAAGATGTCAAAGAATAAATTAACTTGACCCTGCCACCAGGGTCAATAGACACA
GCACCAGCCATCACACCATCCAATATGACACCACAGCTGAAGTCCGCAACAGCTACGGAG
CGTCAGGGCTTGGCTGGTAAATCGAAAACCAGCATCGAAGCCCTGACAGAGAGGTTGGAG
CAAATCGAGATGGACGACACACAGAGACGGAGAATAGAAGTGTTTCTGTGTCAGAAGGAG
25 AAGATCGGGGAGCTTAGTGATGATGATTTTGAAGCTTGGAGAGTTAGGCCAAGGCAAC
GGTGGCGTTGTAATGAAAGTCCGTCACAAGTCAACCGGTCTGATAATGGCGCGAAAGTTA
ATCCATCTGGAAGTCAAGCCGGCAATAAAGAAGCAAATCATCAGGGAGTTGAAAGTCTTA
CACGAATGTAACCTTTCGCGATATCGTCGGCTTCTACGGGGCCTTTTATAGCGACGGCGAG
ATCTCGATTTGTATGGAGTACATGGACGGTGGGTCTTAGACCTTATACTGAAGAAGGCC
30 GGCAAGATTCCTGAATCTATTCTAGGAACAATAACATCCGCCGTGCTGAAAGGTCTGAGC
TACCTCCGGGACAAGCACGCCATCATGCATCGCGACGTGAAACCATCAAACATTCTGGTG
AACAGCAACGGCGAGATCAAGATATGCGATTTTCGGCGTGTCGGTTCAGCTGATCGATTCC
ATGGCCAACCTCTTTTGTGGCACTAGGAGTTATATGTCTCCCGAACGTCTCCAAGGCACG

CACTATTCAGTCCAATCTGACATATGGTCGCTCGGGCTGTCGTTGGTAGAGATGGCAATC
GGAATGTATCCCATACCGCCGCGGACGCGAAGACCCTGGCTGCCATCTTCGGTGGACAG
AATGAAGATCATTCTCCTGGTCAGGCGCCGAAGCTCGCCCCGTCCGATGGCCATATTCGAG
TTGCTGGACTACATCGTGAACGAGCCGCGCCGAAGCTGCCCCGCCGAATATTCTCCGAC
5 GAGTTCAAGGACTTCGTGACCGCTGCTTGAAGAAGAATCCAGACGAACGAGCCGACTTG
AAGACTTTGATGAATCACGAATGGATACGCAAAGCGGACGCAGAAAAGGTGGACATAGCG
GGGTGGGTGTGCAAGACAATGGACCTCATGCCTTCCACTCCAACTCTAACGTGTCTCCT
TTTTCTTCATAA

10 [0227] > *M. sexta*-FOS (MsFOS); Msex2.09858-RA (SEQ ID NO: 37)

ATGCAGAACATCGATCCTCTGGAGATCGCCAACTTCCTCGCCACGGAGCTGTGGTGCCAG
CAGTTGGCGAACCTCGAGGGCCTCCAGTCGGGGGTCCCGACTCGCACAACGGCCACCATC
ACGCCGACGCAACTGCGCAACTTCGAGCAGACTTACATCGAGCTGACCAACTGCCGCAGC
GAGCCCACCACGCACGCCGGCTTCGTGCCGCCGTGAGTCACGCACGCCAACAACACTACGGC
15 ATCCTGAATCCGACGGCGTATTGTGATTTCGGGCCCCGACGACGGCGCTGCACGTGTCGCCG
GGCCCCGCTCTCCGCCAGCGGCGACAGCAGCAGAGCCCCGGCCTGCCACGCCCCAAGCGG
CGCAACATGGGCGGCCGCGGCCCAACAAGGCGCCGCAAGAACTCACGCCCCGAGGAAGAA
GAGCGCAGGAAGATCCGCCGCGAGCGAAACAAAATGGCCGCCGCCGTTGTGCGCAAGCGC
AGACTCGACCACACCAACGAGCTGCAAGAGGAAACCGACAAATTAGAGGAAAAGAAGCAT
20 GCGCTCCAGGAGGAAATCCGCAAACTGAACGCTGACCGGGAGCAGCTGCAAGTGATCCTT
CAGAACCATATGGTATCATGCCGGCTCAACAAGAGATCCATCAGCCCCGCCCGATGTGAAG
CCCTTCCAGGACCCGTACGCCTACCCTGAGATACCCGAGGATGGCGTCCGTGTCAAGGTG
GAAGTGGTCGACCCCTCAGTAGACACGGTCTTAGTGTTGGACAATATTTACTCAACGCCG
CCGACTGACAAAAAATTATGCTGTGTCGTGCGCCAACCCAGCCGTGGTGACGAGTGGGTGCG
25 CCCGCCGCCCTGGAGACCCCGCCGGCGATAGTGCGTCCCAACAGACCCAACTCCCTCCAG
GTGCCGCTCAGCCTCACACCAGCACAGTTACACAACAACAAGGCGCTGGGAAACAACAAA
ATAGCCGGCATAGAGATAAGCACGCCGAGCAACGGCATCCCGTTCAACTTCGAGAGCCTG
ATGGAGGGCGGCACGGGGCTGACGCCGGTGCACGGCCACGCGCTGCCGCTGCCGCACCCG
TGCGCGCAGCAGCAGCGCGCCGCGCCGACGCCTCGCCCGCCGAGCCGGCGCCGAGCTCG
30 CTGGTGAGCCTCTGA

[0228] > *M. sexta*-Jra (MsJra); Msex2.12422-RB (SEQ ID NO: 38)

ATGGTTCTGGCACTCCGGCCACGGCATGGAGACCACTTTCTATGACGAGCAGTATCCCATC
AGCGGCCCCGTGGAGAACCTGAAGCGGCCCCCTCACGTTAGACGTGGGGCGCGGCGTGAAG
CGCGCCAGGCTCGGCGGGGCACCCGTACTCTCATCTCCAGACCTACAGATGCTGAAGCTC
5 GGCTCGCCAGAGCTCGAGAACTGATCATCCAGAACGGCTTGGTGACGACGGCCACCCCC
ACTCCAGGTGCGCCGGTGCTGTTCCCCGCGGTCGCGCCTACCGAAGAGCAAGAGATGTAC
GCGCGGCCATTTCGTGAGGCGCTAGACAAGCTGCACCACGGCGAGGTGACCCCGATCGGG
CGGCGAGTGTACGCCGACCTGGACCGGCGCTCGAGCGGTACCCACGCCCGTGGTGAAG
GACGAGCCGCGACGGTGCCAGCGCCGCCAGCTCGCCTCCACTTTCCCCTATTGACATG
10 GACACGCAGGAGCGGATCAAACCTGGAGCGCAAGCGACAGAGGAATCGAGTGGCCGCTTCC
AAATGCAGGCGGCGCAAGCTCGAACGCATCTCCAAGCTGGAGGACAAGGTGAAGATCCTG
AAGGGCGAGAACGCGGAGCTGGCGCAAATGGTGGTGAAGCTAAAAGAGCACGTACACCGA
CTGAAGGAGCAAGTGCTGGAGCACGCCAACGGCGGCTGCCACATCGAGTCGCACTTCTGA

15 [0229] > *M. sexta*-Caudal (MsCAD1); Msex2.04570-RA (SEQ ID NO: 39)

ATGGTGAATTACGTTAATCCCCCTCGCCATGTACCAAGGCAAGGGCGGGCAATACGGCGGC
GGGTGGTACGGCTGGCAGCATCAGAACTTTGAAGAACAACAATGGTGTGCTTGAACGGT
GCGCCGGCGGGTGCGGAGTGGGCGCCAGATCCACATCATTTTCCCAAAGAGAACCTGGA
GAGAGAGAAATAGCAGACATGCCATCACCGGCACGAGGAGACTTGGCAAGTCCAGCAGAA
20 GGTTTCGCCGAGCTCGGGGTGAGGCCGTCGCAGCCGCCAGCACCGCCGCGTTCCCCATAC
GAATGGATGAAAAACCCAACTACCAGACACAACCTAACCCAGGTAAACGCGCACAAAA
GACAAATACAGGGTGGTGTACAGTGATCATCAGAGGCTGGAGTTAGAGAAGGAGTTCCAC
TACAGCAGGTACATCACTATTTCGTGCAAGGCAGAACTCGCCGTCAGCCTTGGCCTTTCC
GAACGACAGGTCAAATTTGGTTTCAAATAGACGAGCCAAGGAAAGGAAACAGGTGAAG
25 AAACGCGAAGAAGTGGTGATGAAAGAGAAAGGCGACCATGCATCTCTACAGCACGCGCAG
CTGCACCATGCCACCATGCTGCATCACCAGCAGATGATGAACGGCATGATGCACCACCAC
CACTACCACCAAGGCGTGTTGCAAGGCGTGCCGAGCCGCTGGTGCCGGGCGTGCCGCC
GTGCCGCTGCTGTGA

30 [0230] > *M. sexta*-Atg8 (MsAtg8); Msex2.12227-RA (SEQ ID NO: 40)

ATGAAATCCAATACAAAGAAGAACATTCTTTGAAAAAGAGGAAGACTGAAGGCGAAAAG
ATTTCGAGGAAATACCCGGATCGCGTTCCAGTAATTGTAGAGAAAGCCCCGAAGGCTAGA
TTGGGAGACCTCGATAAGAAGAAGTATTTGGTGCCGCTGATTTGACTGTGCGACAATTT

TATTTCTAATTAGGAAACGCATCCATCTTCGGCCTGAGGACGCATTGTTCTTTTTCGTG
 AACAAATGTTATTCCACCAACATCCGCCACCATGGGCTCTCTGTACCAGGAACATCATGAC
 GAAGATTTCTTCCTCTACATTGCATTTTCTGATGAAAATGTTTATGGATTTTAA

5 [0231] > *M. sexta*-Atg13 (MsAtg13); Msex2.06273-RA (SEQ ID NO: 41)

ATGGCACCCGAAGTGGCTTTTTCTAACATAAATGACAAGAATGAATTTACTAAATTCACA
 AAATTCTTAGCTTATAAAGGCGTTCAAGTTATTGTAGAATCGAGGAAGGGTGTAAAAATA
 GATCCTAATAGTAAACCAAGATCATCAGACACTGATTGGTTCAATCTTCAAATACCAGAC
 TCTCCAGAGGTTAACCAGGCAACTAAGAATGCATTGCCTTCAGACAAGGTGTTAGAGATT
 10 ATCAAAGCCCAACTGCACGTGGAATATCAGTACAAACCGAGGATGGCGATGAAATGGTT
 TTGGAGTTGTGGACCCTTGAACCTTGACGAACTCAGTTTGACACTTCTGTAAAGCCACG
 AACACAGTTTACTTCAGAATGGGAATATTACTTAAGTCGCTTATAACTATAACAAGAATT
 ACTCCAGCGTACCACTTGTCTGAGGAAGCAAAGAACAGAGTCGTTTACAATATTCTACAGA
 GTATACAATGGCGAACCGAAAAGTAAAAGCGCTTGGAGAATCAGTGAAGAAAATTCAAGCT
 15 GGAATGCTCAAACTCCACTTGGAGGGATAATATTCTCCGTGGCCTACCGCACAAACTTC
 TCCATTTTCGCCAAACAGATCGGAGAAGGACAAAACATTGCTTTTGAAGAGTGATCATTTT
 GAACTGAGTCCAAACATGTGATATTTGAATCCAAGAAAAAGAAAGACGAGAAAAAAGAA
 TACAAGCCTCTGAAACCTGTTGATTTGAATAAGCCACTTCGATTAGCCGCATTTGTAGAC
 GAGGATGTTGTAAAAAAGGCCCTTGTGACTTCATGGAGAAGATGCCGATTCCCAAATAC
 20 CGAGTGATACGTAGGGAGAGAAGTCCAGAGAGCGACAAGCCTATAGTATCCAAAAGTACT
 CAGGATTTGGACGCTTCTGTGACGTCAAAGAGTCCGACGTCAATGGAAATGCCACCTAAA
 AAGTTCACAGGCTTTTCGCAATGAGAACGAACCTCCATTAAAACCTCTCCATTTCCCATT
 GCTGATAACCATCCGATAAGAGAACTGGCCGAGTTTTACAAAGAGTTCTTCAACGCCCCC
 CATTTGAAGTTAGCTGATGACGTTAGCCTGAAATCGGGCAGTGCTGAATCGGTAAAAGAG
 25 GTGATAGAGATTACAACCTGAAGATTTGTGCGAAAGATCTCGAATTGTATGAGAACTCGGTG
 TTGGAGTTTGATGAGCTCTTGGCAGATATGTGCCGATCGGCTGAGTGGAGTGGGAACCTAG

[0232] > *M. sexta*-IAP1 (MsIAP1); Msex2.05607-RA (SEQ ID NO: 42)

ATGGCATCAGCTGGCGCCGTACCGAATATTCTAGTGTCGTCGTCGCTTTTCAAGACCACT
 30 CCTCGGGATCCTAAAATTTCGTGAAAAACAAGCCCTTTGAAGTTACCACCTTGTGACACA
 CATATAGGCTCGCCTCCACCATCATCCTCTCCGACCTCCTCGTCAACTGATAAAACCGAT
 AATCATGATACTTTTGGTTTCCTTCCTGACATGCGtgatatgCGCGGAAGAAGAACGA
 CTGAAAACCTTCGATAAGTGGCCTAGCACGTACGTGACACCTGAAGAGTTAGCTCGTAAT

GGTTTCTACTACCTTGGGCGCGGTGATGAAGTTCGCTGTGCATTCTGTAAAGTAGAAATT
 ATGCGATGGGCGGAAGGAGACGACCCTGCGAAAGATCACAAACGATGGGCGCCCCAATGT
 CCGTTTTTACGTAATCTTTTGAACGGTACTAATGGCAGCGGAGAAGGTAGTTCGGAAGGT
 CGCGACGAGTGTGGTGC GCGAGCAGCGACGCGGGAGCCTGTGCGTATGCCCCGACCTGTG
 5 CATCCCCGCTATGCAACAGAGTTATCGCGTCTCGCCAGTTTCAAGGATTGGCCGCGTTGC
 ATGCGCCAAAAACCAGAGGAACTCGCGGAAGCAGGATTTTTCTACACCGGCCAAGGGGAT
 AAAACGAAATGTTTCTATTGCGATGGAGGTCTCAAAGATTGGGAAAACGACGATGTTCCA
 TGGGAACAGCATGCCCCGTTGGTTCGATCGTTGTGCGTATGTGCAACTTGTTAAAGGCCGT
 GATTATGTCCAGAGGGTATTATCGGAAGCGTGTGTTATACGTGCCACCGACGAAAAAGCCT
 10 GCGCCTGCACCTCAACCGTCCCAACCAAATGTCTCAGTTGTATCAGAAGAAAAACCTGTC
 GAAGAGGCTAAGATATGCAAAATATGTTATTCCGAAGAACGAAACATATGCTTTGTGCCG
 TGCGGTCATGTGGTCGCTTGTGCAAAGTGTGCCTTATCTACTGATAAATGCCCAATGTGC
 CGGAGGGCTTTTCACAACTGCACTGCGACTCTATTTTTTCGTGA

15 [0233] > *M.sexta*-Chitin synthase 2 (MSCHS2); AY821560.1 (SEQ ID NO: 43)
 ATGGCCGCAACTACACCAGGTTTTAAGAAGTTAGCAGACGATTCTGAGGATTCTAGATACA
 GAATACACCCCGCTGTATGATGACGGTGATGAAATAGATCAAAGAACTGCACAAGAAACA
 AAAGGATGGAATCTATTTTCGAGAGATTCCGGTGAAAAAGGAGAGTGGATCTATGGCCACA
 AAAAATTGGATAGAAACAAGCGTAAAAATCATAAAAGTGCTTGCCTACATATTGGTTTTT
 20 TGTGCTGTACTGGGTTCCGCAGTCATAGCTAAAGGAACTCTTCTATTTATTACGTCACAA
 CTGAAGAAAGACAGACAAATTACTCACTGCAATAGACGACTTGCTTTAGACCAACAGTTC
 ATAACGGTACACAGTTTAGAAGAAAGAATAACATGGCTATGGGCAGCACTTATTGTATTC
 GGTGTGCCGGAGTTAGGGGTGTTTTTGAGATCCGTCAGGATATGCTTCTTCAAAACTGCC
 AAGAAACCAACCAAAACACAGTTTATTATTGCTTTCATAACAGAGACACTACAAGCAATA
 25 GGAATAGCAGCACTTGTATTAATAATTCTACCAGAATTAGACGCTGTGAAAGGAGCCATG
 TTGATGAACGCCACGTGCGCTATCCCTGCATTGCTAAACATTTTCACGAGAGACCGAATG
 GATTCTAAGTTTTCTATAAAATTGATATTGGATGTATTGGCGATATCGGCACAAGCCACG
 GCGTTTGTGTTTGGCCTCTTATGGAAAGAAGCCAGTTCTATGGACCATAACAGTTGCA
 TGTGTGTTAGTGTCTCTAGGCTTCTGGGAGAATTTTGTGACACCTACAATAAAAGTTAT
 30 GTTTTTACGGTGCTGCAGGAACTACGCGACAACCTCAAGAGGACTCGGTACTACACTCAG
 CGGGTGCTATCTGTTTGGAAGATTATAGTGTATTATGGCATGCATTTTAATATCGCTGCAT
 ATGCAAAATGACAATCCGTTTACCTTTTTTCACTCACGCCAGCAAAGCCTTTGGAGAGAGA
 CAGTATGTCGTTAACGAGGTTCTAATAGTAGTCCGAGATGACGAAACCATAGGCTATGAC

GTCACCGGAGGTATATTCTGAATTGGACGCGATATGGACCTCAGCATTGTGGGTTCGCATTA
ATTCAAGTGGGAGCAGCCTACTTCTGTTTCGGAAGTGGCAAGTTTGCTTGCAAAATTTCTT
ATACAAAATTTTAGTTTTCACTTTAGCATTGACTCTCGTCGGGCCCCGTGGCAATCAACCTC
CTTATTGCTTTTCTGCGGAATGAGAAATGCAGACCCTTGCGCTTTCCATAGAACTATACCT
5 GACAATTTGTTTTACGAGATACCACCTGTGTACTTCTTGCGGGAGTACGTGGGCCACGAG
ATGGCGTGGGTGTGGTTATTGTGGCTCATATCTCAAGCGTGGATCGTGTTTTACACGTGG
CAGCCGCGATGCGAGCGCCTCTCCGCAACTGACAACTGTTTGCCAAACCGTGGTACATC
GGACCGCTAATCGACCAATCGTTGCTGCTAAACAGGACTAAGGATTTGGATAATGATTGC
CAGGTTGAGGATTTGAAGGGTCTTGCGGACGATTTCGTTCGGTTGGAAGCGATCTTGCCATC
10 GTAAAAGATATCAAACCGTTTCGATTGATAACCAGAATACAAGTGTGTGCGACAATGTGG
CACGAGACCAATGAGGAGATGATCGAGTTCTTGAAGTCGATATTCCGCCTCGACGAGGAC
CAGAGCGCGCGCCGCGTGGCGCAGAAGTACCTCGGCATCGTCGACCCCGACTACTACGAA
CTCGAGTGTCATATTTTCATGGATGACGCTTTTGAAATATCCGATCACAGTGCCGAAGAC
TCGCAGGTGAATCGCTTCGTGAAGTGCCTAGTGGATGCGGTGGACGAAGCGGCTTCCGAA
15 GTGCATCTGACTAACGTGAGGTAAAGGCCCCCAAGAAATACCCACCCCGTACGGCGGA
AAACTAATTTGGACCATGCCAGGGAAAAATAAGTTGATTTGCCATTTGAAAGATAAATCC
AAGATTCGGGCACAGAAAGAGATGGTCGCAGTTATGTACATGTACTATTTCTGGGGCAT
CGCTTGATGGACCTGCCAATATCCGTGGATCGTAAGGAAGTGATTGCCGAGAACACGTAC
CTATTAGCTTTGGATGGAGACATCGACTTCAAGCCGAGCGCTGTGACGTTGCTGGTCGAT
20 CTTATGAAGAAGGATAAGAACTTGGGCGCCGCTTGCGGTTCGCATTCATCCTGTTCGGCTCT
GGTTTCATGGCCTGGTACCAGATGTTTCGAGTATGCTATTGGTCATTGGCTGCAAAAGGCG
ACTGAACACATGATCGGCTGCGTACTCTGTAGTCCGGGATGCTTCTCCCTCTTCAGAGGA
AAGGCGCTTATGGACGACAACGTCATGAAGAAATACACACTCACTTCTAACGAGGCTCGA
CATTACGTGCAATACGATCAAGGCGAGGACCGTTGGCTGTGTACGTTGCTGCTGCAGCGC
25 GGGTACCGCGTGGAGTACTCGGCGGCGTCGGACGCCTACACGCACTGCCCCGAGCGGTTT
GACGAGTTCTTCAACCAGCGCCGCGCTGGGTGCCCTCCACCATGGCCAACATATTCGAT
CTGCTCGCGGACTCCAAACGCACCGTGCAAGTCAACGACAACATTTCCACTCTGTATATC
GTCTATCAGTGCGATGCTTATGATGGGTACGATTTTGGGTCCGGGAACAATCTTCCTGATG
ATGATTGGCGCAATAAACGCTATAACAGGCATGAGCAATATGCACGCACTTCTCTTTAAC
30 CTGGTGCCCGTGCTTACGTTTTTGGTTGTCTGTATGACATGCAAGTCCGAGACTCAGTTG
ATGCTCGCGAACCTCATTACCTGCTTTTATGCGATGGTAATGATGTTTGTGATCGTCAGT
ATCGTCCTACAAATATCACAAAGATGGTTGGCTAGCGCCATCTAGTATGTTCACTGCGGCA
ACATTTGGAATATTCTTCGTAACAGCGGCTTTGCATCCACAAGAAATAATATGTTTGTG

TACATTTCCATATATTACATCACAATTCCGAGCATGTATATGTTGTTGATTATCTACTCC
CTATGCAATTTGAACAACGTCTCGTGGGGAAGTTCGAGAGGTGGCTCAGAAGAAGACTGCA
AAGGAAATGGAAATGGATAAGAAAGCAGCGGAAGAAGCAAAGAAGAAGATGGATAATCAA
AGCATAATGAAATGGTTCGGCAAGTCGGACGAGACGAGCGGCTCGCTGGAGTTCAGCGTG
5 GCGGGACTGTTCCGCTGCATGTGCTGCACCAACCCTAAGGACCACAAGGACGACTTGCAT
CTCTTGAGATCGCCAACTCCATCGAGAAGATCGAAAAGAGATTGTGCGCACTTGGCGCG
GAGGAGTCCGAGCCGGCGCAGGCGCAGACGCGGCGCCGCTCGTCGCTGGGGCTGCGGCGC
GACTCGCTCGCCACCATGCCCCGAGTACGCCGACAGCGAGCTGTCCGGAGACATTCCCTCGC
GAAGAAAAGAGACGATCTTATAAAACCCCTATTGGGTGGAGGATCCCAATCTGCAGAAAGGT
10 GAAGTAGACTTCTTGACGACGGCTGAAATCGAATTCTGGAAGGACTTGATTGATGTTTAT
TTGAGGCCCTATCGATGAAAACAAGGAAGAGCAGGAACGTATCAAACCGATCTAAAGAAC
TTGCGTGACACGATGGTGTTCGCGTTCGCCATGTTGAACTCGTTATTTCGTGTTGGTGATA
TTCCTGCTGCAGTTCAACCAGGACCAGTTGCACATAAAGTGGCCGTTTCGGGCAGGATGTC
GCGCTTTCTTATGACAAGGAAAGGAATGTTGTATTGGTGGAGCAGGAATTCCTTATGTTG
15 GAGCCTATAGGTTCCCTGTTCCCTCGTGTTCTTCGGGTTTGTAATGTTGATACAGTTCGTG
GCGATGTTGTCCCATCGTTTCGTATACTATTACGCATTTGCTCTCCACAACAGAGCTTCAC
TGGTATTTTCAGCAGACGTCCGGACCAGATGTCAGATGAAAACCTCTTGGAAGGAAGGTG
GTAGAAATAGCGAGAGAGTTGCAGAAGTTAAACACGGACGACCTAGACCGCCGCGCGGTC
GAAACTAACGACGTGTGCGGGCGAAAGACTCTACACAACCTAGAGAAGGCGCGAGACACC
20 AAGCACAGCGTGATGAACCTTGACGCTAACTTCAAGAGGCGACTGACTATACTACAGAGC
GGTGATCCTAACGTGATATCTCGGCTGTCATCGTTGGGCGGCGATGAGGTTACTCGTCGC
GCCACGATACGCGCATTAAAGACGAGGAGGGACTCACTGCTCGCTGAAAAACGACGCTCC
CAGCTGCAAGCGGCGGGCGACGCTACAGGCTACATGTATAACCTGTCAGGCACTGCGGTG
AACGACATGAGCGGCCGAGCTTCGACGGCCAGCGCCTACATTAATAAAGGATACGAACCC
25 GCTTTCGATAGCGACGACGAACCACCGCTCCGCGCAGGAGCACTGTACGCTTCAGA
GAAAACTACACGTAA

[0234] > *M.sexata*-Beta-fructofuranosidase 1 (MsSuc1); GQ293363.1 (SEQ ID
NO: 44)

30 ATGTACATTAAACAGCAACATTTTTGCTGTGCGTTTTCTTGGTAGTGTATCGTCATGT
TGCGTTAATGGGCGGTACTACCCGAGGTACCATTTGTCGCCACCGCATGGCTGGATGAAC
GACCCCAACGGATTCTGCTACTTCAAAGGTGAATACCATATGTTTTACCAGTACAATCCC
ATGTCAAGTTTGGAGGCTGGCATAGCTCATTGGGGTCATGCGAAAAGTAAAGATTTGTGC

CATTGGAAACACTTAGACCTCGCCATCTATCCTGATCAGTGGTACGATCAAACGGGAGTA
 TTTTCTGGAAGTGCCTAGTAGAGAATGACGTCATGTACCTTTATTATACTGGAAATGTA
 AATCTTACTGATGAAATGCCATTTGAGGGACAATTCCAAGCTCTTGGTATCAGTACTGAC
 GGTGTCCACGTAGAAAAGTATAAAGACAATCCAATAATGTACACGCCAAACCATCAACCT
 5 CACATCCGAGACCCAAAAGTTTGGGAACACGACGGCTCTTATTATATGGTCTTAGGAAAC
 GCATATGATGATTATACAAAGGGCCAAATAGTTATGTACGAATCATCAGACAAGATCAAC
 TGGCAAGAAGTAACCTATACTATATAAATCAAATGGATCTTTCGGTTACATGTGGGAGTGT
 CCAGATTTATTTCGAAATAGACGGCAAGTTTGTACTTCTGTTCTCTCTCAAGGCGTGAAG
 TCTGTGGGCGATATGTACCAGAACTGTATCAAGCAGGATACATCGTCGGAGAATTTCGAT
 10 TACGATACTCATTTCATTACAACTAACC GAATTTCAGAGAATTGGATCACGGTCATGAT
 TTTTACGCTACACAAACAATGAAAGATCCTAGTGGAAGAAGAATAGTCGTTGCTTGGGCA
 AGTACTTGGGAGTATGCTTATCCTGAACGAGCAGATGGTTGGGCTGGCATGCTCACACTA
 CCTAGAACTTTAACTTTGACAAAAGATTTAAGACTAATCCAACTCCAATTAGAGAGATC
 GATCAAGTTTTTTAGAAGAAGACTATATTCAGGAAAAGCCTCAGCAGGCAAACTGTCGCT
 15 TTACCAGACAAAGCAGGGAAAAGTAGAACTGAAATGGGATACACCAAGAAATATAAAGGTA
 GTTATAGAATCTCAAAATGAGTGCCAAAACGTAGTAATCAGTTATGATCACGAGGATGGT
 ACTATTACTTTGGACAGAGGAGGCGATGACGCAATCCGCCGCACTCACTGGGATCCTCGA
 GGTCACCTCAAATGGACCATTTTTATTGACGCAAGCTCCATAGAACTCTCTTGTGGTGAT
 GGAGAAGTATGGTTTACAAGCAGATTTTTCCCTGAAGGAGTCGTATCTGTTCCGCTTGGG
 20 GAAGATACTTGTGTTGATAAGTTTACCGTGCATTCTATTCGCCGTACTACTCCAGACCCC
 GAGGCTCATTGTCGTTGTGAATCAGAAGAATAA

[0235] > *M. sexta*-Hemolin (MsHEM); M64346.1-UTRs

5'UTR (SEQ ID NO: 45)

25 TGTTACATTAATTATAAAAAAAAAATACAAAAAGAAATATATAAGTAAGTACTAATAATA
 TGGTCTAGTTTATTATAAGTCTTAGAGACTAACGATAAATAATAAATTTCTCATGAACCA
 CCTATTTATTTATTTGAAAAGCATTTTAAATATATTATAGATTTAAACGTAACGAAGTCT
 TTAAACTCGCGGTAAAAACGCATACTTACTTGACTCTACATCGGCGACACACGAAAAAC
 TTATTTCGTACTGTTTTTTCATTGAATATGTTATGAAAAAGAACTATATGTAATCGCAG
 30 TCACATATATAAACTTTATAAAAAAGTTAACAGAGATAAATAACTTGTTTGGTGTTTCGT
 CATAGCAATAGAGTAGCCGCGGCGCCTAAGGCTACGAAATAAGCTCATTGAACTGTAATG
 GAGTGTGCCTAGTTGTTTCTCTTCTTACCAAGACTCAAGAGGGATTTGGAGCTTCATCTA

CGATTATTATACCTACCTACGTATAGACTATAATGGATAGTAAAAATAGAAAGTAATTTTC
TTTTATATCAACTTTTGTATTCATATGTAAGTACTTACTTATAATTATTTATTTTTTTTAG
GTGAAA

5 **3'UTR (SEQ ID NO: 46)**

GTTAACAATAAACAATACTGTTAACCGTACGTAGTGTTAAATAATACAAATATATGTATT
TTACAATAAGATTTCTGTTTTTAAATTATCCTCACGTAACGTATTGGGTATCTAAGCGG
TTGAGCAGTGAGATAAGTCTACCCCAAAGTAGTCCGTTTCATCAAACGACATAACCATCTC
GTCATTTAGTTAAAACAAAAAAGAATAATGATAAAAGATATAAAATTCTGTATAAGAAC
10 CAATACCTAGCACCTTTCTCACATTGCCAAACATACATTAAAAACAGTATTATGCTTTT
TTCGCTCTTTTATTCTATATTTTATATTAAAAAATACCTATAGTAAATACTGTTTTTCATC
GTCGCCGGTATTCATACACGTAGTATACGTACCTAACTCTGAAACTACTGGTTTGAATTG
AAAAA

15 [0236] > *M. sexta*- Serine Proteinase homolog 3 (MsSPH-3); AF413067.1

5'UTR (SEQ ID NO: 47)

AGCGCTTTGGGAACGTTCCGTGGCACGATA

3'UTR (SEQ ID NO: 48)

20 GATGGTGGAATGTTTAAAAATACAAGAGTGTGAGGCAGTGATTAATGGTCTGTAATATCC
GATTCTTGCTGGCTTCTGTTTCGTAATTAACGTAAAATCTAATTATCATTAGAATATTTT
GGAAAACCTTAGAGTTACCTTCGGAAACTTCACCGTTTGCCGCTGGTGTGAAGATCTGT
TCCCCCATAAACTGATGGGAAATTGTATGTAGGTACTCGAGTTATAATTTCTTTTATA
CCTGCGTTTAAGTTCCATTACAACCTTTCTAATTTTATGAATAAATATCTAATAAACGATT
25 AACAAAATTAAAAA

[0237] > *M. sexta*- Peptidoglycan recognition protein 2 (MsPGRP2);
GQ293365.1

5'UTR (SEQ ID NO: 49)

30 ACGGCATAAATTGTTAGGTCGTCTGAGAGGCGAGTGTTGTATTTTTAATTGCCAAAGAGG
CTGCGAAGTTCGCAATAATCATTAGAAAA

3'UTR (SEQ ID NO: 50)

AATGACCAAAGATAATACGACTGTTTTATAATTTTTGTTAATAAATGTTGTTGCATTATG
GAAAAAAA

- 5 [0238] > *M. sexta*- **Beta-1, 3-glucan-recognition protein 2 (MsβGRP2);
AY135522.1**

3'UTR (SEQ ID NO: 51)

ATTA AAACTAACGAAAAGACTCGTTTCCATAGTGGTATATTTTCAACTCGTCAATTTTCAG
GTACAAGCATGTTTGGTGGAAAGGATATTATCGGCCCCGAATAGGCACTGTACACCAAGTAC
10 AACCATGACTCATCAAAGGTGTCGCGTTCTGGAATCACCTGTATTTCCAACAGGCCGGCA
TAATTGTGTCGTCTAGCGAGGGGATAACTCAATAGTCTATTTGAACGCCATTCTACTTACC
ATTAGGTGTAGTGAAGATATTTGGGGCTAGACAAAATGGAAGGAAATTTATGAGTTGCAT
CGAATGATTATCACTAAGTATTCGAATGATTCATTTTCGTTGTTGGTGCAATAGGATGTCA
AGGGTCAAATGGACATTAAAAGAGAGTTTAAGGTGTTTTTTTACAATTAACGTTGATCTA
15 TCACTTTACTTGCCTATTAAGTAAAGTATTATTTTGAAAAATACAAAATACTTGAGTTTA
TAGTATCTCTTGCGTTTATGGTACTGTCAAAAATATCAGTATTATTCATTTACAAAATTA
AAATTTAATAATCTAAATTATTCTTCATGTAAATGATCATTTATACCTCTGCCTTGATTA
TG

- 20 [0239] > *M. sexta*-**Relish family protein 2A (MsREL2A); HM363513.1**

5'UTR (SEQ ID NO: 52)

AGAGTACGTTTCGATGGCAGTCTGTCTGAACATTGGTAGTTTCCCGTTTGAGTGTGTTTAC
TCCCTTTGAGGGATTAGTTTATTCTCCACGAATATAAACATCGGAAAATCAAAAATAAG
TTGATAAAAAGTTGTGTGCTCCGGTATAATTTTTTGGTATCAGTGACGGACAAAGGTGAT
25 ATAAAA

3'UTR (SEQ ID NO: 53)

TATATTCATGAGAAGGGGACAACCTAAGGATTGAATATCAGCAGAAGTTGAGTTATGTTAA
TGAGGTATTTATATTAGCTTAATACTTAAAGGGGAAAATTCGATTAGCTTTTCAAATATA
30 CTTAAATTTTAGTTTTTGTCAAATATCGGTGTTTCCCATTTTGATATTTTTTTATCCATA
TTTTAATAATAAATATCTTGTCTTAGCAATTTTAATGGGTAATTATAAAGAACTCACGC
ACCATAGTTGCACTAACTACAAAATTACACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

[0240] >*M.sexta*-Dorsal (MsDor); HM363515.1

5'UTR (SEQ ID NO: 54)

ATACAACGATATCACAGGCGTCCGGGGACGGACCAGTTTAAACAAACATTACAGTGAATA
5 GCGATGTGATTATTTTCTTGCTTGTATAGAGTTAAATTTTAAATTAGATTTAAATATTA
AAATATTTGCGAATAAAA

3'UTR (SEQ ID NO: 55)

ACTTAACAATTACATCTATAAATCTCTCCTCTATCAACCTAGTGGGCGTCTCTACAACCT
10 ACCACGTCTGGTATACAAATAGTGACAACCTGAAATTGTGAGATTTAAATTGTGTAGTTA
TGATAAATAACAATAAATCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

[0241] >*M. sexta*-Toll receptor (MsTOLL); EF442782.1

5'UTR (SEQ ID NO: 56)

15 GAAAAGTTATTACAATATGACCCGAAGTGTCAGCGCCGCACATGCGCGGGAGCACTCGT
ACTTATACCAGACATTGTGACTAAATACCTAATTTTATGTTTTGCTCATCGCCCATTGCG
CGACATTAAGCAGTATCCAGTAGTCAGTGATCAGTGTTACTACACTATTTTGCTTCTCAG
CGATTAGTCAACACGCGCATATCGTTTACTTCAACAAACAATTATTACGCAAATCGTGAT
ATTTGAATGTAGAGACACGAATCAAAGATTATTCGTTTAAAGTTATTTTCGCGGGATGTT
20 TCTCTGTTGGGGGGTACTGTTGCGTGGTGTGCAGTCAAAGGTTTATTTTATCGGGTATTG
TGCTCTTTAAGTGTTGACGCGGCGGATTATCGTCGGTTAGACTAATAAATCGTGTCGATT
TATGTGTGACCCACTACGGTGTCGTGCGACGTG

3'UTR (SEQ ID NO: 57)

25 ATCCAGAACTTGCGTGTACCCTTCGATATACAGGGCTATTTTGACATCGTGTTACTAAAT
GAAACCACATTCTCGTCTTCACCTTTGCTGACATTGTGCCAAAAATCATCCATTAATAAC
GAATATTTCCACCAAAAAAAAAAAAAAAAAAAAAA

[0242] >*M. sexta*-Scolexin A (MsSCA1); AF087004.1

3'UTR (SEQ ID NO: 58)

5 TAGACCATACCGTTGTCATTTTGGGCTGTAGTGTATAGATAATAAATATAGACGCGTGTA
CTGGTGTGACGTACGGAAGTGGAGAGTTGGGAGCGACAGCTCACCGCTCACTCCACTCCC
GGCCGCCGCGCAGTAGCAGTGTGAGTGATTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

[0243] >*M. sexta*-Hemolymph proteinase 18 (MsHP18); AY672794.1

5'UTR (SEQ ID NO: 59)

10 GCCAGACGTTTCAGTTTGTTCGAACT

3'UTR (SEQ ID NO: 60)

TTATGAATAAATACAATTTAATAAGCATTATTTATTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

15 [0244] > *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1); AM419170.1

5'UTR (SEQ ID NO: 61)

TACTTCGGGCTACACAATGTACGTGAAAGTA

3'UTR (SEQ ID NO: 62)

20 TCTCCGAACCGAACCTGATCTTAAGTGTAAATAAAATAAGCGATACCCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

[0245] > *M. sexta*-Dredd (MsDRD); Msex2.04297-RC; Currently annotated as
Manduca sexta Caspase-6; HM234679.1 in NCBI

25 **5'UTR (SEQ ID NO: 63)**

TTGGTAACCCCTGTGGGAAGTCCCAAAGTCGAAGCTCGAGAACAGTTTTAAGCAGAGGTT
TTAAGTCTAATTTATTGGTCTCTGGTTTTAAGTTAGTGTCATGTGTCAACAATAATAAA
GCTTTATTTTTGGCTCTATTTATAAGTAAGGTATCATCCTTTCAGCGTTAAAACAAAGG
GCGTAGCTCATGTTTCATGTAGTTCTTTTAAATAAGTGTGAACTAAGTGTATATGTACAT
30 TTATTACTGGTGACA

3'UTR (SEQ ID NO: 64)

CATAATATTTTTATTTAGATATATTGTAAGTACTAAGAATGAAGTGGTGATAGCTTAGTT
 GGGAGTGGAATGGACAGCCAAGACAAATGTCAGCAAGTTCAAATCCAAAGGCATACACCT
 CTGACTTTTAAAAAAAATATGTGTGTATTCTTTGTAAATTATCAGTTGCTTTACGGTGA
 5 AGGAAAACATCATGAGGAACTCTCAATAGTAAAGGTATCCCATGCCCAGCAGTGGGAC
 AGTATATTATACAGGGTTGATATTATTATTATTATATACTATGCTTTGCTCATGCGCTCA
 TTCACTCCAGCATTAAATGACCTTTCCTGGTATTGAAGTTCTGCTAAGTATTTTATGGGAT
 AAAAATACCCTGAATGTTAATCCACACACATTCAGTATGTCAAATTTTCATCTAAATCCAT
 TTAGGTGTGTTCTATTTGATACTAAGTTCCAACAAAAATCTTCATAAACGTCAGGACCCC
 10 TCAGGAGCAACATTATTAATAAGATTAATAATAAATTTTCAATGCATAATAATTTTAATA
 TAATTTATATTACTTAATGTTGAAGTTGATATACTTAA

[0246] > *M. sexta*-Relish F (MsRelF); HM363513.1

5'UTR (SEQ ID NO: 65)

15 AGAGTACGTTTCGATGGCAGTCTGTGCGAACATTGGTAGTTTCCCGTTTGAGTGTGTTTAC
 TCCCTTTGAGGGATTAGTTTATTCTCCACGAATATAAACATCGGAAAATCAAAAATAAG
 TTGATAAAAAGTTGTGTGCTCCGGTATAATTTTTTGGTATCAGTGACGGACAAAGGTGAT
 ATAAAA

20 **3'UTR (SEQ ID NO: 66)**

TATATTCATGAGAAGGGGACAACCTAAGGATTGAATATCAGCAGAACTTGAGTTATGTTAA
 TGAGGTATTTATATTAGCTTAATACTTAAAGGGGAAAAATTCGATTAGCTTTTCAAATATA
 CTAAATTTTAGTTTTTGTCAAATATCGGTGTTTCCCATTTTGATATTTTTTTATCCATA
 TTTTAATAATAAATATCTTGTCTTAGCAATTTTAATGGGTAATTATAAAGAACTCACGC
 25 ACCATAGTTGCACTAACTACAAAATTACACAAAAAAAAAAAAAAAAAAAAAAAAAAAA

[0247] > *M. sexta*-Chitin synthase 2 (MSCHS2); AY821560.1

5'UTR (SEQ ID NO: 67)

ATTACGCTTTGAGCAGCCACTTTGTAAACACTAGCCTATTAACCTCCGTCAGTCTCGGC
 30 GATAACACTTCTGTATATCTGTTATTGTTTGTTAATTTTGGCGCAAGGATATATTTAAT
 ATGTGCTAAGTTTGTGGCTAATTTATATTATGTTTCTACATTAAAGGTATGTATTAGTGA
 TTTTTTGTAACCTATTTAATTACAAACATTATAACATATTTTATTAGAAAAGGGTTTTGT

ATCCTATGTAGCGCCTGTTTCACGATGCCTCTTGAAGTATACTGAAATGGGTACCCGTCG
 ATAGTGTTTGCTTTAATAGGCAACGCATAGTGAAAACCTTTGTACTTTAACCTTTTCAAAA
 GCATGAATAATTAAAAAAAATATTAGAATAATGTGAAAAAGGTGTACAGTGTGATAAAT
 ATGGAGTATACAATATTCTTGTTCCAGTTATAAGATAAGGCACA

5

3'UTR (SEQ ID NO: 68)

TATTTGGCCAAAATTGTGAACTGTAAACATGCAATAAAATGATGAACG

[0248] > *M. sexta*-Beta-fructofuranosidase 1 (MsSuc1); GQ293363.1

10 **5'UTR (SEQ ID NO: 69)**

TGAGAACAAAAACATTAGCTCCGCGTTTAAAA

3'UTR (SEQ ID NO: 70)

TTATCGTGCTAAAGTAATAGTTATTGTTTCACATTATGTTCAAATAAAAAAGTAATTATT
 15 TATGTTCAAATAAAAAAGTAATTATTTAAGTGTCTTGTAATCTGCGAATAAATATACTT
 AATGTATAAAAAAAAAAAAAA

[0249] > *M. sexta*-Sickie (MsSck); Msex2.03324RA (SEQ ID NO: 71)

ATGACGACGTTGACTGCAAATAGGCAAGTGTGCGTGTTGCAGACGTCGATCCCGCTGCCG
 20 GCGTCGGCGGGCGGCGGTGCGGCGCGCTCCGCCGACAAACGACCGCTGCCCCGCCACACCA
 GTACATGCAGGTGGCAAGAGTGGTCTTTCTGCGAGTTCCAGCCGCTCCACCAGTCCATTA
 GGACAGGGTGCAGTCAGTTTTATACCACGTGCGCCTAATTCATCATCTGGATCCCGGCCG
 AACTCGTCCCTCCTTGCGCCCAGTAGCAAATACCCTCCACCGCAACACAAGGGCAACAG
 CATTCACAAACACCCACAGCCCCAAAATGGAACACCCACAAAGCAGTCTATGCTTGACAAG
 25 TTAAAGCTATTCAATAAAGACAAAATTAGCAATGAAAAACAAACAGCAAAAGCACTGCA
 GTATCAAAACGCACCAGTTCTTCCAGTGGTTTCTCATCGGCAAAGAGTGAGAGATCAGAC
 TCGAGTTTAAAGCCTTAATGAGTCTTCTAACATACCCAACACACATATCAAATCGTCTAAT
 TTAATAGGACCTAAAACAATACGGCAACAAAGCGATACTTTATCAAAGACAAATCTGGT
 AAAAATTTAAACCTAAGTTAGTTAATTCTAAATCTCCTAGAGATTCTACAACCTAAGT
 30 AATAGGGCTAGTAGCAAAACAACTAATAATGATAAATCGAGGAATAGTCCAAAACCTTCCT
 GCTAGGGATAAGGAATCGAAACTAGCCACACCTAAAACCATGAGTAACACAAAACCTAAAC
 CAAGTTGAAGATCAACCGAGGGGTTCAAAACCTAAAGTGGAATCGAAAATGGTAAAGCTT

TCCGGTAGCCAAGTTAAGCTGAGTGAACAAAGATCCGATACTCCACAAGACTGTAAAGAA
AATGTAACCTCCTAATGCGAAAAATCATCAGAGTCACTCTCAAACACCATGTGGAGGACAG
GGATTTGGAAC TCCAACCATA CAGGAATACCTAAACCGACTGCCGCTGTCAAGGGAAC T
TTTAAATATCAAAGACGATAGACATGTTATACAGAAAAGTACAAATAGTCAATTAAGT
5 CCTATACAAAGCAATTCTAGTTTAAATTCTACAAATAACATAAGTGC ACTTCCATTCTGT
AGAGAACAATCTAATTTAAGTAAGGATATAACTCAAAAGCAGACACTAGCCGTATCCCCG
ATGCCGGTTATGAGCACAGGGAATCAAATCATAGTTTCGCAAATGTCTGAAAGTTCACAC
TCCAATTCTACGCACAGTACTACAGGCCAACATTCGAACTCTAGCGATAGCAGCGTTATA
TACCGTCCCTTAGCGAATCAGGTTCTGAAATGTGAAAGACTGCTAGTCACAGTGTGGCA
10 TCAAATAAACGGCTAGACATGAATACTACTTATATAAATGACGTTATAAACGAAGCGGAG
ATATCAGAAAAGGAGGCAGCACAAAGACGTCACGTCGATAATTCAATCCCCAAGCAATCG
TTTGATCCCAATAAAACGTTAACCGAAATAAGTAGGAGGCTCGAAAGTGATAGTAGATCT
AGCACACCGTCGCATTGTCTGTGATAATTCTTTAGGCGAAGACGAGAATCCAATGATGAAT
GTTTTACCAATGAGACCGTTACTTCGCGGATACAACAGTCATTTAACCTTGCCCATGAGA
15 ACTTCAGGTTTGGCACAGAAAAATATAAGCGTTTATCCACACCACGCAAATACTGTAAAA
GCAAAC TTTGGACGGGAAAACATAGGTCTTCGCGATCGTATAAACTATGGGCCTGGTTTT
TCGAATCCTGATTATTGTGATCTGGAAATTGCTTCGGGATACATGTCTGATGGTGATTGT
TTGAGAAGAATTAATATCGGTGAGATGGAATGCGGGAGGAACAACGACATGATGGACGGC
TATATGTCCGAGGGTGGTGCTTCACTCTACGGTCGTCCGATGAACTACCAGCAACCACAA
20 TTTCAACAAATGGACGAAAGACGAAGTGGTGGTCGCAATAGAGGCATGGAGGGTGGTAGT
GGTGTAGTCTACAGAGTAGTGGGTGCGCACACGCAGCAAAGCCGACTCCGGACAGCAGACC
GAGCGCCAGCCTCAGCCTTCCCGGCAGGACACCACGTGGAAGAAGTACACTGACTCGCCC
GGGAATCAGCCAGCACCCGCGCCTCCTAGTCCATCTCACTCGCGCAAGGGTGAGAGACGA
ACTGGCCATCATTCACCGCAGCACCACAAACGAGAAAACTCACTGCAGCTCAGCAGCTT
25 GGGATCGCACCTCATCTCAGTATGCCGCTCCAGCTCAAGCAGCTAACCTGTGGTCAG
CATTCCTCTAGAAACCCAGGCCCACAGCTCCAGTCTCCGAGTGGAGGGTCGCGTCCCTCC
AGCGTCTCTAGCGGTGGTAATGGCAGTGCCTGCTCGTCGAAGGCTAAAGTTCTCAAAT
TTTGATATGTGAAAAGACAAAACGGTGTACAGCAGCCGGCACCTCAGGCCAACGGTCCA
CCGCCGCAACATGGAGGCCACACTGGAAGAACCGCCAGGTGTCTGCAGTGCCAAGA ACT
30 AAAGTCAAAGTTTCGGGAGGAACCCAGACATGCACACAGGATTTACAGATTCACAAAAAT
GGTATCGGACCTAAATCGTATTCTCTGGGCGGCACCGCGGCTGCCCACTGTCAGCGTCA
GTGCGAGAGAGACTGCTCGGGTCACAATCACTACCAAAACCTGGAACACACGAATTCGCA
GCGTTATTCCATCACCACAGAATTGCACCCAGAGGCGGCATGAAGATCAGCGATGGCAGC

CTTTCTGACACACAGACATACTCTGAAGTGAAATCAGACTATGGGATACCCCTACGCGCCC
TGGCTCAGGCATAGCAACACATACTCGGCGAGCGGGCGGTTGTCAGAGGGAGAGTCGATG
GAGTCGCTCACGTCGCTGCACTCGGCGCAGGCGCAGGCGCACAACCACACCTCCTCCCCT
AACTCCCACCGCAGCTCACTCACACACAATAAGCTCATCATGCACCGAGATGCACAGGGC
5 TCCAGGCTTAACAGGAGCAACAGCATTAGATCGACTAAGTCAGAAAAATTATATCCGTCTG
ATGCTTCAAAGGTCTTCAGAGAGCGATTATGAACCGTATTATTGTTTACCTGTGCAGTAT
GGACCAACAGGTCAAGGTCTAAACTATGGTGTGTCTGGAGCCGCCGTGCGCGTCGCCGCGC
TCGGCGCTGAGCCCGACGCACGCGCCCGGCAACGTCATGCACACGCCGCGCCACTCACAC
CACTACCCGAAAAAGAACGACGATGTGCACGGTTCGACGGCGTCGCTAGTGTGCACCGCC
10 TCCTCGCTGGCTGCCGGCGCAGGCGCAGAAGAGAGGCACGCCCATGAGGTGCGAAAGCTG
AGAAGAGAACTGGCCGATGCGAAAGAAAAAGTTTCACTTTAACAACGCAGTTAACAACC
AACGCGCACGTGGTGTCCGCATTCGAGCAGAGTCTGTCTGAATATGACGCAGCGCCTGCAG
CAGCTCACCGCAACCGCCGAGAGAAAGGATTTCGGAACGACGGAGCTTCGTCAAACGATT
GAGTTGCTGCGGAAACAGTCGATTCAAGCTGGTCTGACTACTGCTCACATGCAGTCCATG
15 GGAATCCGTGCCGATGGCGTCAACGTCACTGGACAGCAGGACCCAACAACCCAAACGCAG
CAGTCATCACCACAACGTAACGCACAAACGGGCAACGGTGCGATCACGCGGCATCTATCG
ACCGACAGCGTGTCTGAGCATCAACAGCCTGAGCAGCGGCTCCTCAGCGCCTCACGACAAA
AAACACAAGAAAAAAGGATGGCTACGCTCATCGTTTACGAAGGCATTCTCACGGAACGCG
AAGATATCTAAACAGCGAAGCACTCGTCCCTCGGGCAGCTGTCGTACAGGACAGCTCG
20 TCGGGCTCGCATCACTACGACGACCCGCACACGATACGAGAGGGCAGTAATGAGAACAGT
CTAGAACATTCCCACGAGGCTCTTCTGATACTAAGGAGAAGCCGGCGCCTGTCAAGCCT
GAAGAACAAACCAAGATAACAAAGAGGAATCTGTCTTGGTGGATGAGCTGAAGCGGCAA
CTGCGCGAGAAGGATCTCGTGTGACCGACATCAGACTGGAGGCGCTCAGCTCCGCGCAT
CAGTTGGAGAGTCTCAAAGACACCGTTATAAAAATGAGAAACGAGATGTTGAACCTGAAG
25 CAAAACAACGAGCGTTTGCAGCGGCTGGTGACGTACGCTCGCTCGCCGGCAGCCAGAGC
TCGCTCGGCACCGGCGGCTCCGCCGTCGAGGACCCGAGGCGGTTACAGCCTCGCGGACCAG
GCCACCATGCACCAGGCGGCGATCGACATTACGCCCAGCCTCTCGACCTCGACTTCAAC
TGCATGTCAGCCACACCAACCATCGACTTCTCGAAGAAAGGTTACCCAAGTCCGGCATG
GTGGAGCCCATATATGGGAATAAGGCTGCCTGCGAACTGAACGAGAACAATGAGACGCTG
30 CTAGGAGCGTTGAATGGGGCCAGCGATTTGTTCTCCAACGGACTCAATGCTGGAGAGCGG
CTGAGTGGAGATTACGATATAAACAGCGTGTTACCGCCGCCTAAAACACGCGAGCTTGCT
ATTGGTGAAAGCTACTCTGATATTGGTGTAGCAGACAGCCAGGGAGACACGACTGATGGA
AAGAAAAATAGCGATAGCTGTATATTTAGGTCAACCCGAAACATTCCAAAGATATTTCGAA

GAGGTCCAAGACACATTGACGGAGTCCGAGTGCAGATTCTACGCGAAGCAATCGGCAAGC
GCGTACAATCATTTTCGAGAAACAAGCCAGTTTCGAATCGCCGAGAATGTCCACGAATCAC
AGTCCAGAAGTGGAGACACAAGACTACCCGCAAATAAATAAGTCGAACACGAATAGCCTT
AAAAGCAACAAATCTACGCACAGTAGCTCGTATAAGAATGTTTATAATAGTGATTTCGACA
5 ATAAACTGCAACGAGTACACTATAGCGTACACTTATATATCTGGCAAGACGACTTGGCAG
AATTTAGATTATATAGTTAGGAAGTCCTTTAAGGACTACTTGTCTAGGATAGATTTGGGC
ACGAATCTCGGTCTGAACACTGATTCTATAACGTCTGACCATTGTTGGTGAAGCGACGCGT
GGGCCGGAGATCGGCTTCCCGGAGCTGTTGCCATGCGGGTACATCATAGGGACCGTGAAC
ACGCTGTACATCTGCTTGCAAGGAGTCGGCAGTCTGGCGTTCGATAGCCTTATACCAAAA
10 AATATTGTATATAGATACGTTTCTCTGCTATCGGAACACAGGCGAGTGATACTCTGTGGT
CCCAGCGGCACCGGCAAGTCATACTTAGCGGCGAAACTCGCTGAATTTTACGTCCAGAAA
ACACAAAGGCGCGGCAATCCCGCCGAAGCTGTAGCTACATTCAACGTGGACAGAAAAGTCG
TGCAACGAGCTGCGCGCGTACCTGGCGAACATCGCGGAGCAGTGC GGCGCGGCGGCCGCG
GGCGAGGAGGCGCCGCTGCCGTCCGTCTGTGGTGTCTCGACAACCTGCAGCACGCCTCCGCG
15 CTCGGCGACGCCTTCGCGGGGCTGCTGCCGCCCCGACAACAGGAACATGCCCCGTTATTATC
GGTACCATGTCCCAAGCGACGTGCAACACCACGAATCTCCAACCTACATCACAACCTTCAGA
TGGCTCCTCACCCTAACCACATGGAACCCGTCAAAGGATTCTTAGCTAGGTATCTCCGA
AGAAAGTTATTCTCGCTGGAGCTGCGGCTGGGTGCGCGGAGCCGGCGCTGGCGGCGGTG
CTGGAGTGGCTGCCGGGCGTGTGGGCGCGCTCAACGCCTTCCTCGAGGCGCACTCCTCC
20 AGCGACGTCACCGTCGGGCCGCGGCTCTTCCTCGCCTGCCCCATGGACTTGGAGGCCAGC
CAGGCATGGTTTCGAGACGTGTGGAACCTACAGCATAGTGCCGTACGCTTCGGAGGCGGTG
CGCGAGGGCATCGCGCTGTACGGCAGGCGACGACACGCCGCCGTGACCCGCTGCAGCAC
ATCAAGTCTACATACCCCTGGAGAGAACCCAATCACTCGCATACTTTGAGACCCATAACA
GTTGATGATGTTGGCATCGAAGAGTCAAGCCAAGACTCCGCCGTGAACAACAATCAAGAT
25 CCTCTGTTGAACATGCTGATGCGGCTACAAGAAGCGGCGAACTACAGCGGAAACCAAAGC
CAGGACTCTGACAACGCCAGCATGGACTCGAACCTCACACACGACAGCTCTGTAGGGAAC
GAGCTTTAA

[0250] > *M. sexta*-Akirin (MsAki); Msex2.12479-RA (SEQ ID NO: 72)

30 ATGGCGTGTGCTACACTTAAAAGAAATTTGGATTGGGAATCCATGGCGCAATTGCCTGCT
AAAAGGCGAAGATGTTCCGCATTTGCTGCAAGTTCTAGCACAAGTCCTGGATTTAAAGTG
TCTGAAACCAAGCCATCTACATTCGGAGAGGCCGTTAGTGACCTGTGAAAATGACCCCA
GAGCGCATGGCTCAAGAGATCTGCGACGAGATCAAGCGGCTGCAGCGGCGCCGGCAACTG

CGGCTGGCTGGCAGCTCCGCCGCTTCGTGCTCATCGTCGAGCGGCAGCGAGGGCGACTGC
TCGCCGCCACATCGCTCCTCGCACACTTCGCACAAGATGCACAACCGTGCGCTCTTCACT
TTCAAACAGGTGCGCATGATCTGCGAGCGGATGCTGCGCGAGCAGGAGGTGGCTCTGCGC
GCGGAGTACGAGTCGGCGCTCAGCACCAAGCTCGCCGAGCAGTACGAGGCGTTCTGTGCGG
5 TTCAACCTTGATCAGGTGCAGCGCAGACCCCCGCCAGCACGTGCATGCCCCCTCGGCATG
GACGCCGAGCATCACATGCACCAGGACCTCGTACCTAGCTATCTGTCCTAA

[0251] > *M. sexta*-Cactus (MsCac); Msex2.02793-RA (SEQ ID NO: 73)

ATGAGTGCCAAAAAAGGATATGAAACGAAGATTGTGAGGAAGAAAACATGGATTCCGGA
10 ATTGTGTCTGGTGAATTGGAATCTTATGAGATTTTCGGGTGAAGTGGATTTCGGGCGTGATT
GATTGTGATAAGAAATACGAAGGGGTTCCAAGTGAGGTGTTGGAATTGACGGACAAGTTC
AAAAGTGTAATGTGAGAGAGAAGAGCTGTCCTGATGTTCCACCACTGGCGGACCTGTTT
CACCTTGACAACGACGGAGATACACAACCTACACATTGCATCGGTACACGGCTGCGAGAAA
TCAGTGAGCACGATCATCAGGGTGTGCCCTGACAAGGAGTGGCTGGACCTGCCCCAACGAC
15 TACGGCCACACGCCCCCTCCACCTCGCGGTGATGAGCGGCAATGCCGTGGTGACAAGGATG
CTGGTGATAGCCGGCGCTTCGCTCGCTATTTCGCGACTTCATGGGAGAGACGCCCTTACAC
AAGGCGACCGCAGCGCGAAACCAGGAGTGTCTCAAAGCCCTGCTTGCCCCCTGTACCGGAA
CAGCCCCAATAGGAAATTGTCTTCAATACTCGACCAGAGGAACATAACGGTCAATGTTGT
GTCCACCTGGCGGCGTCAATTGGAAGCGTAGAGACGCTACAGACCCTGGTCTACTACGGA
20 GCCGATATCAATGCCAGGGAGAACCTGGCGGGCTGGACGGCGCTGCACATCGCGGCGCGG
CGCGGCGACGTGCGCGTGGTGCAGTTCTTCGCGGTGCGGCTGCGCCGGCGCGGCGACGCGG
CCGCGGGACTACGCCGGCCGCACGCCGCGCCGCTCGCGCGCCGCACCAAGGCCGCCGCC
GCCTTCGACGACAAGGACGACAGCGACTCCGACTCCGACTCGGACGATGATGATATGTAC
GACAGTGATAGCGAGACGTTGTTGAAAACTCCGCGAGAGCCTGAGCACGTGATCAAC
25 GTCGCCTGA

[0252] > *M. sexta*-Gloverin (MsGLV); GI110649240 (SEQ ID NO: 74)

CCACGACAACCACTGATGAAGTTATTTTTTATAGCAATTCTTTTCGCTGCCATCGTCGCT
TGCGCGTGCGCTCAAGTGTGATGCCCCGCAATACGCTCAGATATATCCAGAATATTAC
30 AAGTACTCCAAACAAGTCCGCCATCCCAGAGACGTGACCTGGGACAAGCAAGTCGGCAAC
AATGGGAAGGTCTTCGGAACCTCTGGGACAGAATGACCAGGGTCTTTTCGGTAAAGGAGGC
TATCAACACCAATTCTTCGATGATCACCGCGGCAAACTGACAGGACAGGGTTACGGGTCC
AGGGTCCTCGGACCTTACGGAGACAGCACCAACTTCGGCGGCCGGCTTGACTGGGCCAAC

AAGAATGCTAACGCTGCTCTTGATGTGACCAAGAGCATTGGCGGTAGGACTGGGCTGACT
GCCAGTGGATCAGGCGTGTGGCAACTTGGGAAGAACACGGATTTATCTGCGGGAGGCACT
CTGTCTCAGACGCTTGGACATGGGAAGCCTGATGTGCGCTTCCAAGGTCTCTTCCAGCAT
AGATGGTGA

5

[0253] > *M. sexta*- Beta-1 tubulin (Ms β Tub); AF030547 (SEQ ID NO: 75)

ATGAGGGAAATCGTGACATCCAGGCTGGCCAATGCGGCAACCAGATCGGAGCTAAGTTC
TGGGAGATCATCTCTGACGAGCATGGCATCGACCCACCGGCGCTTACCATGGCGACTCG
GACCTGCAGCTGGAGCGCATCAACGTGTACTACAATGAGGCCTCCGGCGGCAAGTACGTG
10 CCGCGCGCCATCCTCGTGGACCTCGAGCCCGGCACCATGGACTCTGTCCGCTCCGGACCT
TTCGGACAGATCTTCCGCCCCGACAACCTTCGTCTTCGGACAGTCCGGCGCCGGTAACAAC
TGGGCCAAGGGACACTACACAGAGGGCGCCGAGCTTGTGACTCGGTCTTAGACGTCGTA
CGTAAGGAAGCAGAATCATGCGACTGCCTCCAGGGATTCCAACACACACTCGCTCGGC
GGCGGTACCGGTTCCGGAATGGGCACCCTCCTTATCTCCAAAATCAGGGAAGAATACCCC
15 GACAGAATTATGAACACATATTCAGTTGTACCATCACCCAAAGTGTCTGATACAGTAGTA
GAACCTTACAATGCAACACTGTCAGTCCACCAACTCGTAGAAAACACCGACGAAACCTAC
TGTATCGACAATGAGGCTCTCTATGACATCTGCTTCCGCACGCTCAAACCTTCCACACCC
ACATATGGCGACCTTAACCACCTGGTGTGCTCACAATGTCCGGCGTGACCACCTGCCTC
AGGTTCCCCGGTCAGCTGAATGCGGATCTCCGCAAGCTGGCGGTGAACATGGTGCCCTTC
20 CCGCGTCTGCACTTCTTCATGCCGGGCTTCGCTCCGCTCACGTCGCGCGGCAGCCAGCAG
TACCGCGCCCTCACCGTGCCCCGAACACCCAGCAGATGTTGACGCTAAGAACATGATG
GCGGCGTGCGACCCGCGTCACGGCCGCTACCTCACCGTCGCCGCCATCTTCCGTGGTTCG
ATGTCCATGAAGGAGGTCGACGAGCAGATGCTCAACATCCAGAACAAGAACTCGTCGTAC
TTCGTTGAATGGATCCCCAACACGTGAAGACCGCCGTGTGCGACATCCCGCCCCGTGGT
25 CTCAAGATGTGCGCCACTTTCATCGGCAACTCCACCGCTATCCAGGAGCTGTTCAAGCGC
ATCTCTGAACAGTTCACCGCTATGTTCAAGCGCAAGGCTTCTTGCATTGGTACACCGGC
GAGGGCATGGACGAGATGGAGTTCACCGAGGCCGAGAGCAACATGAACGACCTGGTGTCC
GAGTACCAACAGTACCAGGAGGCCACCGCCGACGAGGACGCCGAGTTCGACGAGGAGCAA
GAGCAGGAGATCGAGGACAACCTAG

30

[0254] > *P. xylostella*- Peptidoglycan recognition protein 2 (PxPGRP2);
ACB32179.1 (SEQ ID NO: 76)

ATGACGTTGTCTTTTGGCGTGTTTCTGCTGATATCTTCAGTGTTTTGTTGTTGTGCTCAT
GCAGGGTGTGGCGTGGTGACCAGACAGCAGTGGGATGGGCTGGACCCGATACAGTTGGAG
5 TACCTGCCCCGGCCCCCTGGGGCTGGTGGTGGTCCAGCACACCGCCACCCCGCGTGTGAC
ACTGACGCCGCGTGTGTGGAGCTGGTGCAGAACATACAGACCAATCATATGGATGTGCTG
AAGTTTTGGGATATTGGACCGAACTTCCTGATTGGTGGGAACGGCAAGGTGTACGAGGGC
CCTGGTTGGCTGCACGTCGGCGCCACACTTACGGCTACAACAGGAAGTCTATCGGGATC
TCTTTCATTAGGAATTTTAATGCTAAGACCCCAACAAAAGCAGCGTTGAATGCGGCTGAA
10 GCATTGCTGAAGTGTGGAGTGAGAGAAGGACACCTGTCTCACTCATACGCAGTGGTCGGC
CATAGACAACCTGATCGCAACAGAGAGCCAGGCAGGAACTGTACCAATCATCAGGCGC
TGGCCAAACTACCTCGAGGATATTGATAAGATTAAAAACAACAAGTAG

[0255] > *P. xylostella*- Immune Deficiency Protein (PxIMD); Px003008 (SEQ
15 ID NO: 77)

ATGTCTATCCTAAAATCAAAGTTATTCGAACTATTGCAAAAAGTTTCAAGTCTGATGCA
GTCCCGAAGCCACCTAGAGAACCGGTAGAGACTACAGAGACATCACAAAATAATACCGAA
AATCAACCTTACAATGTCTGAAGAAGAGGAAATACCCGAACCAGAAAAGCCTAAGAAAGAA
AAAAAGAATCCCAAGCCTACCAAAAAAATTTCTTTAATCGTGACAAAATAACAAACAC
20 GACGATACCCGCAAACATACAAAATCCGGAAAGGACCAGACATCAATTAATACTCAAGGT
AACTTGAAAATTATACTTCCTGTAACTTAAACGGCCCGTTGACCCAGTTTACCTTTCGC
CTTTCTTGATATATTTTTGTAATCCAGCCTTACTTTGGTAATACATACTTGCCCCACTTG
TATTTAGTTAATGGTGGCACTAGCTAGATAGTAATGTTAAATGATGATAAGCAGTAGTGA
TTCATCATTCAAATGTATCATTGTCCTTTAATGTTAAGCGCAAATAGATTTTCATTGTTT
25 TCCCATGTGCTTCATGTTTTATGTATTTATAGGTAGGTACTTAATGTTTTATAAATATTT
TTTTGTTAATTGGGAATCCCCAGTCCCCATTGTCTGGACCAGTTTATATATAATTGAACT
AACAAGAGTGTGCTTTAAATACTATTCTCTGCAATTATGATAATTAAACAACATGAATTT
CTCTTCACTTCCCTTCTCTTATTTAAATAATATTGTAGGAACTGTAATAACTAATACAA
GATTATAAATTTTATTCTAGCAACTGGTGTATGTAATCCATGTGGTAAATTCCAAAGATGT
30 GCAGGTCGGCCATCAGTATGTGTACAACATGGGAACCCCGAGCTAACTCACAGAAGAA
TAACCCATTTGATGATGAAGAAACAGTAGAAAAGACAAATCTAATAACTCTGGTCATGGA
AGCAAAAATTATGGTAATAACACATTTTTAACTAGGCATAAGGTCATAATTTAGCCAGAA
TCATCAGCTTGTCTGTGGCTCTTGTTGAGCTGGTGGAAAGAATACATAGGTAATGAATA

TTTTGATCAATACTCATTGCAAAAATCACAATAATGCCATTGAAAATCTATAACATGTTCT
 CTTAAGTATCAGTTATCATCAATCCAATTAAGTCATCACACAGATCAATCGGTTAGTTCT
 GTTTATTTACTTCTTTTCAGCTGGAACATGAATACATGGACTATGTCTCGAAGAACCCTCGG
 CAGGAACTGGCACAGCTTCTTCAGAACGCTCGGCTTCACGCGGGGGCGCATCGAGACTGT
 5 GGAAGTGGATGAGGGCAGAAATGGTGTTCAGAGGTATGAAAAAACATACATGTTAATT
 TGTGTTGTTTGGCTGATGTGGCAACTAAGTTCGTAAGTGCATGATCAACTGTTTGTGTCT
 ATAGGTATTTTTTTTTGCCCTTCCACACATCTGAGGTAACAAGGACACCTCCTGCACTCAA
 AACACAACTGCTATGTCCTACTGATGAGTCCTAGGAACTCAGAAACCATCTGTTTCCCC
 CATTCTCAATTCCATAAAGCTAAAAAGTGGTAGTTACACAATTCACAATTCATAAACATG
 10 CTTTGTTCATAGTTAGAAAAGCAGCTCAGCTATGAGGCATCCACTCCACAGTCCACTCACG
 AAAGCCCTCTTTAAAAACATAAAATCATCATCATCAGCCCTCAATTGCCCACTGTTGCAT
 ATAGGCCTTCTTTTGATTATGCCAAGTTTTTCGTTTCTCTAGTCCACAGACTTGACATAG
 TTGTCACAAATTTATTCTACGTACTTGTATTTCCAGGTGCGCTACAAGTTGCTCCTGGAG
 TGGGCCCCGCACCGACGAGGACCCACGCTGGGGCGGCTCGCCACGCGGCTGTGGGACGAG
 15 GGAGAGCGGCAGACCGTCAAGGAACTCGCCATCTTGTATAATAATAATTTCAAGCAACAA
 TGTGTA

[0256] > *P. xylostella*- Relish (PxRel); Px002858 (SEQ ID NO:78)

ATGGTAGTGGTGAAAAGCCAATTAAAAATGCAAAGTGACCAGGACACGGACTCGTCCACT
 20 GCCGGTGCTTCGCCGCGCAGCTTCTACATCGAGTCGCCGCACAGCTCGCCGGGACAACAA
 GTGCCTTATTTAACTAATTACATGACAGTACTGTCTGTGCAGATAATAACTTAATGGAT
 ACAGGAAGCAATGGACCATTCTTGAGCATCACGGAGCAGCCATGTGACCACTTCAGGTTC
 CGCTACAAGAGCGAGATGGTCGGCACCCACGGCTGCATCGTCGGCAAGACCAGCGCCAGC
 AACCGCACCAAGACATAACCCTTCTGTTGTTCTGCTCAACTACAAAGGCCGCGCCACCATC
 25 AAGTGCAGCCTCGCGCAGCACACAACCGCAAGCAGCACCCGCACCAGCTGGTCGAGGAT
 GACCAGGAGCGCGACCTGAGCGCCGAGGTCAACCCCGAGAAGGGCTATGAAGTTGGATTT
 CGTGGCATGGGCATAATACATACAGCGAAGAAAGATGTTCCGGCACTCCTATACAAGAAA
 TTGAGTGAGAGACTGCCACATTTCAATGCCCGTGAGCTGAAGGCCAGTGTGAGAACGAG
 GCGCGCAGTATAAACCTCAACATCGTGCGCCTCAAGTTCAGTGCGCACAATGTCGACACG
 30 GACGAGGAGATATGCGCTCCGGTGTCTCGGAACCTATCCACAACATGAAAAGCGCCGCG
 ACGAACGACCTGAAGATCTGCCGCATGAGCCGCACGTGCGGGCGCCCGCGCGGCGGCGAC
 GACGTCTACCTACTACCGAGAAGGTTAACAAAAAGAACATCGACATTGCTTCGTGCAA
 CTGGAGCGCGGCGAGGTGTGCTGGACCGCAAGGCCAGGTTCTCATGAGCGACGTGCAC

CACCAGTACGCTATTGTGATCAGAACACCAGCATACAAGAACCCCGAGATTACGTCTGAC
 GTAAAAGTGTACGTAGAACTATTCCGCCCGTCCGATGGCCGCTCCAGCGAACGCATAGAG
 TTCACGTACAAGGCAGAAGAAGTCTACAAGCAAAGCAAGAAACGGAAGGCCAACTCTTAC
 TCCTCTATCGGAAGTTCATCTAGCGGTAATTCTATCAAAAAGCGTCAGTGATCTTCCAGCA
 5 ACTGTTATTATGGCCAATGAAATGAATGCGGCTAACAACAACCTTTAGTAAAATCTCTTCA
 ATGCTGAGCCCCAAACAATATACCAGAAATACCGACACAAACGACTGTGGGTCTATCAGAC
 GCTCTCTACGACATAACAGTGACAGAAGACCACCAAATGCACATCAGTCCCATGCTATGC
 CAACCACTGGAAGAGTATCCCCCTAAAGCTTAACTCGCAGGATATCATACAAGTGAATTTG
 AACTCTAAGGACATCGACCAACTGCTCAAAGTCAACAGTGTGCCTGATACCGATAAAGAC
 10 TTTGCTGACTTCAATTTTAGTGACTACTACAAGGCACTCGATAGCAACTTTTTAGCTGAT
 GGTGGTGGTGATAGCTTCAGTCAGTGTATCTTCAACTCTATGCAACTGAGGCCTGACTCT
 GGGAGAGGCACG

[0257] > *P. xylostella*- Toll receptor (PxToll2); Px006338 (SEQ ID NO: 79)

15 ATGCCTAAAGTAATAATCGCCAGTTTTGCTTATATAGTAGGTGTGTTTGTCTGTGTGCT
 GGGCTAGAAACAAGTCCAACCTGTTCCAGCATCGAAGGACCTACTCCAGGTGAATTCATA
 ATACAAAGAGGTATCGTACCGGACAATGATTAGCCACCACAGTAAGCTTCGAGGCTGC
 CGAATATCTGACATTCAGCCGAGAGCATTCCATGGGCTACCTTCCCTGCAATACATAGAC
 TTATCAAGAAATAGCATTAAAAACCTGAAACTTGGCATTCTTAATGACGTCAGTACTC
 20 ACTCATCTGAACTTGTCTTATAACTTCATCAGCGATTTAGAAGAGAGTTTGTTCACCAA
 TCGTCAAGGTTGGAGGTGTTGGATCTCCGGTGAATAAGATTGAAGTTATGAAAGTGGGC
 GTTTTAGTCCATTGAAGAGATTGAAGTATTTGGATCTGTCCGACAACGAAATAGTTGGG
 GCCAGCCTGAGCCCCGCTATGTTTGATTCTGTAAAGCTCTATCCACTATCAATTTTTCA
 AGAAATGATATGTCTGGTGCTCCCACTGATTTGCTTCGAGCTGTGGAGGTACTGGACACA
 25 CTGAAACTGGATGGGTGCTTTTTTGAACAAGTTCCGGAATTTGCTACGAGGAGCAATACC
 GGCACAATGAAGAACTTATTTTATCATCGAACCAAGTGAGCACTGTGAACTTACTACG
 TTCATCAGTTTAAACAACCTGGAGGAAGTAGATTTGAGTTCAAATGTAATTTTCAAGATTG
 CATGAAGACGTATTCAAGCCATTAAAAAACTTGAAAATTATTATTTTACGCTCGAACCGA
 CTGGAAAAAATTCCTGATAAGTTGTTTTATAATATGTTACGATTAAGGAAGGTAGATTTA
 30 TCTTTTAATTCTTTGATGATAATACCTGTGAATGCCTTTCGTTTTACGACGATAGAAATG
 TTGAATATATCGCATAATAAGTTCACATATTTAGTCGACAACTTTTGTGTTGGAAGTTAGA
 AACTCGGGAGTGAACTGAAAAAGTTTTACTTCAACAGTAATCCCTGGCAGTGTCTTGC
 TTGAGGGATTTATTAAAGGAAATGAAGACGTATAGAATATCGTACAATAATGCTAAATAC

GATGGTAAAAATGCAGTTTGTATTTTCAGGAGACATTATTAATACTTGCTTGAGACAACCT
GATGTCAATGAACACTTCAATGATTTGTACTATTCTGACTAA

[0258] > *P. xylostella*- Cactus (PxCac); Px016665 (SEQ ID NO: 80)

5 ATGAGTTTCAAGAAGGATTTTCGACACCTCAAAGAAGATCCAGGAGGATGAAAACACAGAC
TCTGGGTTCTTATCTGGGCCGATAAGTGAGCAGCTGACCTCGGAAGATTGTGATTTAGCG
GAGGAAAGTGAGCGTGCTCGCAGCAGGCTTAGTGAGGAAGATCCTGAGCCTGAGCTGCAG
TTGGACAGTGGGCTGGACCTCTCGGAGTGTCTGTCTGAGTGTTAAGCTTAGTGATAGTGCA
GTGTACACACCCACCTCGCAGACCACCCCCACAGTCACTATAGGTGATGAGAAAACATCAT
10 GACATCCCACCCCTCGCCATCCTGTTCCAGCAGGATGACGATGGAGACACACAACACTACAC
ATTGCAGCGGTACATGGGTGCGAAAAATCAGTAGGAACATTAGTAAGAGTTTGCCCTGAC
AAAGATTGGCTAAATGTACCAAATGACTTTGGACAGACCGCCTTACACTTAGCAGCCATG
AGTGGGCATGCAGTAGTCACACGCATGCTGGTGATGGCCGGTGCATCTCTTGGCATTCTGA
GACCTTGTGGCAACACACCTTTACATGTGGCAGCCGCGAGCGGGCTACGTCGGCTGTCTC
15 CAAGCTTTACTGGCTCCTGCTCCAGAACAACAGCAGAGAAGGCTAGCATCCACGTTGAAC
CAGAAAAATTACAATGGTCAAACGTGCGTCCATGTGGCTGCGATGGCCGGCCACGTCGAC
GCGCTGCAGACATTGGTCTATTACGGAGCTAACATCAATGCTGCGGAGGGTCTATGCGGG
TGGACACCTCTACACGTAGCGGCGGCGGAGGCGACGTCGACACGGCTCGCTACTTGCTC
GAGAAGTGCCTGGCGTCGATCCCTCTGCCCTGGACTACGCCGGTCGTACGGCCAGGAAA
20 CTGGCGTTGAAGAATAAAGCGGCCGCCCTGTTTGACGGCAGTGAGGGCAGCGAGGAGGAG
GATAGTGACAGTGAGGATGAGATGCTTCTGGAAAGCGACCAGAGTCTGTTTCGACCGGATC
CGTGACGGTATGAACGCCATCAACGTCGCCTGA

[0259] > *P. xylostella*- Dorsal (PxDor); Px000110 (SEQ ID NO: 81)

25 ATGAACGCGCCCGCCGACTCCGCGTGGTGACGTTACCAACCTGGGCATCCAGTGCGTG
AAGCGGAGAGACATCGAGGACGCCCTGGCTGTGAGAGAGGAGATGCGAGTTGACCCCTTC
AAGACCGGATTCAGCCACAAGAACTCCCCGCAAAGCATCGACCTGAACGCCGTCCGACTC
TGCTTCCAAGTGTTCTGCGGACGAGCGATCCGGCAAGATCCGCCACGCGCTGCCGCCG
GTCGTGTCCGATGTCATCTATGACAAGAAGGCCATGAGTGACCTGGTTATCACGAGGCTG
30 AGTCATTGTTCTGCGCCCGCGCAGGGCGGCAAGCAAGTTATATTGCTGTGTGAGAAGGTG
GCCCCGGAAGACATAACCGTAACCTTCTTCGAGAAGTCCGGCGAGCGCGTGACGTGGCAG
GCGGACGCGGCGGACGTGTTCTGTGCACAAGCAGGTGGCCATCTGCTTACCACGCCGCCT
TACCGCGACCCGCATGTGCAGGACCATGTGCAGGCGTACATCCAGCTGCGTCTGTCGACG

GACAACGCGACGAGCGAGCCGCTCCCCCTTCGAGCTGCTCCCGTCCAGCGCAGATCCGAAT
TATCTGAAGCGAAAGCGACAGAAACCGATACAGAACTTCAGTCGGTACTTACAGCCGATC
GATAGCGACATGAAGCAGCAGCTGCCGGACTATTTCCAGGACAACATGGCGCTGTCCAGC
ATCCCCCTCCGTGAAGCTGGAGCCCCGAGATAAGACTCCTCCTCACAAACATGAGCAGCCCCG
5 CCGCTGCTGTTCCCCCCCCGCGCACGCCGCGCCCGCACACCATGACCCCTACGCGTGGAAC
ATGCAACTAGACAACATGCAGTCGGGTCTGACGGCGCCCGGGCCGAGCCGCCTGCCGCAG
TACAGCCAGGACATGGCCTGGACCAACCAGATGGGCCACGTGTCCCTATGCACCAGGCC
ATGTCCCCCTAACATGGGTACAGTCTCCCCCATGCATCAAGCCATGTCCCCAAATATGGGC
CATGTCTCTCCCATGCACCAAGCTATGTCTCCAAATATGGTCCAGTCACCTATGGGTCA
10 GTGTCCCCCTAACATGGGCCATGTATCCCCTAATATGGGTCAATGTGTCCCCTAATTTGGGT
CATGTGTACCTAACCTGTGCCAGCAACCAATGGCTCCTATGGCGCAGCAGCTGATGGAC
CCGTCCCCCAGCGACCCACCTCCATCACGGGGCTGCTGATGGATCGCCCGGACCAGCCC
TACTCCGGGGAGCTGTCTGGACTCTCCGCCCTGCTGGCTGAGGCAGCCCCCGCAGAGATG
CTCAGCGATAGCCTCAACAGACTGTCTACGGGGGACTTGTTGAGACAAGTTGATATGTGA
15

[0260] > *P. xylostella*- Hemolin (PxHem); ACN69054.1 (SEQ ID NO: 82)

ATGACTTTAATTTTCAAGAGTGTTTTATTTTGGGCTTAATATTGACTACTTTTATTGTT
TCCGCTCAGCCTGTGAAACAAGATGGCGGCTCAGCACACGAAGAAATATTGTTCCGTGAG
CACGGCCAGCCGGTGGTGTGACCTGCGCGCGCGCAGACGACCCCAACCAAGGTGGCATT
20 AGAACGTGGTTGAGAAACGGGACGCCATTAGAAGACGGCAAAATGTCTCCCGAAATAAAA
TTCTCGACGACAAATCACTCTGGTGTGTCAGCCCTCACCAGCCGTGGAAGGGGTCTACC
AATGCTTCACCGAAACCCATAAGGGCATTGCAACCTCCCCGAAATTCAGCGTGAAACAGA
CTTATCTCAAAGCTCCAGAGACTACGCCTTCAGTCAATATCAAACCAGCAAAAGGCCTTC
CCTTTAGCTTGGACTGTGACGTCCCTGAAGGATATCCGAAGCCTGAAGTGCAATGGTTCC
25 TACAACACGGGAAAGATCACACCCTGATTGAGGCAATTATCAATAAACGGATCACACAGG
CTCCGAACGGAGCTCTTTACTTCTCAAATGCTACAACCGAAGATGTGAATGTGGGAGACT
TTAGATACGTCTGTATGGCGAGGAATGATGCGGTAGACTTACCAGTGGTGGTGTGCGAAG
CTGTCAATCACAGGTCTGAGCAGCGAGGGTGGTAAGGGTAGATTGGTGGAGCAGTACGTCA
GTAAAGAAGTTAGGGCGGTTGCGGGGGAGACCACAGCGCTATTTTGCATTTTCGGTGGCA
30 CCCCCTAGCCCACCCAGACTGGACGAAAGACGGCAAGAATGTGAACGGGGCGCCCGGCG
ACCGAGTGACCCGACACAACAGGAGCTCAGGAAGACGACTCATCATCAAGAACCCACTC
TAGAAGATGCTGGAACCTACCAGTGCGCCGTTGACAACGGCGTTGGGACTGAAATGCGTT
CTGTCAAGGTTACTGTTGAAGCGAAACCTTCAATAACGATTGTGAATGAAGTAGCAGCGA

AGCTTGGAGAAGAAGTCAAGATTTGCGAAGCGACCGGAGTCCCAACGCCAAAAC TAACGA
TAACTCACAACGCTAAACCGTTGGTTGCGTCAAATAACGTTGTTATAACCAACGATGGAG
TTGTTATAAAGAATATTCAGGCTATTGATCGAGGGTATTATGGGTGTGATGCTGTCAACG
AGCTAGGAAGCGAATTTTCGTGAAACTTATCTAAGTATTGCCTGA

5

[0261] > *P. xylostella*- Sph-3 (PxSph3); XP_004922188.1 (SEQ ID NO: 83)

ATGCAGCTTAATTTCTGTATCAATGTGATCGCGACCATATTGTTGATTGTGACTGGCGGG
GATTCCCAAAAACGAGTGGGTGACATTTGCATTGATCAATACACGAACACGTACGGAAGG
TGTGTTTTCTCGGATCGATGTCCATCAGCTTTACGTAATTATCAACAGAACGGCATTCCG
10 CCATCAATATGCACTTACAACCTCGACAATGCACTGGTGTGTTGTACTGAACGCGGAAAT
ATTCTTCAAACGGCGAGGCCCGCCACCGCCTGATCAGGAAGACAGATTTTCAGTCCTCT
GCTGGAAACAACAACAACAATAAACCTAACATTAGAGTTAGCGAAAGAAAATGCCGC
GAGTACAGCAAATCAGTAACGTTACGGTGAGCTTCAGCTCGCTGCTGCCGGAGCCCGAG
TTGCAGTCCATCTCGCGGCCGCGCTGCAGCCGGAGCGGCGTGGGGCTCGTGCTCGGCGGC
15 CGGGACGCCGCGCCGGAGGAGTTCCCGCACATGGCAGCGATCGGCTTCGCATCAGCGGAA
GGCTACGACTTCAAGTGCGGGGGGTCCCTCATCAGCGCGCGCTGGCCGCTGACCGCGCCC
TGCGCGCGCGCCCGCGCCTCCAGCCGGCCCGTGGTGGCGCGCTTAGGAGATAGGAATATC
AACCCGAAAGCGCAGGACGACGCCACGCCTGTCGACGTGCCAATCCGGAACATCATCGTG
GACGTGGACCTCAGCAACAGCATCCGCCCCGCGTGCTGTGGCCCGGCGGACCCCTCCAC
20 GAGGATAAGGCTATAGCTACGGGCTGGGGGGTGGTGAACCAACGCACGCAAGAGAAAGCG
GACCTCCTCCAGAAGGTCTCGCTCACTCTGCTCGAGAACTCATACTGCGACCGTCTGCTG
AGGAACAACCGCAACCGACACTGGCAGGGCTTCCGCGACTCGCAGTTGTGCGCCGGCGAG
GTGCGCGGCGGCATGGACACGTGTCAGGGCGACTCCGGCGCACCGCTCCAGATCGTGTC
AAGGAGAACCAGTGCATCTACCACCTCATCGGCCTGACCTCCTTCGGCTACAAGTGCGCG
25 GAGCAGAACAAGCCGTCCGTCTACACCAGGGTGTGCGACTTACGTGGACTGGATAGAGTCT
GTGGTGTGGCCGGAGGAGTATGCGGCTTGGGCGGCGGGGAGGAGTAAATAA

[0262] > *P. xylostella*- Transferrin (PxTrs); BAF36848.1 (SEQ ID NO: 84)

ATGATAGTGAAAATAGCCATTTTGGTGATAGCAATAACGTTCAACGATGTGTCTGCGAAA
30 ACTTCGTACAAGATCTGCGTACCGTCTCAGTTCATGAAGGCATGTGAACAAATGCTTGAA
GTGGAAACGAAGAGCAAAGCGATACTGGAATGTTTGCCGGCCAGAGATCGAGTGGAATGC
CTGACCCTGGTGCAGCAACGGCAGGCGGACCTCGTCCCAGTGGACCCTGAAGACATGTAC
GTGGCGAGTAAGCTGCCCAACCAGGACTTTGTGCTTTTCCAGGAGTTCCGGACCGATGAA

GAGCCGGATGCGGAGTTCCGTTACGAGGCCGTCATAGTTGTTTACAAGGACCTTCCAGTT
ACCAACTTGGACCAGCTTAAGGGCTTGAAGTCATGCCATACTGGAATCAATAGAAATGTG
GGGTACAAGATAACCTAACGATGCTGATGAAGCGCTCCGTGTTCCCTGCGATGACAGAC
CGCAGCATCTCTCCTAAAGAGAACGAGCTGAAGGCTCTCTCGACGTTCTTCAGCAAGTCC
5 TGCATCGTCGGCCAGTGGTCGCCTGACCCGAAGACCAACACTTTTCTGGAAGTCCCAATCC
AGCAAGCTATGCTCCATGTGCGAGGACCCTGCCAAGTGCGACTACCCCGACAACCTACAGC
GGCTACGAGGGCGCGCTGCGCTGCCTGGCGCACAAACGGCGGCGACGTGGCCTTCACTAAG
GTCATCTATGTGCGGAAGTTCTTTGGGCTCCCAGTAGGCACAAGCCCCGGCGACTCCTTCT
TCTGAGAACCCGGACAACCTTCGCGTACCTTTGCGCGGACGGGTCCAAGGTCCCTATCAGA
10 GGAAAGGCATGTTCTTGGGCCCGCAAGACCGTGGCAGGGGTGTTGGGACATCAGGACGTT
CTGGCCAAATTGTCGCCTTTGAGGGAGAAGATTAAGCAGCTGTCTAGAGCTGGAGCAGAA
TCGAAGCCGGAGTGGTTCACCAACGTTCTAGGCCTCTCTGAAAAGATCCACTTGGTCGCC
GACAACATTCCCATTCGTCCCGTCGACTATCTGCAGAAGGCCAACTACACTGAGGTCATC
GAGAGAGGGGCACGGCCCCGCCTGAACCTGTTGTGAGACTCTGCGTGACGAGCTCGGTGGCG
15 CTGGCGAAATGCCGCGCCATGTCCGTGTTGCGCTTCAGTAGAGACATCCGCCCCCGGCTG
GACTGTGTGCAAGAGGCTTCGGAAAGCGATTGCTTGAAAAGTGTCCAAGACAATGGCTCA
GACCTGGCGTCAGTAGACGACATGCGGGTAGCGTCAGCATCCAACAAGTACAACCTACAT
CCAGTATTCCACGAGGTATATGGAGTCAGCAAGACCCCTAACTATGCGGTAGCTGTCGTC
AAGAAGAATACTCAGTATGGAAAGATTGAGGATTTGAGGGGAAACGGTCCTGTCACAATC
20 CTTTATGGAAGCTTCAGTGGCTTTGATGCCCCCTCTGTACTACCTATTAATAAGAAAATC
ATAGGCACTGAACAGTGCCTGAAAAAGCTTGGAGAATTTTTCGCAGCCGGATCTTGCTTA
CCTGGAGTAGGCAAATTAGAGAACAAACCCTACAGGAGATAATGTGCGATAATCTGAAGAAA
CAATGTTCTGGAGACAACAGCCCAATAAAATGCTTACAAGAAGACAAAGGAGACATAGCA
TTTGTGTCAAGTGCTGACCTGAAAAACCTGGATGCCTCTCAATATGAGCTGCTCTGTCTA
25 AACAGAGAGAACGGTGGGCGAGACTCAATAACCAACTACGCTACATGCAACATTGCCATG
GCCCCATCCCGAACCTGGCTCTCAGCTAAAGACTTCCTGTCCGATGTGTCCATAGCACAC
ACTCCGCTGAGCTTAGCACAACTACTGGATACCAGAAAGGATCTGTTTAACATTTACGGA
GAGTTTTTGAAGAATAATAATGTTATTTTTTAATAATGCTGCCACTGGACTGGCCACAACA
GAAAAGATGGACTTTGAAAAGTTCAAGGCAATCCATGATGTTATCTCATCTTGTGGTGTG
30 GCATAA

[0263] > *P. xylostella*- Transferrin (PxTrs); BAF36848.1 (SEQ ID NO: 85)

ATGCTGCTTAGGACGATACATTTGTTGTTAATTGTTTGTGTGCGTGGTGCATGAAGTG
CCTCCGGCTAAATTGGAAGCTATTTATCCAGCTGGCTTGCGAGTGTCAATACCCGACGAT
GGCTTCTCGCTATTTCGCCTTCCACGGCAAGTTGAACGAGGAGATGGAGGGCCTGGAGGCG
5 GGCCACTGGTCCAGAGACATCACCAGACCCAAGAACAACCGCTGGGTCTTCAGCGATAAA
CAGGCCAGGCTCAAGATAGGGGACAAAGTGTTCTTCTGGACGTATGTTATCAAGAACGGA
CTCGGGTACCGACAGGATGACGGGGTGTGGACTGTTGAAGGATTTCGTCGACGTCGAAGGC
AACCCGGTTGACCCCGCGAATGGACAACCCATCTCAGCGCCGACCAGACCTCCAACCCAA
CCAGGCCGGGTGCCAATGTCCCCATGCCGTGTGACATCTCAGTCACCACGGCATCAGTG
10 CCAGGGTACATCTGCAAGGGACAGCTGCTCTTTGAAGACAACTTCAATGGGGCTCTGGAG
AAAGGAAAAGATATGGACGCCGGAGATTATGATGCCTGATGAACCGGATTACCCGTTCAAC
ATCTACCTGAACGACAGGAACCTGCGCGTGAGGGACGGCCGGCTGTCTATCAAGCCCGTC
ACGCTCGAGTCCAAGTACGGGGAGGAGTTCCTGGCCAAACTAGACTTGTCTGCCAGGTGT
ACTGGTAACGTGGGTACTACCCAATGCAGCAGAGAGTCCATTGGGGCCCAGATCATACCT
15 CCGATAATCACAGCCAAGGTTACCACCAAGAACAAGTTCAGCTTCAAGTATGGAAGGATT
GAAGTGAGCGCCAGAATGCCGCGCGGTGATTGGTTGATTCCAGATATTCTGCTGGAGCCG
AAAGAAAACCTTTACGGAGTACGCAATTACGCGTCAGGTCTACTCAGCATAGCCTCAGTC
AGAGGAAACACTGCTTACTCGAAGACCCTCAAAGGAGGCCCCATACTGTGTGACAAGGAA
CCGCAGAGAAGTGCCAAGTTGAGCGAAAAAGTTGGATATGACCATTGGAATAAAGCCTTC
20 CATAACTACACCATGATTTGGGCACCAAGTGGCATCACCATGCTGGTGGACGGCGAGCAG
TACGGGGACATCCGTCCCGGCGACGGCTTCAGCCAGGACCCGGCGGTGAGCAGCGTGGTG
GCCGCGCCGCAAGTGGCTGAAGGGCACCAGCATGGCGCCCTTTGATGTTATGTTCTACATA
TCCCTTGGTCTCCGCGTGGGCGGAGTGAACGACTTCCCCGACACTCCTGAGAAGCCGTGG
AAGAACAAGGCCACTAAAGCCATGCTGAATTTCTGGAACGCCCGGGAACAGTGGCAGAGC
25 AGCTGGTTTGAGGACACCACTGCACTCCTCATAGACTATGTCAGGGTTTATGCGCTGTGA

[0264] > *P. xylostella*- Gloverin (PxGlv); ACM69342.1 (SEQ ID NO: 86)

ATGTACCGATTTGCAGTTATTTTATCTGTAGTCGCCGCGTGTGCCGTGGCTCAAGTTTCT
CTACCTCCTGGATATAATGATAAATACCCAGGCTTCTACAAATACTCCAAGCTAGCCCGG
30 CATCCGCGACAAGTGACGTGGGACAAGAATGTCGGCCGTGGGAAGGTGTTCCGGCACCTC
GGCGGCACTGACGATAGTCTCTATGGTAAGGCGGGCTACCGTCAGGACATCTTCAACGAC
CACCGCGGCCACCTGCAGGGTGAGGCTTCTGGCACCAGGGTACTCAGTCCCTACGGAGAC
AGCAGTCACCTGGGCGGTAGACTCGACTATAGCAACAAGCACGCCAACGCCAACCTGGAT

GTCAGCAAGCGGATCGGAGGCGTCACTAGTTGGCAAGCAGAAGGCAAGGCTAGATGGCCG
ATTGGCAAGAACAGTGAGCTATCAGCCGGCGGAATGATCAGACAAGACCACTTCGGCCAC
GGGAGACCAGACTACGGAGTCGTCGGTGGGTTTAAATCTAGGTTTTAA

5 [0265] > *P. xylostella*- Chitin synthase 1 (PxCHS1); KX420688.1 (SEQ ID NO:
87)

ATGGCGACGTCGGGGGAGTGCGGGGGCGGCGGGAGGAGGGCAGCGACAACCTCGGACGAC
GAGCTGACCCCGCTCCAGCAGGAGATCTACGGCGGCAGCCAACGCACAGTACAAGAAACA
AAAGGATGGGATGTGTTCCGAGAGATCCCGCCGAAGCAGGACAGCGGGTCGATGGAGAGC
10 CAGCGCTGCCTGGAGATCACCGTGCGCATCATGAAGATCCTGGCCTACCTGGTGACCTTC
GTCGTGGTGCTGGGTTTCAGGGGTGCTGGCCAAGGGGTCTGTGCTCTTCATGACCTCGCAG
CTGAAGAAAGATAGAAGACTGGCGTATTGTAATAAGAATTTAGGTAGAGATAAGCAGTTT
ATAGTGACGTTGCCGGACGAGGAGCGGGTGGCGTGGATGTGGGCGCTGTTTCATCGCATTT
ATGGTCCCCGAGATCGGGACCCCTTATCAGATCTGTCCGGATATGCTTCTTCAAGTCCTCC
15 AGAACTCCAAGCAGCGCTCAATTTATTGTGATTTTTGTATCGGAATCTCTCCACACCATC
GGATTGGCGCTTTTGATGTTCAAAGTGTGTCAGAAATCGACGTGGTCAAAGGAGCTATG
ATAACGAATTGCCTCTGCATCATTCAGCCATTCTGGGGCTATTGTCTAGAACTCAAGG
GACTCGAAAAGGTTTCATGAAAGTTATAGTAGACATGGCTGCGATTGGGGCTCAAGTCACA
GGATTTCATATTATGGCCACTGCTGGAGAATAAGCCGGTCTTATGGCTGATACCGATCTCG
20 TCAATCTGCATATCACTAGGCTGGTGGGAGAACTATGTCACCTCGGCAGAGTCCAATCGGT
ATAATCAAGAGCCTCGGCCGCCTCAAGGAGGAGCTGAACCACACGCGCTACTACACGTAC
CGCTTCATCTCCGTGTGGAAGATCCTGCTGTTCTCATGTGCATCCTCACCAGCATCTGG
CTGGACGGCGACGAGCCCGCATGTTCTTCCAGCTCTTCAGCGAGGGGTTTCGGACCGCAT
AACATTGTTGTCGAAGAGATCCAACCTCCAGACGGGAGGCACAATGATCCCGGACTTAGCC
25 AACGCCACACTAACCGGAGACTCAGTGGAGGTGGCAGCGGCCTACAACCTCTGCCGTCTAC
GTCATCCTCATAAAGTGTGTTGCCGCTTACTTCTGCTACATATTCGGGAAGTTCGCCAGC
AAGATCCTGATCCAAGGGTTCAGTTACGCCTTCCCGATCAACTTGGTCATACCGCTGGTC
GTGAACTTCTTGATTGCTGCTTGCGGTATCCGGAATGGTGATACGTGCTGGTTCCATGGG
ACTATTCCGATTATCTGTTCTTTGAGAGCCCACCAGTGTACTACTAAGCGACTTCATA
30 TCCCGCCAAATGGCATGGGTTTGGCTGCTATGGCTTCTGTCTCAGACGTGGATCACCATC
CACATCTGGACGCCCAAGGCCGAGCGTCTGGCGTCCACGGAGAACTGTTTCGTACTGCCC
ATGTATAACGGACTGCTCATCGACCAAAGCATGGCGCTAAATCGTAAGAGAGATGACCAG
AAGGATGTTAAGACTGAGGATCTGGCCGAAATCGAAAAGGAGAAGGGCGACGAGTACTAC

GAAACTATTTCTGTGCACACCGACAACACTGGGTCTCTCCCAGAGCCGTAAAATCTTCC
GATCAGATCACAAGAATCTACGCATGCGCGACGATGTGGCACGAGACGAAGGACGAGATG
ATGGAGTTCCTCAAGTCCATCCTGCGGCCGGACGAGGACCAGTGCGCGCGCCGCGTCGCG
CAGAAGTACCTCAGAGTCGTGGACCCCGACTACTACGAGTTTGA AACCCACATATTCTTG
5 GACGACGCTTTTCGAAATATCGGACCACAGTGACGACGATTCCCAGGTGAATCGATTCTG
AAACTGTTGGTGGACACGATTGACGAGGCTGCGTCAGAGGTGCACCAGACTAATATTCTG
ATGAGGCCGCCGAAGAAATTACCTGCCCCGTACGGGGGACGGCTGACCTGGGTGCTGCCT
GGGAAGACCAAGATGATCTGCCACTTGAAGGACAAGGCCAAGATTCGACACAGGAAGCGA
TGGTCTCAGGTGATGTACATGTACTACCTGCTCGGCCACCGTCTCATGGAGCTGCCCATC
10 TCCGTGGACCGCAAGGAGGTGATGGCTGAGAACACGTACCTCCTGACACTGGACGGAGAC
ATCGACTTCCAACCGCACGCTGTCAGGCTGCTGATTGATTTGATGAAGAAGAACAAGAAC
CTGGGCGCTGCTTGCGGACGCATCCATCCTGTTGGCTCTGGGCCAATGGTGTGGTACCAG
ATGTTTCGAGTACGCGATCGGTCA TTGGCTGCAGAAGGCGACGGAACACATGATTGGCTGC
GTGCTGTGTAGCCCCGGATGCTTCTCGCTCTTCAGAGGGAAGGCTCTCATGGACGACAAC
15 GTCATGAAGAAATACACGCTGCGATCCGACGAGGCTAGGCATTACGTGCAGTACGATCAA
GGGGAGGATCGTTGGTTATGCACATTGCTGTTACAACGAGGATACCGAGTAGAGTACTCA
GCCGCCCTCCGACGCCTACACGCACTGCCCTGAAGGTTTCAGCGAGTTCTATAACCAGCGT
CGTCGCTGGGTACCCTCCACTATCGCCAACATCATGGACTTGCTTGCCGACTACAAACAT
ACCATCAAAATCAACGACAATATCTCCACACCGTACATCGCTTACCAGATGATGTTGATT
20 GGCGGTACGATCTTGGGCCCCGGA ACTATATTCTTATGTTGGTGGGAGCCTTCGTGGCT
GCGTTTGAATCGACA ACTGGACTTCATTGAATACAACCTCTACCCGATATTGATCTTC
ATGTTTCGTTTGTTCACGATGAAATCTGAGATACAGTTACTGGTGGCACAAATACTCTCT
ACGGCATATGCAATGATAATGATGGCGGTAATCGTGGGTACAGCTTTACAATTGGGCGAG
GACGGAATAGGTTGCCATCGGCTATCTTCTTGATATCACTGTCAAGTTCATTCTTCATA
25 GCCGCTGTTTGCATCCTCAAGAGTTTTGGTGTATCGTCCCCGGTATCATTTACCTTCTG
TCTATTCCTTCTATGTATCTCCTGTTGATTTTGTATTTCGACTATAAATCTTAACGTCGTA
TCTTGGGGTACCCGAGAGGTGCAGGTTAAGAAA ACTAAGAAGGAAATCGAGCAAGAAAAG
AAAGAAGCGGAAGACGCAAAGAAGAGTGCGAAACAGAAGTCTTTACTCGGGTTCTTGCAA
GGAGCAAACCAGAATGAGGATGAAGGGTCAATAGAGTTCTCATTCGCGGGTCTATTCAAG
30 TGCATGTTGTGCACACACCCTAAAGGCAACGAGGAAAAGGTGCAACTGTTGCATATCGCA
TCTACACTTGACAAGCTCGAGAAGAACTGGAACTGTTGAAAAGACCCTCGACCCTCAC
GGCCTCCACAGAGGTAGGAAGCTGTCGATAGGCCACCGCGGCAGTACCAACGGAGACCAC
GGGCTGGACGCCCTGGCTGAAGACAATGAGGACCACAACCTCGACTCTGACACCGACACT

CTATCCACGGCACCTAGAGAACAAAGAGACGAATTAATAAATCCATACTGGATTGAGGAC
CCAGAATTAAAGAAGGGAGAGGTAGACTTCTTGAGTCAGTCCGAGATTCACTTCTGGAAG
GATCTGATTGATAAGTATCTGTACCCGATCGATGCCAATAAGGAGGAGCAGGCCCGTATC
TCGCACGACCTGAAAGAGCTGCGAAACTCATCCGTCTTTTCCTTCTTTATGATCAATGCC
5 CTCTTTGTTCTCATCGTATTCTTGCTGCAACTGAACAAGGACAACCTCCACATAAAGTGG
CCCTTCGGAGTCAAACTAACATTACGTATGATGAGGTGACGCAAGAGGTGCTGATCTCC
AAGGATACCTGCAACTAGAGCCTATTGGTCTGGTGTTCGTGTTCTTTTTTCGCATTGATTT
TAGTCATCCAGTTCCTGCCATGTTGTTCCATCGATTCCGGAACCTTTGTGCGCATATATTAT
CGTCTACGGAAGTGAAGTGGTTCGCAATAAGAAGGCGGAAGACTTATCTCAAGACGCAC
10 TGCTAGATAAGAATGCGATAGCAATAGTGAAGGATCTCCAGAACTAAACGGGCTCGATG
ACGGGTATGACAATGACTCGGGGTCGGGCCCCGACAATGTGGGAAGGAGAAAGACGATAC
ACAACCTGGAGAAAGCGAGACAGAAGAAGAGGAACATAGGAACGCTCGACGTCGCTTTCA
AGAAGCGATTCTTCAACATGAACGCTAATGAAGGACCAGGAACACCAGTTCTGAACCGCA
AGATGACGTTGCGAAGAGAGACGTTGAAGGCGTTGGAAACGAGGAGGAATTCTGTGATGG
15 CCGAACGAAGGAAGTCGCAATGCAAACACTTGGAGCTAACAACGAATATGGAGTCACTG
GAATCTTAAACAACAACCCAGCGGTGATGCCGCGCCACCGGCCGTCGACAGCCAACATTT
CGGTCAAGGACGTCTTCGCGGAACCCAACGGGGGACAAGTGAACCGAGGGTACGAGACCA
CGCACGGCGACGAGGGAGACGGCAACTCCATCAGACTGCAGCCGAGAACCAACCAGGTC
TCCTTCCAGGGGAGATACCAATAA

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[0266] > *P. xylostella*- Beta tubulin (Px β TUB); KX420688.1 (SEQ ID NO: 88)

GCGGCAGCCAGCAGTACCGCGCGCTGACCGTGCCCGAGCTCACACAGCAGATGTTGACG
CCAAGAACATGATGGCGGCTTTCGACCCGCGCCACGGCCGCTACCTCACCGTGCCGCCA
TCTTCCGCGGACGCATGTCCATGAAGGAGGTCGACGAGCAAATGTTGAACATCCAGAACA
25 AGAACAGCAGCTACTTCGTGCAATGGATCCCGAACACGTCAAAACGGCCGTGTGCGACA
TACCGCCTCGTGGACTGAAGATGTCTGCCACCTTTATCGGGAACACGACAGCAATCCAAG
AGCTCTTCAAGAGGATTTCTGAGCAGTTCCTGCTATGTTTCAGGAGGGAAGCGTTCCTCC
ACTGGTATACTGGTGAAGGCATGGACGAGATGGAGTTCACAGAGGCGGAGAGCAACATGA
ACGACCTGGTCTCCGAGTACCAGCAGTACCAGGACGCCACGGCTGAAGACGAGGGAGAAT
30 TCGACGAGGATATTGAAGACGAGTGA

[0267] > *S. frugiperda*-Peptidoglycan recognition protein 1 (SfPGRP1);
rep_c7951 (SEQ ID NO: 89)

GCATTAACATCTCAGGATTTGATTTCGAAAGTAAGGTCTGAATTTAGTCCTTACATTTACT
TAAAATTAGGTCCTTTTTTGGTTTGTACTGAAATGAAAGTTTTTCTGTTCTTGGTCTTAAT
5 TGTGAAGATAATGGCTGAGGCAAAAGGAGATTGTGATGTGATCCCGATTACGCAGTGGGG
AGATTACCTCTTAAAAGGGAGGATYCTCTTCCAAATCCAGTGAATATTGTTGTCGTCCA
AYACRCTGTGGTACCGGAGTGTAACAATGATGAAGAGTGTGAGAAAGCAGCCAMTGAAT
CAGGAGCTACCACATTAACAAACGTGGATTCACTGATATAGGACAATCGTTCCTGATTGG
TGGAAACGGGAGAGTTTATGAAGGAGCCGGCTGGCATCACGTTGGGGCCCATACTTTGGG
10 ATACAATGCAAGATCTGTGGGGATCTCCTTCATTGGCGATTTTAGAACAAAATTACCAAC
ACCCGAAGCACTGAAAGCCTTCAACAGTCTCCTGGAATGTGGAGTCACGAACAATTATCT
GTCAAAGGACTATCACCTGGTGGCCCATAGTCAGCTCTCTATGACTGACAGTCCYGGAGA
CATGYTGAGGAAGCAGGTGGAATCGTGGCCTCMTTGGCTGGATAATGCCAAAGACATACT
TAAGTAGAARAAGACTAAACGCCGTACTTTGAGCCATTTAATGGTTACTTAACCCAGTCC
15 TTAGCAATTTGATACAAGGCCAATGTCTCTAAGGGCGGCAGTAAAGGTCAAAAACATTT
AATGAGTGTGTTTAAGATTTTGCTAGTGAAAATTGTTTTGAAGTACGTATTTGATGTAAG
TGATGATATCAGTACCCTTAGTATGAGTTTGCTTTACGTTCCACGAGATGGAAACGAGAG
CGCGTTTCGGCGCTCTGATTGGTTCGTTTCATTTCATGCCGGCCAATCATAGCGCCGAATGGG
CTCTCATTTTCGTTTTTCGTTCAACGTAAAGTAAATTCGTACTAAGGGTACTGACTTTAAAA
20 TAAGTTACCAAAAAGAGTATTACCTATTTACATTATTTTATTTATTTTAGGTGTATTGTA
ATTCAAGTATTAAATTAATTAGTGTAGATTAATKSCATGCATTTTATATTTGATTTTCATT
GAATAA

[0268] *S. frugiperda*-Attacin (SfAtta); rep_c9395 (SEQ ID NO: 90)

ATCATTCCAGATCCTCTCTCATACATCCAACACTTGAAGCAAACCAATCCACATACATTA
25 TAGCAACATGTTTCGCTCTCAAGTTGGTACTAGCTGCAGTGCTGGTGGTCGCAAGCGCCAG
ACATCTACCACAGGACCACTCAACGTACGACCAAGTACAACCTCCTCGGGTTCGACGAAGA
TGGACGACCAGTGTTTGAGCACGAAGACTTACTCCCAGAACTAGAGGAGTCCTACCAGCC
AGAGCACCTGGCGAGGACTCGCAGACAGGCGCAGGGCAGCGTCACCCTCAACTCCGACGG
30 CGGCATAGGCCTGGGCGCTAAGATCCCGCTCGCACACAACGACAAGAATGTGGTGAGCGC
CATCGGCTCCATGGACTTCAACAACAAGTTGCAGCCTGCTTCCAAGGGCTTCGGTCTGGC
TCTGGACAACGTCAACGGGCACGGAAGTACGGTGATGAAGGAAAGTATCCCCGGGTTCGG
GGACAGGCTGTCGGGCGCTGGCAAGCTGAACGTGTTCCACAACGACAACCACAACGTGGC

CGTGACCGGCTCTCTCGCCAGGAACATGCCCAGCATCCCGAACGTGCCCAACTTCAACAC
GTACGGCGGGGGCGTCGACTACATGTACAAGAACAAGGTGGGAGCGTCTCTGGGCATGGC
CAGTACTCCGTTCTTGGACCGCAAGGACTACTCCGCGATGGGCAACCTGAACCTGTTCCG
CAGCCCCGACCACTACCGTGGACTTCAGCGGCGGCTTTAAGAAGTTCGAATCTCCCTTCAT
5 GAGCAGCGGCTGGAAGCCTAACTTCGGCCTTACTTTCGGCAGATCTTCTAGATATATTT
TGTAATCTAAATTTAACTTTAACTTTGTTGTATAATATTTTGTGCAATTAAGATCAGTAT
TGTTCACTAATAATATTATATTATCAGTGTTTCTTATAAAATTAA

[0269] ***S. frugiperda*-CtypeLectin15 (SfCTL15); Joint2_rep_c488 (SEQ ID NO:**
10 **91)**

AGTTTTCGTGCTTAGCACACAGAGCGCCGAACGCGCTCTCGTTTCAATTACTTTAAACGT
AAAGCAAACCTCGCACTAAGGTTACTGTGACCTTTGTAAACATGTACAATGCAATACTATG
TTGTTATTTTCGATACAATCATATAAAAGACAACGTTTAAAAAAAAGCATAGCACAGAC
CACAGTACAAGTATCGAGACCAAACTTTTGTTAAACTTATTTTCGTTCTGTGCAGCAACT
15 CTAATGCGAATAATGTGCAAATTATAATAAATATGTTTTGTATATAAACATGTGTTATCT
CAAGTTCAAGACATTCCGGCTCCTACAGTCAACAGATACAGTGCACAAAAATGTTAAAAA
TATATTTAATTTGTTTGTCTTACTTGTTCATGTTAAACTTAGACAGGGCACAATGCACCC
CCCAGTATTGGTTCAACATGGATGCGAATGGTTGGCTGAAAGTGCACACGATACCCGCCA
CGTGAGGAAGCATTTCCTTCGGTGTCACTATGAAGGTGCGGTACTTGCGTCCCCCTTGA
20 CGCAACAACCTGAGTAAGGCTCTTMAAAACAAGTTTGCAGKCWTCGGTAACCCATCAATCC
ACTTGGGGACACATGATTTGTACTCCASTGGTTACTACTTTTCTGTAGAAGGAGTACCAA
TGGACAGCTTGGTGCTGAAATGGAGTAATATCAGAGGTACGGGCGAYTGCCTGGCGATGT
CACGCGACGGGGAAGCATTTTTTACGAAATGCGAGCAACCTCGACCCTACATCTGCTACA
AGAAGCTGGACAATCTGACGATGAACATCTGTGGAACATTYGATGACGCKTATCAATTCT
25 ACGATAAGACTGGCAGCTGCTATAAGAGACACAACGYCTATCAGACATGGCCTGACGCGT
TCAAGATATGCGCTGCCGAGGGAGGSTACCTGGTGATCCTGAACGATGACACAGAGGCCG
CCATCATCAAGGATATGTTCCCCGTACGGCCAGGAAAGCCCAACGAATGGGAGAACTTCC
ACGTGGGKCTGCGGGCATGGGGACCGGAACGTACTTGGATCACTATTCATGGAGAAAAAA
TTGATGATGTATTCCATAATTGGAACCCGGGACAGCCGGACAACCTACAAGGGAGTCCAGG
30 ACGTGGCGCTTTCTTAGARMAGGCACTTTAGACGATCATGCCGCTGGTGACAAATGTA
TGTTTGTCTGTGAGAAGGATCCTAAAGTAAACGCTTCGAAGAGYTACCCGAAGGATTGG
CMGAAGTTTTAGGACAATAGGCCGCTAGTCAAATATTGTTTCATATACCTWAGTTTTAATT

ATGTAAAAATAATARTCGATTGCAGAATTTAATAAAATTTAACTAAAAAAAAAAAAAAAA
AAAAAGGTMAAACATGTC

[0270] *S. frugiperda*-Galectin4 (SfGlc4); rep_c2653 (SEQ ID NO: 92)

5 GCCTTGTAGTTCGACAGTCAAATCCAACGGGTGTCAGAAACAATTTCCGTTTTTCCGGCT
ATTGATCGTCATATAAATAACTCCGAAGGAAAAATGACTACAATCGACAATCCGACAGTA
CCGTTACAGAGACCCATTCTGCGCATCYGCTCCCCGGCCGCAAATGGTCGTTAAGGGT
GCAATCTCTCCAGATCAGATAGGTTCTCAATAAACTTGAAATGTGGTAGCGAGGACATC
GCTTTCCACTTCAACCCTCGCTTCAGTGAGCAGAAAATAGTTCGCAACTCTTATATTTCT
10 GGCAAGTGGGGTCATGAGGAGATCAGTGGAGGCATGCCGTTGGTAAGGGGAGAGCATTTT
GAAGCGCAATTTGAATGCAATGAAGATAATTTTTCGGTGGAGTTGAACGGGAAACATTTT
TGCAATTACTCTTATCGCATCCCAATCCATAAGATCACCCACGTCAACGTGGACGGTGAC
GTCACGATAAGTCAGATCACCTTCGTGGACGCCTGAGCCATCGCCCGATCTTACAATGGT
ACTTTTTTTTTACTTATGAACTAATGCTGGAAACCAAACCTCTTTATTCAAATATTTTTT
15 TTTTGTCTTTATGACTATCAGTGTTTTTTATTGCAATAAAAAAG

[0271] *S. frugiperda*-Lysozyme (SfLys); rep_c18992 (SEQ ID NO: 93)

ATCAGTGTGGTGTCTTCAACCCAAGTGCATTGTATTGCTTGGTAAATAATAACTGASAAC
AAAAATCTTGGTTATTGCTTGAACAGGTTTTCGCCTATCAATTAGCCGAATATTGTTACCC
20 TTGACACGCAATAATTGGTTACTCGATTAAAGCTTGAAGAGGTAAAGTGCCGAAATGACG
CGCGCCATTCTGTTTGTGTTGTTTTATGCTTTATTGCAAAATGCTATGGAAAAACATTC
ACKGAATGTGAATTAGTTTCAGGAGCTAAGAAGGCAAGGATTTCTGAACATGAGCTTAAA
GATTGGGTRTGYCTGATCGAAGCGGAGAGTTCCAAACGAACCAACGCCATTGGTAACGGC
AATTCAGATGGCTCTCTCGACTATGGCTTATTCCAAATCAAATAACCGCTACTGGTGCAG
25 CGAYGGTGACCATCCAGGCAAGGGATGCAACGATACCGCTAGTAAAGATCTGTTGCTGGA
TGACATCACAATAGCGTCTCAGTGCGCTAAGACCATTTTCGGTGTCCACGGATTTAACGC
CTGGGTCGCATGGGTGAACAAATGCAAAGGAAGGACCTTACCYAACCTTCACTGTTAGTT
ATTTATTGAGAAAATGTAATAAGGTATATGGTTACTTTGTACCTAAATATAGGTATTAG
GCATATATTGTCCACTCTCATCAAATTTTTACTTTTATATCAGT
30

[0272] *S. frugiperda*-Hemolymph proteinase 10 (SfHP10); c12881 (SEQ ID NO: 94)

ATTTCGCTGTACGCACCTCGGATTGTGCGGTCAACTWTACAAGGCTCGTACCTTGCAGTTG
AACCGACAATCTATTCTAAAGCCTTTTTAAGGTCAGGAAAAATAGTTCCTACATCTAAA
5 TGCAGTAGAATTTGCGAAACGAATTTAAATAAAAATGGCGTCGATTGTGTTTGTGATTTT
GTGTGTTACCGTCGCTGCGGTGAAAAGCGCGATTTTAAACCCGTGGAGTAAAGTTGAGGC
CAACAAATGTGGTGTAGAAGCCAGTACTAAGTTGGTCCATCACAATCCATGGTTGGTCTA
CATCGAGTATTGGCGTGGAACTCAGATACTGAGATCCGATGCGCCGGTACTTTAATCGA
CAGCAAACATGTCGTCACAGCTGCCCACTGCGTTAGGACTCTGAAGTTTAGTCATTTGAT
10 CGCCCGTCTTGGCGAATACGACGTAAATTCTAAGGAGGACTGCGTTCAGGGCGTGTGTGC
CGATCCCATCGTCAGAATCAAGGTGGCTGAGATCATCGTGCATCCTAACTACAGCAACCG
GGAACATGACATTGCAATCTTAAGGCTGGAGGAGGAAGCTCCTTATACCGATTTCACTCC
GGCCCATCTGTCTGCCTTCTGGTGATCTCGCGGAAGACACCCAGTTCTTAGCAGCCGGCT
GGGGTGARATCCCCACGAAAGGCTTCTTCAGCCACGTGAAGAAAATCGTCCCCCTACGTAC
15 TGAATCGAGAGAGATGCCAAAAGGTGTACCAGTACAATTATATCCCGGAGAACGTGATC
TGTGCCGGT

[0273] *S. frugiperda*- Trypsin like serine protease (SfTSP); rep_c48453 (SEQ ID NO: 95)

CAAGTAGCAACAAAATGCGTGTCTCGCTTGCTTGGCCCTTCTCTTAGCTGTGGTAGCAG
CCGTCCCCCTCAATCCCCAGAGGATTGTGGGTGGTTCGGTCACCACCATTGACCGGTACC
CCACCATTCATCCCTGCTGTACTCGTGGAACCTTGAGTTCCTACTGGCAGGCGTGCGGTG
GTTCCATCTTGAACAACCGTGCCATCCTTACTGCTGCCCACTGCACAGTTGGTGACGCCG
CCAACAGATGGAGAATCCGTCTTGGCTCCACCTGGGCCAACAGCGGTGGTGTGTTTACA
25 ACGTCAACACTAACATCGTCCACCCCTCATACAACCTCTGCAACTTTGAACAACGACATCG
CTATCCTCCGCTCCGCCACCACCTTCTCCTTCAACAACAATGTTTCAAGGCTGCCTCCATTG
CTGGTGCCAACTACTTGCCCGGTGACAACACCGCCGCTGGGCCGCTGGATGGGGAAC
CCTCCGCTGGTGGCTCTAGCTCTGAGCAGCTCCATCACGTTGAGCTGCGCATCATCAACC
AGGCTACTTGCAAAAACAATTACGCTACCCGCGGTATCACCATCACCTACAACATGTTGT
30 GCTCTGGCTGGCCACCGGTGGTCGCGACCAGTGCCAGGGTGAATCTGGTGGTCTCTCT
ACCACAACGGCATCGTTGTTGGTGTCTGCTCTTTTCGGTATTGGCTGTGCTCAGGCTGCCT
TCCCCGGTGTCAACGCTCGTGTATCCCGCTACACTGCCTGGATCTCTTCCAACGCATAAG
ATGTTACTTGGTGCTAATAATATTTTTTTGTAATAAAATGTTACTTTTATCCTCC

[0274] *S. frugiperda*- C Type Lectin 6 (SfCTL6); Joint2_ rep_c448 (SEQ ID NO: 96)

AACAGTTTTCTATTGGCAGTCAAAGACTTCAGTCGAAAAATAATCCTCATCAGAGTCGTG
 5 AAGCAAGGTGCCCAAAATATAATGTAACCTAGATACCTATTAATAAATTATTTGTCAACC
 AAAACGTTACGTTCAAAGTCCTTAAAATCAAATATCTTATGATTAGTTTTGATTTAAAA
 ATAGAGGTTTCGAAATCGCCAACCCAAATAGGTTTAGTTTACGATTTCAGGAAAAATCCTAA
 CGTAGGGAAACATTATTTTACAAGACTTTTGGCTTAAAACTTTGAGAACCAATGTCAAA
 TTTGATAATAACTAATGAGGTATAAAAGCTTGATCCTATTAGGACTTATTTTCATAACAC
 10 CATCGAGTTTGTATTTAATRRAGACGTGKGTAACTAACAACATGAAGACCGGTGTAAAA
 TATTCTGTTMTTGGATATTCTCTCTATTYTGTCTATATAGAGGCAACATTTCTGTTGTGAC
 TACACGTACAGCAAGGAAGCGAAGGGCTGGTTCAAACATGTGGTGATAACCAGCTACTTGG
 GCTGACGCACGWCTGCACTGCACGTTGGAAGGTGCAACGCTGGCTTCTCCACTCAACCAG
 GCTATMAGTAATGAGATGCAGTCCMTCTGGCRAACCTCTCGGCGCTGCAATCAGAAGTC
 15 TTTACTGGAATTCACRCGACTKTTTCACGRMRCAACTTATATCATACYATYGAAGGTATA
 CCTCTTAGTAAAATTCCATTAGATTGGGCAACAAATGAGCCAAATGGTGGGAGAGATGAA
 AACTGTATCACGTTTAACTCCGATGGCCAAGCGGCAGACAGATCCTGTAARGAGACTCGA
 CCTTACATCTGCTACCGACACACWACTAAAGTGAAGTGTGKCCAATGAATGTGGGACTGTA
 GATCCTGAATACAATTTGGATAAAAAGAACGGGCKCYTGCTATAAGTTCCACACRGTACCT
 20 CGCACGTTTCGAGCGTGCCAACTTCGCGTGTTCTGCTGAAGGTGGMCACCTTGCCATAATC
 AACRGTGATRTCGAAGCTGCAGTACTGAAGGAAGTCTTCGAAAGGAATCCACCTGCAAAG
 ATGTTTCGGTACTTTCTGGAAAGACGTTGCTTTTCATTGGTTTCCATGACTGGGGTGAATAT
 GGTGACTGGAGGACAATTCACGGTCAAACGCTAGTAGAGGCAGGATACAGCAAGTTTTCA
 TCTGGAGAGCCAAATAATTCTCGACGGGAGAATTCTGTGGTTCCATCTATCGGAATGGT
 25 ATGCTCAACGACCTTTGGTGTGGGCATCCTAAACCATTCTCTGTGAGAAGGACCCGAAA
 TATCCAGCCGTATGTTGTGTTACAGAATCAGAACCAGAATTGGACCCTACTCACTTCTTA
 GAGTAATTCAAATTGGATCTTTTTTTATAATTCTACATCATTAGAAATATGATGTTTAGT
 TGAATCTGCTTTTGAAGATTGATT

30 [0275] *S. frugiperda*- Serine protease homolog 13 (SfSph13); rep_c1904 (SEQ ID NO: 97)

GAAKAGTGTCAATTTATTTAATTGTCAAAATCGCGTTGAATGTAAGATTGCTATAGAAAT
 TATTTGTAAAACTTTCTCAAAAATTTAATTCTAAAATGTAAAGGAACCTAAAATCAGAT

ACCGATAACACATTTTGTAAATGGTTTAATATTGAAACGAACTTCTAAACATTTTGGT
GAAATACACATAATAATATAACTTCTTCGAAAAGTAGGTAGATAGACTTCAACTCAGTTT
TTATTAGCGAGCTAGAAGATACAGAGATTATCTAAGATGGTGTGTGATGGTCCGGATCCT
CCAGAGAACAATCCTCACGAAATTGTTCCACCTCCTAGGAATGAATTGATAATGAATGGT
5 AATCAAGGGGATGACAGTGATGAAGAACATGAATATTTTGGCTATGAACCTTTGGCGCAA
GGTCCAGAAGTAGCAGTCTCAGATCACGATAGTGATGATGACCCAGAGAGTGCTGAAACA
CCTCCAGCTGATGTTCCAAATATAGAGCCAATGGAAAATGTACTAAGCCGGGAAGTTTGG
AGTGCCCCGAGRCATACAGATGCTATACAAATGGATAATGAACGGGCTCAACAGGTGATG
AGAGCTATGGCAAATTTTGGCTCTACCCCAGGCCTCAWTTCCAGAATGGGCTCAGAGCATC
10 TCTGAAGAACAATGGAAGCAAACTCTGAATGAACAAATAGAAAGATTGAAAAATAAAAGA
TAAACTAATTATATGTAGTATAATAATAATTAAGATTTAAGTGATAAAAATAACAATTAT
AACTTATATGTTTAAAAAATGTATATAAACTGTAACTTTAAGCTTATTCACATTACTTT
AAATATAGAAAAATATGTGTACCTATTTATTGTTTGGCTACATAATCCAATATAGATTA
AATTGCAAATGTTTAATGTAATTATTTAGTTGGATCAAAAATAACAGCACTAAAGGTCAC
15 TAGTTTAGTTCTTTCATTTTCGAATGAAAAAGTAAATGGAGAATCTGCATAGAAAATTTTC
AGCTGACCGTGTTAATGTTCCACTTGTTGCGGCTACTGCTTCTGTTCCAACTCATTAAT
TGTTAACTTTACATCATGAATTATGGAATCCACATGTATTCCAGGGTTGGGTAGACTGTC
CAAAATGTTTGTCCCATTTCTTCGTTTTCTGAGTATCTGTCTGATTCTCCTTCAGATTT
ATTCACAACTGATTGGTGTTATTTACCATAAGTGCGAAGTTTGCTTGGCCTGGTATAAA
20 CATACTTTGTATCCCAATAGATTGCAAGGTGCTCTCTAGCTTTGTGGTGCTTTTAATTTT
CATCTTAGGGAAACGAATAACACAATTTTTCACATGCATTTTCATTGATGGTATCATCAAT
AACTTTGTTGTTAATATTTTCCATGAGTTCCAATAATGTTAATCGYTTATGAGATAATGG
TTTTAAAGCGTACATAAAAGTTTCACTGTGCTTATATGGCAATGCTATCATGTGGAAATC
ATGTTCCCTCAGAAACCTTGTAACGAACTCCCCAAAATTCAACATCATGTGAGCCATAAC
25 TTCATCTGTGGCCCTTTTGAATTCCATCTTTCTTGTGAATTGCGGTGCAAAGGCTGTTT
CCATGTGCCACTAAAGTACAATGCAGTTAAAAGTACTACTTTAGTATGGGGAGGCAGAGA
ATCTTTCAAAAAATCGTCTATATTTCTTCTGTGTGCTTGCTCACCCACTCATTGATGCT
GTTTTTAGATCCTTCGGTTTCTTGAAAATCAGTACGTAACACATCGCCTCCGTAAACACC
ATGCAGATAACTTCTGTACAACTCTCGCAATTCTACTTGGTTGTCTACAAATATCGCGTC
30 AGCGTACAAAGTTTTTGAAAAGCTCGTTCATATTTAACTCTGTAGTAGTTCCGCCGAAGTG
TTCGTGGTTCTTGCAGTTTCTGTAGAATATCTTGGGAAAATCCGAGTGTCTCTGCGATTTT
ATCATGTGTCATCCCAACACTTCCGAGTAATGTCATGGCAAGCAGACCAGCGACACCTAT
TGGTGATATCACGATGTTTTCGTTTTCTTTTCGTTTCATCATTTTGACTAGTAAATTATA

TCCAAAATTATTTATAGCTTTTGGTATCGAGTTATCTTTCGTATTTGTTGTTTCTAAGTT
ATCATTTTTCAGCAGTTGTGGTTGGTATTATCGTGCTTGAAATCTGACTGTCTCTTCATT
TTGTCCAGAATATTGAAAATATAATGTTGTTATAATTAAAAATAACAATGACTTGCTATC
CATGTTGTGGTGCTTAAATAAGGTATTAAACGTAAACTTCACACTAACAGGAACAGGTTT
5 CTATTATTTCCCACTTAAATCGTGAACCTTACGGCATAGACACTATACACGTCTACTCGTT
TGACCAACTCTGAGAGCAACTCAAAAACAACCTTGTGTGTGTATGAATAACGAACTAAAA
T

[0276] S. frugiperda- Cecropin (SfCec); rep_c42380 (SEQ ID NO: 98)

10 TTCGTGTCGTATCACTAGAGTTCGAAATACAAAATAATAATACATTTATTATTTTGCCAT
AATTAATAATAAAGTTATTTTATTTTCATAATAATAATGAATTTACAAAGATATTTTGT
TGTTTTTGTCTTGCTTTGTTTTGATGGCGACCGTGTGAGGAGCTCCTGAACCGAGGTGGA
AATTCTTCAAGAAAGTGGAGAAGTTGGGCCAAAACATCCGCKATGGTATCATAAAGGCAG
GACCCGCAGTGGCCGTGGTGGGATCAGCRGCAGCCATWGGAAAGTGAKCCCTACGACCTG
15 AGACATGAAGACTAATATCCAYTAAAATAASAATATTGAGGCKTATAATATTAATTTATT
RTRTTTGTAATTAAATTATTTGTAAGATAA

[0277] S. frugiperda- Relish (SfRel); c13122 (SEQ ID NO: 99)

ATAATATGAAGAGTGCTGCGACTAACGATTTAAGAATCTGTCTGTATAAGTCCGGTCGTCCG
20 GAATTGCTTCTGGCGGCGAAGATGTCTTCATTCTGGTGGAAGTTAATAAGAAAAACA
TAATGATTCGATTCTTCGAGTTGGATGAAAACGGAGAAAAGAGGTTGGACCAATGTTGGG
CGATTTGTGCAAAGCGATGTTTCATCACCAATACGCAATCGTCTTTCGTACTCTCCATAC
AAAAACCCTGAGACGCCAGTCGATGTGGAAGTGTATATCGAACTGGTTTCGTCCATCGGAC
GGCCGTACCAGTGAACCGAAGCAATTCAGTACAGAGCCAACCAAGCGTACAAACAGATC
25 AAGAAGAGGAAGACTGGATCTTCTACTGTTCTATTGGCAGCTCATCTAGTGGATCGTTG
AAAAGTGGTTGCGACATTCCCATATCTGTTGTCAATCATCAACCAGAAGAAGTTCCCATG
GATCGCGAGCCACCGGTGCCGTGTCGATGTATGTTTTACCCAGGTGCATGATTCGACG
ACACCAAACCAATGCGATCTGGCCAGTGCTCTGTACTCTGCTCCTGGTTTCGGAGACCAGC
CAGTCTCCTATATCGAGTCCGATGTGGAGTGAGCCTCACAGCGTGATGCTGCCGATGTGCG
30 CCCATTGCCAACCTTCAGCTCAACTCCGCAGACTTCGAACAGATCACAGTACCCACT

[0278] S. frugiperda- Toll (SfToll);joint2_ c3284 (SEQ ID NO: 100)

AAAACCGAATAACCGGTATACCGGATAACTTCTTCAAGGATTTGAAGAATATAGAGCATT
TAGATTTGAGCTTCAATAAGATAACTAAATTGACCAGTGGAGTGTTGTCACCAATGAAAC
AATTGAAGTATTTGAACCTGAATCGAAAYCATTGGAAGTTTTRCCTGAATTCCTCTTCG
5 CTGGCCTCAGRAAACTAGARAAWGTRWCAATMAACGAAAATCTACTCACTTCCATAGATT
CTTTAGCATTCCAAGGRGCWACGGCWTTGCATACAATATCTTTATACGGCAACAGATTAA
CATTGAAGTCCAATGAACACATCCAAGACTATATGGACTTAGATCTCTACTCACCCCTTYA
ACACTTTGAGCGAATTAAAAAATTTGAACCTTAGTAAGAAAYAYATAAGCTCTATATTCG
ATGATTGGMGGATWGTGYTRCTCAATYTGGAGTTGCTGGATCTATCTTATAAYCATATTG
10 GAGAGTTATTGCCGGACACCTGYCAATTCCTAAGCAACAARRTYACAGTGGACCTGCAGC
ACAATGACATAAGTACTGTTATTTTATATCCTACGTCTCATATGGACTTCACAGAACCCA
GCATGCCATCAAACAATGTGTTTCTCTTAGACAACAACCCATTTAACTGTGATTGCCACA
TATATAACCTAGCTATGCGTCTACAAGGCAAAAAGCTGCCCTACGAACCTACTTTCAACG
TAGGCAAGGCCGAATGCAAATCCCCACGCCACTTAAGTGGGGATTTGTTGTACATGTAT
15 CCCCCTCGACTTATACTGCGAAGAAATGTCGCCTGATGTTTCGTTTTAATTGTAGTTCGG
TTAAAAATGAGGCCTGCGTACAATGATTTGGCGTACGACTGTGATGATGTACCACCTTACT
TCTCTGATGACATTAAAACTACTCTTTGAAATTACGACACCCACCAAAAGACTTACGCA
ACCTAACACTAAGTCTACTAAACCTAACCGGCATAGGATTACAAGAAATCCCMTTTACRC
CGTCAGAAATCGGTAAAAGTAATCGATTTATCGAACAACAATCTCACAGAGATACCKATMM
20 GATTCTTAGAATCGAATACGACRTTGTWTTTATCGAATAATCCATTTGTTTGCGATTGTT
CTTCRAAAGATGATATTTTAGCTTTAMGRGCRAGTTAYAATGTGAATGATTTGGATATAG
TYAGCTGTTCAAACGGCGTTTTGGTAACAGATTTAGAAAATATCATCGCTATGCTATACAA
GAACTTTAATAGCAGAAATAGGTGGTATAYTAATATTCTTAYTAATAATCTTAGTRTTTA
TAATAACATTYATATTTCTAGACAAATGGTACTRTATTGTGGTCATAGGCTMTTTCCKT
25 GCTGGTATATCGACGATCCAGAACTACGGCAAAAGAATATGACATATTCATATCTTATG
CTCATAAAGACCAAAAATATAGTGAATAAGCTACTCCCGTAACTAGAAAATGATTTCAA
GTTAAAAGTCTGCGTTCATTACCGAGATTGGGAAGTCGGTGATTTCAATCCGGATCAGAT
CAATCGATCAGTATCGAATTCGAGAAAAACGATTATTCTTTTATCGAATAGCTTTCTCGA
TTCGACTTTCGCGAATTTGGAATTTTCGTACCGCGCATAATTTAGCTTTGAAAGAGGGAAG
30 AGAGAGGGTCATTTTAATACTTTTAGAGGACGTTAGTAAACATGAGAAGTTATCTGAAGA
ATTAAAGTATCATATGAATATGAATACGTATCTTACATGGGATGATATTAGATTTGATGA
AAAGTTAAAACGAAGGACGATACCACAGAAATATAATAGAAAGAAATTCGTAGCGCCGGC
CATTTTAAAACCTATATTCAGACAGGCTACTGAGAATAATTTGAAAAAGGCACTCGATGT

ACACTTTGAATAGTGCAGGCCAATTGGTGAATTTAGCTCAAAATAAGAAGAATATTGATA
TGGTATAGCTTTTCCCAAATAAGGCTCTTTTAAACATGTAAAGCCCTCTCTCACCCGACC
TCTCTGACTACCGCACTCAGAGACATTTTAATGTATWTTTTTTTTTTAATTGGGTACAAG
CCCGCCACAACATCCCAGACCGCT

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**[0279] *S. frugiperda*- Beta 1, 3 glucanase recognition protein (SfβGRP2);
EF641300 (SEQ ID NO: 101)**

ATGTGGTCGGTGTTAGCCGGAGTATTGGCGATCGCGTCGCTAGGCGCGGCTTGCACCCCC
AGTTTGACCACCGTCAGTGGTACCCACGCACCGGTCACCGTCTGCTCTGGTGCTCTGATC
10 TTCGCTGATGGCTTCGACACTTTTGACCTCGAGAAATGGCAGCACGAGAATACTTTAGCT
GGTGGCGGTAAC TGGGAGTTCCAATACTACGGCAACAATCGCACCAACTCTTTCTGTGCGC
AGTGGAAGTTTGTTCATCCGTCCCTCTCTAACATCAGACGAGTTCGGAGAAGCTTTCCTC
TCATCTGGACACTGGAACGTCGAGGGTGGTGCTCCTGCTGATAGATGCACAAATCCACAA
TGGTGGGGTTGCGAGAGAACAGGCACGCCGACCAACATTTTGAACCCAATCAAGAGTGCT
15 CGTGTCCGTACCGTCAATTCCCTCAGCTTCCGTTACGGACGCCTCGAAGTCCGCGCTAAA
ATGCCCCGCCGGAGATTGGATTTGGCCAGCTATCTGGTTGATGCCTGCGTACAACACTTAC
GGTACTTGGCCCGCATCAGGAGAGATTGACTTAGTTGAGTCCCAGGCAACCGTAACATG
TTCCACAATGGTGTCCATATCGGTACACAGGAAGCAGGCTCGACCTTGCACTACGGACCT
TACCCAGCGATGAACGGTTGGGAGCGCGCCCATTTGGGTCAGAAGGAACCCCTGCTGGCTAC
20 AACAGCAACTTCCACCGTTACCAACTTGAATGGACACCAACTTACTTGCGATTTCAGTATC
GACGACATGGAGCTTGGACGTGTAACCCCTGGCAATGGCGGCTTCTGGGAATACGGTGGT
TTCAACAGCAACCCTAACATTGAGAACCCATGGAGATTCGGAAGCAGAATGGCGCCTTTC
GATGAGAAGTTCTACCTTATCATGAATGTGGCTGTGCGGTGGTACCAACGGATTCTTCCCT
GATGGCGTCAGCAACCCATCACCCAAACCCTGGTGGAACGGATCACCAACCGCCCCAAGA
25 GACTTCTGGAACGCGAGATCAGCTTGGTTGAACACCTGGAACCTGAATGTCAACGATGGA
CAGGACGCATCCATGCAAGTCGACTACGTCCGCATCTGGGCTTTGTAA

[0280] *S. frugiperda*- c20042 (Sfc20042); Un-annotated (SEQ ID NO: 102)

ATCAGTCGTCCCTCGTACATCCAACACTTCAAACCAAATATCTCCATATACATAGTAACA
30 ACATGTTGCGCCCTAAAGTTGGTACTAGCTGCAGTGCTGGTGGTCGCAAGCGCCAGACATC
TACCACAGGACCACTCAACGTACCGAACATGTACAGCTGCTCGGGTTCGACGAAGATGGA
CGGCCAGTGTTTGAGCACGAAGACCTGCTCGCAGAACCAGAGGAGTTCTATCAGCCAGAG
CACCTGGCGAGGACTCGCAGACAGGCACAGGGCAGCGTCACCCTCAACTCCGACGGCGGC

ATGGGCCTGGGCGCTAAGATCCCGCTCGCACACAACGACAAGAATGTGGTGAGCGCTATC
GGCTCCATGGACTTCAACAACAAGCTGCAGCCTGCTTCCAAGGGCTTCGGTCTGGCTCTG
GACAACGTCAACGGGCACGGACTGACGGTGATGAAGGAAAGTATCCCCGGGTTCGGGGAC
AGGCTGTCTGGGCGCTGGCAAGCTGAACGTGTTCCACAACGACAACCACAACGTGGCCCTG
5 ACCGGCTCTCTTGCCAGGAACATGCCCAGCATCCCGAACGTGCCCAACTTCAACACGTAC
GGCGGGGGCGTCTGACTACATGTACAAGAACAAGGTGGGAGCGACTCTGGGCATGGCCAGT
ACTCCGTTCTTGACCGCAAGGACTACTCCGCGATGGGCAACCTGAACCTGTTCCGCAGC
CCGACCACTACCGTGGACTTCAGCGGCGGCTTCAAGAAGTTCGAATCTCCCTTCATGAGC
AGCGGCTGGAAGCCTAACTTCTCCTTTAATCTTGGCAGGTCATTCTAGAAATATTTTAA
10 ACTCTTATTTAAAAATTAAATGTAAAAAATCCWGTTTGTTTCATGATAATAAGAATAAATR
ACAGTATTGTTCTGACTATTTACTATGTAATCTATAAATTGTATTAATAAATGAAAATTA
A

[0281] *S. frugiperda*- rc16438 (Sfr16438); Un-annotated (SEQ ID NO: 103)

15 ATCAGTCGTCCCTCGTACATCCAACACTTCAAACCAAATATCTCCATATACATAGTAACA
ACATGTTCCGCCTAAAGTTGGTACTAGCTGCAGTGCTGGTGGTCGCAAGCGCCAGACATC
TACCACAGGACCACTCAACGTACCGAACATGTACAGCTGCTCGGGTTCGACGAAGATGGA
CGGCCAGTGTTTGAGCACGAAGACCTGCTCGCAGAACAGAGGAGTTCTATCAGCCAGAG
CACCTGGCGAGGACTCGCAGACAGGCACAGGGCAGCGTCACCCTCAACTCCGACGGCGGC
20 ATGGGCCTGGGCGCTAAGATCCCGCTCGCACACAACGACAAGAATGTGGTGAGCGCTATC
GGCTCCATGGACTTCAACAACAAGCTGCAGCCTGCTTCCAAGGGCTTCGGTCTGGCTCTG
GACAACGTCAACGGGCACGGACTGACGGTGATGAAGGAAAGTATCCCCGGGTTCGGGGAC
AGGCTGTCTGGGCGCTGGCAAGCTGAACGTGTTCCACAACGACAACCACAACGTGGCCCTG
ACCGGCTCTCTTGCCAGGAACATGCCCAGCATCCCGAACGTGCCCAACTTCAACACGTAC
25 GCGGGGGCGTCTGACTACATGTACAAGAACAAGGTGGGAGCGACTCTGGGCATGGCCAGT
ACTCCGTTCTTGACCGCAAGGACTACTCCGCGATGGGCAACCTGAACCTGTTCCGCAGC
CCGACCACTACCGTGGACTTCAGCGGCGGCTTCAAGAAGTTCGAATCTCCCTTCATGAGC
AGCGGCTGGAAGCCTAACTTCTCCTTTAATCTTGGCAGGTCATTCTAGAAATATTTTAA
ACTCTTATTTAAAAATTAAATGTAAAAAATCCWGTTTGTTTCATGATAATAAGAATAAATR
30 ACAGTATTGTTCTGACTATTTACTATGTAATCTATAAATTGTATTAATAAATGAAAATTA
ACTATMTAAMWAAAAAAAAAAAAAAAAAAAAAAAAACATGTC

[0282] *S. frugiperda*- j2rc2367 (Sfrc2367); Un-annotated (SEQ ID NO: 104)

ATCAGTCGTCCCTCGTACATCCAACACTTCAAACCAAATATCTCCATATACATAGTAACA
ACATGTTTCGCCCTAAAGTTGGTACTAGCTGCAGTGCTGGTGGTCGCAAGCGCCAGACATC
TACCACAGGACCACTCAACGTACCGAACATGTACAGCTGCTCGGGTTCGACGAAGATGGA
5 CGGCCAGTGTTTGAGCACGAAGACCTGCTCGCAGAACCAGAGGAGTTCTATCAGCCAGAG
CACCTGGCGAGGACTCGCAGACAGGCACAGGGCAGCGTCACCCTCAACTCCGACGGCGGC
ATGGGCCTGGGCGCTAAGATCCCGCTCGCACACAACGACAAGAATGTGGTGAGCGCTATC
GGCTCCATGGACTTCAACAACAAGCTGCAGCCTGCTTCCAAGGGCTTCGGTCTGGCTCTG
GACAACGTCAACGGGCACGGACTGACGGTGATGAAGGAAAGTATCCCCGGGTTCGGGGAC
10 AGGCTGTTCGGGCGCTGGCAAGCTGAACGTGTTCCACAACGACAACCACAACGTGGCCCTG
ACCGGCTCTCTTGCCAGGAACATGCCCAGCATCCCGAACGTGCCCAACTTCAACACGTAC
GGCGGGGGCGTCGACTACATGTACAAGAACAAGGTGGGAGCGACTCTGGGCATGGCCAGT
ACTCCGTTCTTGACCGCAAGGACTACTCCGCGATGGGCAACCTGAACCTGTTCCGCAGC
CCGACCACTACCGTGGACTTCAGCGGCGGCTTCAAGAAGTTCGAATCTCCCTTCATGAGC
15 AGCGGCTGGAAGCCTAACTTCTCCTTTAATCTTGGCAGGTCATTCTAGAAA

[0283] *S. frugiperda*- Chitin synthase B (SfChsB);AY52599) (SEQ ID NO: 105)

ATGGCGAGACCAAGACCTTATGGTTTTAGGGCTTTAGATGAGGAGAGTGATGACAATTTCG
GAGTTGACTCCGTTGCACGATGATAATGATGACCTAGGACAAAGAACAGCTCAAGAGGCA
20 AAAGGATGGAATCTGTTTCGAGAGATTCCGGTGAAGAAGGAGAGTGGGTCTATGGCCTCA
ACTGCCGGGATAGACTTCAGTGTAAGATCCTTAAAGTCCTGGCGTATATTTTTATATTT
GGCATAGTGCTCGGATCTGCGGTTGTGTCTAAGGGTACGCTGCTTTTTATCACATCACAA
CTGAAAAAGGGCAAAGCAATCGTTCAGTGTAAATAGACAGTTAGAACTGGACAAGCAGTTT
ATAACAATCCATTCGTTGCAAGAGCGTGTGACGTGGCTATGGGCAGCCTTCATAGCATTC
25 AGTATTCCAGAAGTTGGCGTTTTCTTGAGATCAGTCAGAAATATGCTTCTTCAAAACAGCA
CCGAAGCCTTCTGTTTTACAGTTTTTGACGGCCTTCGTAGTAGACACCCTTCATACAATA
GGCATTGGATTACTGGTGCTTTTCATCCTGCCAGAATTAGACGTGGTTAAAGGAACAATG
CTAATGAATGCTATGTGCTTCATGCCTGGAATACTAAACGCTGTGACCAGAGACCGCACG
GACTCTCGATACATGTTGAAAATGGCACTAGATGTACTAGCTATCTCCGCTCAAGCCACC
30 GCGTTCGTCTGCTGGCCTCTGCTAAAAGGCGTTAGTATGCTCTGGACGATTCTGTGCA
TGCGTATTATCTCACTCGGATGGTGGGAAAATTTTCGTGCGGATATCGGAAAACAATGG
CCAGTCCTGGAACCTGTACAAGAACTTCGTGACAATTTAAAGAAGACTCGTTACTACACA
CAGAGGGTGTTGTCTTTGTGGAAGATATTCATATTCATGTGTTGCATCCTGATATCTTTG

GCGGCACAAGATGACAGCCCGCTTTCTTTCTTCACGGAGTTTGCTACTGGATTTGGTGAG
CGCTTCTACAAAGTTCATGAGGTTTCGAGCGATACAGGACGAATTTGAAGGTTTTCTGGGC
TACAAAATTATGGACTTATACTTCGATCAAATGCCAGCGGCATGGGCCACCCCACTGTGG
GTGGTGCTGATCCAGGTCCTGGCTTCTTTAGTCTGTTTTATGGCAAGTTTGTCTGCCTGC
5 AAGATTCTGATACAAAACCTTCAGCTTTACATTTGCGTTGAGTCTTGTTGGACCTGTCACC
ATCAACTTGTTGATTTGGCTTTGCGGCGAGAGGAACGCAGATCCCTGCGCATATAGTAAT
ACGATACCAGATTATCTGTTCTTCGACATACCACCGGTGTATTTCTGAAGGAGTTTGTG
GTGAAAGAGATGTCGTGGATTTGGTTGCTGTGGCTGGTGTGCGAGGCGTGGGTGACGGCC
CACAAC TGGCGCTCCCGGGCCGAGCGTCTCGCCGCCAGCGACAAGCTCTTCAACAGGCCT
10 TGGTACTGCAGCCCCGTCTCGACGTCTCCATGCTGTTGAACAGAACCAAGAATGAAGAA
GCGGAAATAACGATAGAGGATCTAAAAGAAACAGAGAGTGAGGGTGGGTCTATGATGAGC
GGATTTGAAGCAAAGAAAGACATAAAGCCTTCTGACAACATTACGAGGATATATGTCTGC
GCGACTATGTGGCACGAAACGAAAGAAGAAATGATGGACTTCTTGAAGTCTATCCTGCGT
TTCGATGAGGATCAGAGCGCGCTCGCGTCGCACAGAAGTACTTGGGCATTGTAGATCCT
15 GATTACTATGAACTCGAAGTACACATCTTCATGGACGATGCTTTTGAAGTGTGCGGACCAC
AGCGCGGACGACTCGAAAGTGAATCCCTTCGTGACGTGTCTCGTGGAGACTGTGACGAG
GCTGCTTCAGAGGTCCATCTCACCAACGTGAGGTTGAGGCCACCGAAGAAATTCCCCACA
CCGTACGGCGGCCGACTGGTCTGGACTCTCCCAGGAAAGAACAAAATGATATGCCACCTC
AAAGACAAGTCCAAAATACGACACAGGAAAAGATGGTCTCAAGTGATGTACATGTACTAC
20 CTATTGGGCCACCGCCTGATGGACGTGCCGATCTCAGTGGACCGCAAGGAAGTCATCGCA
GGGAACACCTACTTACTGGCTTTGGACGGCGACATTGACTTCAAACCGACAGCAGTCACG
TTACTAATCGATTTGATGAAGAAGGATAAGAATTTAGGAGCAGCGTGCGGGCGCATCCAT
CCTGTGGGCTCAGGCTTCATGGCATGGTATCAAATGTTGAGTACGCTATTGGTCATTGG
CTGCAAAAAGGCGACTGAACACATGATTGGCTGTGTACTCTGTAGCCCTGGATGCTTCTCC
25 CTCTTCAGAGGAAAGGCTTTGATGGACGACAACGTTATGAAGAAATATACCTTAACTTCC
CACGAGGCACGACACTATGTGCAATACGATCAAGGCGAGGACCGTTGGTGCACGCTACTG
CTGCAGCGCGGGTACCGCGTGGAGTACAGCGCGGTGTGCGACGCGTACACGCACTGCCCC
GAGCACTTCGACGAGTTCTTCAACCAGCGCCGCGCTGGGTGCCCTCCACGCTCGCCAAC
ATCTTCGACCTGCTCGGCAGCGCCAAGCTCACCGTCAAGTCCAACGACAACATCTCCACC
30 CTCTATATAGTCTATCAGTTCATGTTGATAGTGGGTACGGTGTGGGTCCCGGCACGATC
TTCCTGATGATGGGGGAGCCATGAACGCCATCATTAGATCAGCAACGCGTACGCGATG
ATGTTGAACCTCGTACCACTCGTCATCTTCCTTATAGTCTGTATGACTTGTGAGTCAAAG
ACGCAGCTCTTCCTCGCTAACCTCATAACATGCGCATACGCAATGGTGATGATGATCGTG

ATAGTGGGGATAGTTCTGCAGATAGTGGAGGATGGATGGCTGGCTCCGTCCAGTATGTTT
ACAGCTTTAATATTTCGGTACATTCTTCGTCACCGCGGCACTACACCCGCAAGAGATCAAA
TGTTTGTTGTTTCATAGCAGTGTACTATGTAACCATCCCTAGTATGTACATGTTGTTGATC
ATATACTCCATCTGTAATCTCAACAACGTATCCTGGGGTACCAGGGAGACACCGCAGAAG
5 AAAACTGCTAAGGAAATGGAATGGAACAGAAGGAAGCAGAAGAAGCGAAGAAAAAATG
GAGAGTCAGGGTTTGAAGAAGTTGTTTGCCAAGGGAGAAGAGAAGAGTGGTTTCGTTAGAG
TTCAGTGTGGCGGGCCTGTTGCGATGTATGTGCTGCACCAATCCAGAGGATCATAAGGAC
GATCTCAACATGATGCAGATCTCACACGCGTTGGAGAAGATAAATAAGAGATTGGATCAA
CTCGATGTCCCTCCTGAGCCGACCCACCAGCCCTCGCATCCGCACACACACGTGGAGACG
10 GTCGGTGTTCGTGATTACGAAGACAGCGAGATTTCCACTGAAATTCCTAAGGAAGAACGA
GACGACCTGATTAACCCCTACTGGATCGAGGACGTGGAACCTCAGAAGGGCGAGGTAGAC
TTCCTCACCACCGCTGAGACCAACTTCTGGAAGGATGTCATCGATGAATACTTACTGCCT
ATTGATGAGGACAAGCGTGAAATTGAACGTATAAGAAAAGATTTGAAGAAGTTGCGAGAT
AAGATGGTGTGTTGCGTTCGTGATGTTGAACTCTCTGTTTCGTGCTCGTCATCTTCCTGCTG
15 CAGCTCAGCCAGGACCAGCTGCACTTCAAGTGGCCATTTCGGACAGAAGTCCAGCATGGAG
TACGATAATGATATGAATATGTTTCATCATAACCCAAGACTACTTAACGCTGGAACCTATC
GGTTTCGTGTTCTCCTGTTCTTCGGCTCCATCATCATGATCCAGTTCACCGCCATGTTG
TTCCATCGCCTGGACACGCTGGCCCATCTGCTGTCCACCACCAAGCTGGATTGGTATTTT
AGTAAGAZGCCGGACGACCTATCAGACGATGCGCTAATAGACTCTTGGGCGTTGACAATA
20 GCGAAGGATCTTCAACGTCTGAACACCGACGACTTGGATAAACGAAATAACAACGAACAC
GTGTCCAGGAGGAAGACCATATATAACTTGGAGAAAGGGAAGGAAACCAAACCGGCTGTT
ATCAACCTCGATGCCAACGCCAAGAGGAGATTGACTATCCTGCAGAATGAAGACTCAGAA
TTGATCTCCCGCCTGCCATCTCTGGGACCTAATTTGGCAACTCGTCGTGCCACGGTGCGT
GCAATAAACACTCGACGCGCATCTGTCATGGCGGAGCGACGCAGGTCTCAGTTCCAAGCG
25 CGACCTTCCGGGGGATCATAATGTATAATAACCCTCAAAACACGATTTCAGCTGGACGAT
ATGGTCGGGGGGCCGTGACGTCGGGAGTGACGTGAACCGAGGGTACGAGCCCGCCCTG
GACAGCGACATCGAGGACACGCCCGTGCCACAGACGATCCGTTGTACACTTCACCGAC
CATTTTCGCGTGATAACCACCAAAATCTGACTAACATCTCCATATTACATTTTCTACTCTG
TTACGAAACGATAAAGTTTAAAGTGATTAAATAAATTGGACAGATTTGAGTAGGTTTCA
30 CGTTTGTGTTTAAATAATTTATGAAAATAACATACCTATTGCTTTATGACCGCTTTAATA
TTAAAAGAACTCAATATATGCATTAA

**[0284] *T. castaneum*- Peptidoglycan recognition protein LC (TcPGRPLC);
DT786101.1 (SEQ ID NO:106)**

ATATAAAAAAAAAAATATTAGGCAATTTATTTACACAAATAGCACAATTTATCAATTC
ACAAGTTGTGTATTTTATTATAAATACTAAATCAACAATAGCGACTAACAATTAACACAA
5 TTTTATTTCACTTCCTGTCACTATCGCGAGTAATAAATTCCTGCATCAAAATGCGGCCAA
TTTTTGATCTCTTTGTAAACATTTGGCCCCGACTTTCCGTTCTAAACGTCTGATTGTGA
GCTACCAGTTTATAATCCCTGGCCAATTTTCCACTCTTTACCCCCTCATCTAGCAATTTT
TTCGCCACGCTGATCATCTCCGTCGTCAAATGATCATGAAAAAATTCCTCAATAAACTA
ATCCCGATCGAATCATCCATGTGAAAATTCCTGATATCCCAGCCTCGTCCAACATACGCA
10 TTCCCATCTCCACCAATTACGAAATTTGTACCCAATATCGGGACTTTTCAAATTTGCCACA
TGGTAGTCCTGCATGGACTGCACCCTTTGCGAACATGCAGGAAAGTCGCTACAAGTCGGG
GTAACAGTGTGTGAAACGATGACAAAATGAGTGGGATGTGGCAGTGGTTTAGAGAAGTTT
AAGGTGGCACGGCCTCCCCAAATTTTTTTCTCGATGATGGCACCGGGGCCCAAAGGAAGT
CTTGAGTTCGCAGTGTAGTGTGCGGAGTTTTCGGGAGACTTTTCAGTTTTCCGTGGGAGT
15 ATTACAACGCAAGTTGTGGTGACGAGGATTACGATTACGACTAGAGAAATGCCCAAATAT
TTCACAGGTTTGGAGTATAAAAAAGGAGTTTTTTTGGTTTTTCAGCGGGGGGAGAGTCGG
AAACAGGGGCTTTTCAGACTTGACGAAGTTTACCAATGGAATCAGTTGAATTAACAAATC
CTTTTCCCTAAAGTCCTCTAAAAACAGATGATGGGGCCCCAT

**20 [0285] *T. castaneum*- Peptidoglycan recognition protein 2 (TcPGRP2);
XM_965754.3 (SEQ ID NO:107)**

ATGAGTGGCAGTGACCCTTTAACAAATACCCAACAATCCGATCAAGATTATTACCATCCA
CTCTGTTATTCAATTCAAGTGGACGACGAAAATGAACAATCAGCTCTCCTGCCCGCATTT
CATCAAAGGAAAAGTTTGCAGATTGAGGATAAAATCTTTATTGTATTTTTATTTCAATT
25 CTAATTACCGGACTAGCCATTGGCCTCTATCTCCTTGCAACTGAGGGACACGAATGGAAA
GCTGCAGGAGTCTATAATATTACAGTTTCGGGAACAGTGGCAAGCTCACGTCCCTTCATCA
ACAATGCCAAAGTTGGAACCTCCCGTAAGAAGAGTTTTATTTCTTCCTGCAAAATACCACT
AGCTGCGGCAGCAAATCCCACTGTGCCAAAGTCTCCAGGAACTACAATTACAGCATATG
CTGCAGTGGAAGAACCTGACATCTCCTACAATTTTATAATGACTGCAGATGGCAGAATT
30 TTCGAGGGGAGAGGATGGGACTTTGAACTTCTGTTCAAAATTGTACGGTTAATGATACT
GTGACAGTTGCTTTTTTGGACGAATTAGATGCGAAAGCACCGACGTTTAGACAAGCTGAA
GCGGCAAAAATGTTTCTGGAAGTGGCAGTAACAGAGGGAAAATTAGAACGGTGTTTTAAT

ACCGCGGTCTGGGGAGGAAATAAATTCTTCATTGATTTGGCTCGAAATGTTCAAGACGTC
TTATCGGAATGCGAGGGAATTACTTAA

[0286] *T. castaneum*- Beta 1-3 glucan binding protein (TcβGRP2);

5 XM_966587.4 (SEQ ID NO: 108)

ATGTGCGTTTGCAAGACTGTGCTATTAATCGTTGGGCTGGGGGGTTGTTTTGCGGGTCCG
GTCCGTAATTATGGGCCATTGAGACATTACAACGTTCCGCGACCCTCAATCCAAGCATT
AGGCCCCGTGGCTTCAAAGTGAGCATCCCTCATACTGAAGGCATCCAATTATTCGCCTTT
CATGGAAATATTAATAAACCCCTGCACGGTCTCGAGGCCGGACAATTTTCCCAAGACGTC
10 CTCCAAAGGGAGGGAGACGAGTGGGTGTTCCAAGACTCCAGTGCCAAATTAAACGTGGGA
GATAAAATCTATTATTGGCTCTTTATCATTAAAGAAGACCTGGGCTACAGATACGATCAC
GGCGAGTACGAAGTGAAAGTTTTAGCCACCCGTGACTTCGATTCTCCTCAAACAACCTCT
GTGACGCCGAATCTTGCCCCAATCTCGGCATTTGCGAAAAGGTGATGGTAAATCTCACG
CGGAAGCTGCTCGATTTGCAGCAAGAAATTGAGTCCCTTAGGGAGACGAACGATATTTTG
15 GAGGATATGGTTCAGAAGCACACTGATACGGCGACTACTCTCACTTTGGACGGCTTGATG
ATAAAGGATGACGACGAACCTGTTTCGGTGATTCAAGCAATTATTAAAGATAAACTTGGA
CTAAAAAGCAGGATTCAAAATGTGACGAGGCAGGAGAATGGAATGGTCAAGTTTCAAGTG
GCGAGTTTGAGAGAAAAGTTGGAGGTTGTCAAAGCGGCCAAAAGAAAACCAAGTCGTCG
AGCTTTACGATCACGTATTAA

20

[0287] *T. castaneum*- midgut protein (TcMDGP); XM_971351 (SEQ ID NO:
109)

ATGTATCCGTTGAAGAGGATGCCAGTGAAGAAATCAGTATCAGTGATCTGCCTAGCGAA
ATGAAAGAAGTTTTACTAGAAATTAGCCCGAAGTTTGATGAAAATCTGAAACGGGCTTTC
25 AGGAACGAAGGAGTGAGGCTGCAGAGAGTGCAGAACAATGGACGATTTATTCATCAGCTG
GACGACGTTCTCTTATCCATAGACGATACCAAAATCGAGTTACGCAACCTGAAATTCCCC
TGGATCCCCGACTTCCGCATCGTGGACTTGTCAGCGACCTGCCCATGTCATGCCTCGAC
CTAAACCTAAACCTGGGCAATTTGCGAATTGAGGGCGAGTACGAAGCCAACAACACCACA
CTCAGGCGATGGCTCCCGGTATCTCACATTGGTCTGAATCGTGATCGGTTTTAACAACGTC
30 CGAGCGAACGGAAGTCGGACTCGTGCTCGAGCAGGATTCTTTCGTTCCGCAGAATTAT
GATATTAGATATGAGCCGACGGATGTTGTTATTAGGGTTAGCTATCACGTGGATGGCGAG
AATGAGGTGCAAAATGAGATTAGCAATTCAGATATTGAGGCCACGCTAGGCAAGACCGTG
TGGGTGCAGTTGACTGAGATATTGTCCAACCTGTTGCATAGGCAATTGGGCGAGGTTGTA

GTGGAGTTTTCCGTGACGGAACCTCTCGTCGATAGGGACGAGGAATACAGGGAATACGCC
AAGGGACAAGCAGCGCGCGCCAATAAACTCCTGGACTCGCTTTTGTGCTCAGCCAAGGAC
TATTTAGTCGCGAAGGACTTGAGGACGGTCAAACGCCACCCTTCGACGTCTCTTCAA
GGGAAAGTCTCGGGGGTGCAGCAGGGGACCTTCAGCACGGGGGAAGGGTTCTCTCAAGAC
5 CTGCCCCTTTGACGCGGAGACACAGCTTTAGTTTGTACGAAGACAAACACAACTCACG
ATATATGGGGGGATCAGGCTGAGGGAGTTTAACTCGGGTATGGGGGCTACCAGGGGCCAG
TACGAGGAAACGGCCGTCTCAGGCAGCATCAAAGGCTCGCTCTACAAGAACGAGATTTTC
GTCAAGATCACTGTGAAAAAAGAAGGCGAGCGGTGCTCGACTCAGTTAGATTCCGTCCAA
GTTGTTGTTGTAAAGTAA

10

[0288] ***T. castaneum*- Chitin synthase 2 (TcCHS2); EFA 10719.1 (SEQ ID NO:
110)**

ATGGCGGCGCGTCATCGCTTTGCCACAGGGAGCCCTGAGGAAACAGAGCCCCCTGTATTCTG
TCGACGCAAATGCCCCGAAAAAGTCCGGGAAAAATGGAACGTCTTCGACGACCCCCCAAGA
15 GAGCCCCTTCGGTTCGGAAGTCAAAGAACCTACATCGAGTGGGGGGTGAAGTTTTTGA
AAGTTGTGACAATCATAACTGTGTTTTTTGTGGTCTTGGTGCTGCAGTGGTTTCGAAAG
GGACAACCTTGTTTCATGACGTCACAAATAAAAAAGAATGTGACAAGGGCTTATTGCAACA
AAAAGATAGACCGCAACCTCCAATTCGTCTGCTCCTCCCCGAAGTGGAGCGCGTGCAAT
GGATCTGGCTCCTCATTTTTCGCTTACTTGATCCCCGAAGTGGGTACCTGGATCCGCGCCG
20 TCCGCAAATGCCTCTACAAGCTCTGGAATATGCCCTCCCTCTCCGAATTCCTCTCCCTCT
TCGGCACGGAAACGTGCCCCGCCATCGGAAGCGCAATTTTGATATTCGTCTGCTCCTCCCCG
AGCTGGACGTCGTCAAAGGGGCGATGCTCACAACGCGGTTTGTTCGTGCCCCGAGTTG
TGGCAATGTTCTCGCGCAAACCGTGCTCCATAAACGAGAACCTGAAAATGGGGCTGGACA
TCGCCAGCATAACTGCACAGGCGTCAAGCTTCGTGGTGTGGCCCTTGTTGAAAAATAACC
25 CGACCTTGACCTAATCCCCGTTTCCGTGATTTTGATTTTCGGTGGGTGGTGGGAGAATT
TCGTGTCGGAAACGTCTTACTTACCGTTTATCCGGGCTCTGGGCAAGAGCAAAAAGGAGT
TTAAGACAAGGACGTACTTCATTTACGCGTTTCGTGGCCCCGGTTAAATGCCTGGCGTTTT
TTTGACCCGCTTTGGTCATTTTTTACTGCCAGGAGGGCAGTGTTGACTTTTTTATTGATA
ATTTTTTCAGCCGCGTTTCAGGATCATAACATTGAAATTACCGAAGTCGCGCCCCGTCTTGC
30 CGGGGAATTACGCAAATGCAGTTCGGTTCGGAGCCGAAACCCCATCCACACAAGCAGTTA
CATGACGGGGATTTGGGTTTGGTTGATTAACATTTCCGGCGACTTATATTTGCTACGCGTT
TGGGAAATTCTCTGCAAAGTCATGATCCAGAGCGTTAGCTTCGCTTTTCCGATCAATTT
GTCGGTCCCTGTCCTCTTATCCGGACTGATCGCAATGTGTGGCATGTACTACAGGGATGA

GTGTTCTTTCGCTGAGTCAATTCCCTCCATATTTGTTTTTCGTTCCCTCCACCTCTCATGTT
CCTACAAGATTTTCTCTCGCACCAACACGCCTGGATTTGGCTGGTTTGGTTGCTGTGACA
AGCCTGGATTTTCGGTGCACATTTGGTCCCCAACTGTGACAACTTTCAAGCACCGAACA
GTTGTTTATTCGGCCCATGTATGACGCGTTTTTTGATCGATCAAAGCCTGGCGTTAAACCG
5 GAGACGTGACGAAAATCCCAGAAATTACAGAAGCGACGAAGGGCCTCAAATTACAGAGCT
CGAGCCGGAAACGATCGAGAGTCAGGACGCCATAACCCGGATTTACGCCTGCGGGACAAT
GTGGCACGAACTCCCGAAGAAATGATGGAATTTTTGAAATCGGTGTTCCGCTTGGACCA
AGACCAGTGTTCCACAGGATTGTGAGGGAGCATTTGGGACTCAAGCATGACAATTACTA
CGAATTGGGAGACTCATATATTTTTTCGATGATGCGTTTATTCGGACCAGTGAAGACGATAA
10 TGATCCCCACGTCAACGAATACGTTGAGTCACTTGCGTCCATTATCGACGAGGCTGCGAC
TAAGGTTACGGTACCACGGTGAGGGTGCCTCCGCCCCAAAGTGTACCCACGCCTTACGG
CGGACGCCTGGTCTGGACGCTCCCAGGGAAAACAAAAATGATCGCCCACTTGAAGGACAA
GAAGAAGATTAGGGCGAAAAAGCGCTGGTCTCAGTGCATGTACATGTACTTTTTGCTCGG
ATTCAGATTGCAAGCCAACGACGAACTCTCCGCCCACAGCAAGGAAATCCGCGGCGAAAA
15 CACCTACATCCTCGCCCTGGACGGCGACATCGATTTCCAACCCGAAGCCCTGCACCTCTT
GGTGGACTACATGAAGAAGAACAAAACGTTGGGGGCGGCCCTGCGGCCGCATCCACCCCAT
CGGCAGCGGCGGCATGGTCTGGTACCAAATGTTTGAATACGCCGTGCGTCACTGGATGCA
AAAAGCCACCGAGCACGTCATAGGCTGCGTCTCTGCAGCCCCGGCTGTTTCTCCCTGTT
CCGGGGAAAAGCCCTCATGGACAAAAGCGTCATGAAGAAGTACACCACTCGATCGACCCA
20 AGCCAAGCACTACGTGCAGTACGATCAAGGGGAGGACCGGTGGTTGTGCACTTTGTTACT
CCAGAGGGGCTACCGTGTGGAATACTCCGCAGCCTCGGACGCTTTCACGCACTGTCCGGA
AGGCTTCAACGAGTTTTTACAACCAGCGGAGGCGCTGGATGCCGTCCACTATGGCCAACAT
TTTGGACCTTTTGATGGATTACGAGCACACGGTCAAAATCAACGAAAATATTTCCATGCT
GTACATCGGGTACCAAATTATTTAATGATCGGTACGGTCATTGGCCCCGGTACTATTTT
25 CCTCATGTTGGTCGGCGCCTTCGTGGCTGCCTTTGGGCTCGACCAATGGAGCAGTTTCTA
CTGGAATTTACTACCAATCGCAGTTTTTATCCTAGTATGTGCCACTTGTAGCTCCGATAT
CCAATTATTTTTCGCCGGCCTTATCAGCGCCATTTACGGCCTGATAATGATGGCTGTTTT
CGTCGGTGTGATGCTCCAAATCAGCCAAGACGGCCCACTTGCGCCTTCCTCCCTTTTCTT
CTTCTGCATGGCTGCTGAATTTATAATCGCAGCACTGCTGCATCCGCAAGAATCAACTG
30 TTTGAAATACGGGGTCATTTACTACGTCACGGTCCCCAGCATGTACCTCCTCCTAGTCAT
CTACTCGGTCTTCAATATGAACAACGTGTCCTGGGGGACGCGCGAAGTGACAGTCGTGCC
CAAGCCTGACCCCAACGCCGTCCAGAAAATCGAAGAGAAAAAACCGGAGAAGAAAGACAA
AGTTTTGACGTTTCTGGGCGCGAATGCCCAGGACGACGAAGGCGGGCTTGAATTTTCGGT

CAACAAACTTTTCAAATGCATGATTTGTACGTACAAGGCCGATAACAAGGAAAACGAGCA
 GTTGAGGAAAATACAAGAGTCGTTGAGAGACTTGAATAGGAAAATCGAGTCGCTGGAAAA
 AATGCAATATCCGGATTTGAGGTCTCCTGCCGTTAGCAACGTTACAACGTTTCATGGAGGG
 CTCAAAGGCGACGGTTAAGAACAACGTGGAGGATAACTACATGGAGGCTCCGCAAGACAA
 5 TGTTCGCAACCGTCGGATGAGGTCATGGAGAATAGTTGGTTCTACGATGGGCCTTTGAT
 TAGGGGGGAAGTGCATTACTTGAATAGGAATGAGGAAACGTTTTGGAATGAACTGATAGA
 GCAGTATTTACACCCGATTGAGGATGACAAGAAGAAGGTTTCGGCTGAATTGAAAAGATTT
 GAGGGACAAAATGGTGTCTTACTTTCTGATGTTGAATTCGCTCTACGTTATTGTGATTTT
 TTTGCTCACTTTGAAGAAGGATTTGCTCCATCTGGACTGGCCGTTTGACCCCAAAGTGAA
 10 CTTACAGTATTTTCGAGGACAAAAATGAGATTGGCGTTTACATAACATACCTCCAGCTGGA
 GCCCATCGGTTTCGTGTTCTCATATTTTCGCCCTGCTTATGGTGATCCAGTTCTTCGC
 AATGATGATCCACCGCTTCGGCACCTTCTCCCAAATCATCACAAAACACAATTAGACTT
 CGATCTGTGCAGCAAACCAATCGACGAAATGACTGTGGACGAACTCAGGTCCCGCGACCC
 TATAAAAAATAGTCGCAGATTTACAAAACTAAAAGGTATAAACAACGAATACGAGGACCA
 15 AACGGAAGTTCCGGTCGAAATGCGAAAAACAGTAAGTAATTTGGCGCAAACGAGCGGTGG
 TGGTGAGAACAAGCCCATATTTTATTTGGATGAAGCGTTCCAAAGGCGAGTCACTCAAAT
 AGGGAGCACTTCAAGCAACAACCCGAGCATTAGCGCCTTTAGGAAGAAAAGCCTTGCTTA
 CGTCCAACAAAGAATGAGCATAGCCCCAAATCGGGTGTACAAGCCCGGCCTAGTGTGCA
 GTTACGGTACCCCAATGGAAAAGCCAACGAAAATTTGTTTTGACGAAAACGGGTCAGA
 20 CGTGGAGGCATAA

[0289] > M. sexta-Peptidoglycan recognition protein 2 (MsPGRP2);
GQ293365.1 (SEQ ID NO: 111)

TAATCATTAGAAAAATGGCGAGCTTCGCTTTAATAGTTATCCTTAGCGTAATTGGCTTTA
 25 TATCGGCCATCCTAGTCCTGAAGGTTACAGTTCTGCCTTCAACTTTCCATTTCGTAACCA
 AGGAGCAGTGGGGCGGCAGGGAGGCACGCACGTGACGCCACTCAACCACCCAGTGCAGT
 TCGTGGTGATCCACCACAGTTACATTCGCGCGTGTGCCTCAGCCGGGACGAGTGCAGCGC
 GCAGCATGCGCTCCATGCAGAACTTCCACATGAACAGTAACGGGTGGAGTGATATTGGAT
 ACAACTTCGCTGTGCGCGGTGAAGGTCGGTGTACGAGGGCCGCGGCTGGGACGCGGTGCG
 30 GCGCACACGCAGCTGGCTATAACAGTAACAGTATCGGCATCGTGCTCATCGGCGATTTTG
 TTTCAAACCTCCCGCCGGCGGTGCAAATGCAAACACACAAGAATTGATCGCAGCGGGCG
 TGCGACTCGGTTACATCAGGCCCAACTACATGCTCATCGGGCATCGTCAGGTCTCCGCCA
 CTGAGTGCCAGGAACCAGACTCTTCAACGAAATCACCAACTGGAACAACCTTCGTGAGG

[0290] > *M. sexta*-Beta-1, 3-glucan-recognition protein 2 (Ms β GRP2);
AY135522.1 (SEQ ID NO: 112)

GAGCGTCTGTTTGTTCGCAACCATTCGCGGGCTGCTTGGGCCAGCGAGGGGGTCCATACAA
5 GGTGCCCTGATGCGAACTCGAAGCTATCTACCCCAAAGGCTTGAGAGTCTCTGTGCCAGA
TGATGGCTACTCCCTATTTGCCTTCCACGGCAAGCTCAATGAGGAGATGGAAGGTTTAGA
GGCTGGCCATTGGTCCAGAGACATCACCAAAGCGAAGCAGGGCAGATGGATATTCAGAGA
TAGGAATGCTGAGCTGAAGCTTGGAGACAAAATTTACTTCTGGACTTACGTTATTAAGGA
TGGATTGGGATACAGGCAGGACAATGGAGAATGGACTGTTACAGAATTCGTCAATGAGAA
10 CGGTACAGTGGTGGACACTAGTACAGCGCCGCCACCAGTAGCACCCGCCGTTTCAGAGGA
AGATCAATCGCCAGGTCCTCAGTGGAGACCTTGCGAAAGATCCCTGACTGAGTCCTTGGC
CCGCGAACGCGTTTGCAAAGGCAGCCTTGTCTTTAGCGAGGACTTTGATGGTTCCAGTTT
GGCCGACTTGGGCAATTGGACCGCTGAAGTCAGATTCCCTGGCGAACC GGACTACCCGTA
CAACTTGTACACTACGGACGGCACTGTGGGATTGCGAAAGTGGGTCTCTGGTGGTGAGACC
15 CGTCATGACCGAGTCCAAATACCACGAGGGCATCATATACGACCGCCTCGACCTTGAGAG
ATGTACAGGACAGCTGGGTACGCTGGAATGCAGGCGAGAGAGCAGCGGCGGTGAGATTGT
ACCACCTGTGATGACAGCTAAACTGGCCACTCGACGCAGCTTCGCGTTCAAGTTCGGCAG
GATCGATATAAAGGCGAAGATGCCGCGCGGGGACTGGTTGATACCAGAACTCAACCTCGA
ACCTTTAGATAACATATACGGCAACCAGCGATACGCTTCGGGTCTCATGCGGGTCGCGTT
20 CGTGAGAGGAAACGATGTATACGCCAAGAAGCTCTACGGAGGTCCGATAATGTCCGACGC
GGACCCGTTTCAGGTCCATGCTGTTGAAGGACAAGCAAGGGTTGGCCAACTGGAATAATGA
TTACCACGTCTACTCGCTGCTGTGGAAGCCTAACGGTTTAGAGCTGATGGTGGACGGTGA
AGTGTACGGCACCATCGACGCTGGCGATGGCTTCTACCAGATTGCGAAGAACAACCTCGT
GAGCCACGCCTCGCAGTGGCTCAAGGGCACCGTCATGGCGCCGTTTGATGAAAAGTTCTT
25 CATCACTCTGGGTCTTCGCGTGGCGGGTATCCACGACTTCACGGACGGTCCGGGCAAACC
TTGGGAGAACAAGGG

[0291] > *M. sexta*-Relish family protein 2A (MsREL2A); HM363513.1 (SEQ ID
NO: 113)

30 ATGTCTCTTGTCCAAGCGACTATGATCCCAGTGAATCGTCCAAATCTCCACAAAGTATT
TGGGAGTCAGGAGGATACAGTTCTCCGTCGCAACAAGTTCCTCAATTGACTTCTAACTTA
ACAGAAATTGTCTGTTGATCACAGCTATAGATACAATGGAAATGGACCATATCTACAGATC
ACAGAGCAACCACAGAAATACTTTCGGTTCCGTTATGTTAGCGAGATGGTGGGAACACAT

GGATGTTTGCTTGGCAAATCTTATACAACAAACAAAGTTAAAACTCATCCGACAGTTGAA
CTCGTGAATTACACCGGTTCGAGCCCTGATAAAGTGCCAACTATCGCAAAACAAGAGCGAA
GACGAACACCCGCACAAACTGCTCGATGAACAAGACAGAGACATGAGCCACCACGTTCCC
GAGCACGGCAGTTATAGAGTGGTATTTGCTGGTATGGGTATAATTCATGCTGCCAAAAAG
5 GAAGTTGCGGGGTGGCTCTATAGAAAATATATACAGCAGAACAAGAATGAAAAGTTTAAAT
AAGAAAAGAGCTCGAAGCGCATTGTGAGAGGATGTCCAAAGAGATCGATTTAAATATAGTT
AGACTGAAGTTTACGCTCACGATATTGACACTGGCATTGAAATTTGCCGGCCAGTGTTT
TCTGAACCCATTTATAATTTGAAGTGTGCGTCTACGAATGATTTGAAAATATGCCGCATA
AGCCGTTGTTACGGTAGACCGAGAGGCGGCGAAGATATCTTCATATTTGTGCGAAAAGGTC
10 AACAAGAAAAACATCCAAGTTCGGTTCCTTTAGACTGGAAAACGGGGAGCGCACCTGGTCA
GCGATGGCGAACTTTCTGCTAAGCGATGTTACCACCAATACGCTATCGCTTTTAGAACG
CCACCGTACGTCAATCACCAAATTTCTGAAGACGTGCAAGTTTTTATAGAACTCGTACGC
CCTTCAGACGGTAGGACGAGCGCTCCCATGGAGTTCACATACAAGGCTGAGCAAACTCTAT
AAACAGAACAAGAAACGTAAAACTACTTCGTCTGCTACTCGTCGCTCGACAGCTCCTCAGGT
15 TCGGCCGGTTCAATTAAAAGCATCAGCGAACTGCCCCGCGCCCGTTGTTTTTGTGAAAAC
GTAAGTTTTTTCTATGACACATTACTCATTCTTCAACCCATGACGAATCTATAA

[0292] > *M. sexta*-Spätzle (MsSPZ1A); GQ249944.1 (SEQ ID NO: 114)

ACGAACAACCTGACAGACGGATAGCGGGACGGTCAGCACAAATACGAACATTTAAGAACAA
20 ACGAGAGGTCTCTCCCGGTCTACAGCGAGACCCAGAGGATACAAGCAGAAGAGAGAAGAA
GACACAGTTCGAGACTAGAAGAACCGAGACAACGTGCTGAGAATGGTTCATATAAGATAT
TGAATAACCCTCCGAAACCCTGTATTACTAATAGGAGAAGTCAAATTGATTCGTCTGAATG
ATAGGGTAGTGTTCCCGGTCCGACTTCAGAAAGGTCTGACGTACCCGAAGTGCCAGAGG
AATGCAAGAAAATCGGCATATGCGACAGTATACCGAATTACCCAGAAGAACACGTAGCTA
25 ATATTATATCTCGACTTGGAGACAAAGGAAAAGTATTACAAATAGACGAACTGGACGTAT
CAGACACTCCAGATATCGCCCAGAGGTTGGGTCCGCAGGAGGACAACATGGAACCTATGTA
GCTTTAGAGAAAAGATTTTTTACCCCAAGGCAGCGCCAGACAAAGATGGAAATTGGTTCT
TCGTTGTGAATTCAAAGAAAACCCAGTACAGGGTTATAAAGTTGAAATTTGCGACCGTC
AGCAATTACCATGCGCGGAGTTCGCGAGCTTCCAACAGGGATATGAAGCGAGGTGCATCC
30 AGAAATACGTTCCCGGACCATGTTGGCGTTGGATCCCAAGGGTCAGATGACCGACATGC
CCCTTAAAGTGCCAGCTGTTGCTCATGCGTGGCCAAATTGAC

[0293] > *M. sexta*-Toll receptor (MsTOLL); EF442782.1 (SEQ ID NO: 115)

ATGCAGGCTCGGCGGTGGTGC GCGGCACTGCTATTAATGCAGATGCTGAGCTGGCTCGGA
GTCAGTGGACACTTACCGCGTCCCGAGTGC GCGCCAGCCGCAGATTGCCAACTTATACGA
GACAACATAATCGATGGATATGCACAATTCTACTTCAACGTATCAGGACATGAAGTGAAA
5 TTTGAACATTACATCGGAAACGACTTCGATGTGCAATTGTCATGCAATTACATCGCCATG
GACAACGCAATGCTGCCGCGGTTCTCAACGACCTTTTCAGTCAACGTAATAGTGGTTAAA
GAATGTGCTTTGCCAAGAAGTGGGTCAATCGATGCCGCTGTCGCTGCACTTAATATCAAC
GTTTTGACGGAGCTGACTCTGGACAAATTCTAGAGCCGCGGTGATCACGCGCGCACAT
CTTACCAGTTTACAACGACTAGAGAGGCTGGAGCTACACGGTAACTCAAACACAAGCCTC
10 GCCCCCGGCGCACTGGCCGCGCTCTCCGCGCGTCCGCACTGAAATGTCTTGTATTGCAT
GCAGTACGCGTGCCCGCGCTGACCTGGCGCGCTTGCCGTCGTCAGTCAAGAACTAGCG
TTGTTGGATGTGGGCGCTGCGAGTATGCATTTAGATTTCATCGGTTAATTTGACGTCCTC
TTCGTAATCGATACACATTATCCTGTCGTCGTGAATGTGAGCAACGCCGTTGCGCTCAGA
GACTTGCACATAAATACCCCAAGTACTGTGTTGACCGAAGACGTGCTCCCGTCGTCCTC
15 AACTCACTTGAACTAGAGGGGTGGAACGAAACGCATCCGGTGCCTAAGACACGTTGTGTA
CTACTTAAGGAACTTAATGTAATCGGCACCGACAATGATGCCTATCCGGTGACTCT

[0294] > *M. sexta*-Valine Rich Midgut Protein (MsVMP1); NCBI accession number not assigned as yet (SEQ ID NO: 116)

ACGGACCTTCCGTTGGACCNCCATCATCGGCGCTGGAGACATCGCTGTGCGGCCCTGCTA
20 TCGTCGACTTCCCTTTCCCCGACGGCGGTGCCGTGTCTGCCCCCGTTGAGCCTTCCCCCA
TCGCCATCGGACCCGCTATCGTCGGTGAATCCCCTATCTCCGTGCGACCTGCCATCGTTG
AGGCCGGAGACATCGCTGTTGGACCCGCTATCATCGACTTCCCCCTTCCCGACGGTGGCG
CCGTGTCCGCCCCCGTTGAGGTTTCTCCCGTCGACTCCGTGTCGTCGCGCCCTGCCGCCG
25 GCTCTCAGAGCTCTCCCCTCGTCCAGATCATCATCAACGTTAAGGCCCGCTGGTGCCG
GCCCCGTTGTCGATGCCGTCGCTGACAAGCCCATGGACATCATTGATGTTATGCCCGTCG
TCGACCCTGCTGATTTTCGTGGACCTACCCCCGTTGTAGAGCCTGTAGAAGTCGTCGACA
TTGTCGATGTCATGCCCGTGGTTGACCCCATCAACATCATCGATGTTATGCCTGTTGTTA
AGCCCGTAAACCCCTTGCCCCGTTCTT

30

[0295] > *M. sexta*-Chitin synthase 2 (MSCHS2); AY821560.1 (SEQ ID NO: 117)

ATGGCCGCAACTACACCAGGTTTTAAGAAGTTAGCAGACGATTCTGAGGATTCTAGATACA
GAATACACCCCGCTGTATGATGACGGTGATGAAATAGATCAAAGAACTGCACAAGAAACA

AAAGGATGGAATCTATTTTCGAGAGATTCCGGTGAAAAAGGAGAGTGGATCTATGGCCACA
AAAAATTGGATAGAAACAAGCGTAAAAATCATAAAAGTGCTTGCCTACATATTGGTTTTT
TGTGCTGTACTGGGTTCCGCAGTCATAGCTAAAGGAACTCTTCTATTTATTACGTCACAA
CTGAAGAAAGACAGACAAATTACTCACTGCAATAGACGACTTGCTTTAGACCAACAGTTC
5 ATAACGGTACACAGTTT TAGAAGAAAGAATAACATGGCTATGGGCAGCACTTATTGTATTC
GGTGTGCCGAGTTAGGGGTGTTTTTGAGATCCGTCAGGATATGCTTCTTCAAAACTGCC
AAGAAACCAACCAAAACACAGTTTATTATTGCTTTCATAACAGAGACACTACAAGCAATA
GGAATAGCAGCACTTGTATTAATAATTCTACCAGAATTAGACGCTGTGAAAGGAGCCATG
TTGATGAACGCCACGTGCGCTATCCCTGCATTGCTAAACATTTTCACGAGAGACCGAATG
10 GATTCTAAGTTTTCTATAAAATTGATATTGGATGTATTGGCGATATCGGCACAAGCCACG
GCGTTTGTGTTTGGCCTCTTATGGAAAGAACGCCAGTTCTATGGACCATAACAGTTGCA
TGTGTGTTAGTGTCTCTAGGCTTCTGGGAGAATTTTGTGACACCTACAATAAAAAGTTAT
GTTTTTACGGTGCTGCAGGAACTACGCGACAACCTCAAGAGGACTCGGTACTACACTCAG
CGGGTGCTATCTGTTTGAAGATTATAGTGTATGATGCGCATTTTAATATCGCTGCAT
15 ATGCAAAATGACAATCCGTTTACCTTTTTCTACTACGCCAGCAAAGCCTTTGGAGAGAGA
CAGTATGTCGTTAACGAGGTTCTAATAGTAGTCCGAGATGACGAAACCATAGGCTATGAC
GTCACCGGAGGTATATTGCAATTGGACGCGATATGGACCTCAGCATTGTGGGTGCGATTA
ATTCAAGTGGGAGCAGCCTACTTCTGTTTCGGAAGTGGCAAGTTTGCTTGCAAAATTTCTT
ATACAAAATTTTAGTTTTCACTTTAGCATTGACTCTCGTCGGGCCCCGTGGCAATCAACCTC
20 CTTATTGCTTTCTGCGGAATGAGAAATGCAGACCCTTGCGCTTTCCATAGAACTATACCT
GACAATTTGTTTTACGAGATACCACCTGTG

[0296] > *M.sexita*-Beta-fructofuranosidase 1 (MsSuc1); GQ293363.1 (SEQ ID
NO: 118)

25 TTGCTGTGCGTTTTCTTGGTAGTGTATCGTCATGTTGCGTTAATGGGCGGTACTACCCG
AGGTACCATTGTGCGCCACCGCATGGCTGGATGAACGACCCCAACGGATTCTGCTACTTC
AAAGGTGAATACCATATGTTTTACCAGTACAATCCCATGTCAAGTTTGGAGGCTGGCATA
GCTCATTGGGGTCATGCGAAAAGTAAAGATTTGTGCCATTGGAAACACTTAGACCCGCCA
TCTATCCTGATCAGTGGTACGATCAAACGGGAGTATTTCTGGAAGTGCCTAGTAGAGA
30 ATGACGTCATGTACCTTTATTATACTGGAAATGTAAATCTTACTGATGAAATGCCATTTG
AGGGACAATTCCAAGCTCTTGGTATCAGTACTGACGGTGTCCACGTAGAAAAGTATAAAG
ACAATCCAATAATGTACACGCCAAACCATCAACCTCACATCCGAGACCCAAAAGTTTGGG
AACACGACGGCTCTTATTATATGGTCTTAGGAAACGCATATGATGATTATACAAAGGGCC

AAATAGTTATGTACGAATCATCAGACAAGATCAACTGGCAAGAAGTAACTATACTATATA
AATCAAATGGATCTTTTCGGTTACATGTGGGAGTGTCCAGATTTATTTCGAAATAGACGGCA
AGTTTGTACTTCTGTTCTCTCCTCAAGGCGTGAAGTCTGTGGGCGATATGTACCAGAATC
TGTATCAAGCAGGATACATCGTCGGAGAATTTCGATTACGATACTCATTTCATTACACAATAC
5 TAACCGAATTTCAGAGAATTGGATCACGGTCATGATTTTTTACGCTACACAAACAATGAAAG
ATCCTAGTGAAGAAGAATAGTCGTTGCTTGGGCAAGT

[0297] > *M. sexta*- Beta-1 tubulin (MsβTub); AF030547 (SEQ ID NO: 119)

ATGAGGGAAATCGTGACATCCAGGCTGGCCAATGCGGCAACCAGATCGGAGCTAAGTTC
10 TGGGAGATCATCTCTGACGAGCATGGCATCGACCCCAACGGCGCTTACCATGGCGACTCG
GACCTGCAGCTGGAGCGCATCAACGTGTACTACAATGAGGCCTCCGGCGGCAAGTACGTG
CCGCGCGCCATCCTCGTGGACCTCGAGCCCGGCACCATGGACTCTGTCCGCTCCGGACCT
TTCGGACAGATCTTCCGCCCGGACAACCTTCGTCTTCGGACAGTCCGGCGCCGGTAACAAC
TGGGCCAAGGGACACTACACAGAGGGCGCCGAGCTTGTCGACTCGGTCTTAGACGTCGTA
15 CGTAAGGAAGCAGAATCATGCGACTGCCTCCAGGGATTCCAACCTCACACACTCGCTCGGC
GGCGGTACCGGTTCCGGAATGGGCACCCTCCTTATCTCCAAAATCAGGGAAGAATACCCC
GACAGAATTATGAACACATATTCAGTTGTACCATCACCCAAAGTGTCTGATACAGTAGTA
GAACCTTACAATGCAACACTGTCAGTCCACCAACTCGTAGAAAACACCGACGAAACCTAC
TGTATCGACAATGAGGCTCTCTATGACATCTGCTTCCGCACGCTCAAACCTTCCACACCC
20 ACATATGGCGACCTTAACCACCTGGTGTGCTCACAATGTCCGGCGTGACCACCTGCCTC
AGGTTCCCCGGTCAGCTGAATGCGGATCTCCGCAAGCTGGCGGTGAACATGGTGCCCTTC
CCGCGTCTGCACTTCTTCATGCCGGGCTTCGCTCCGCTCACGTGCGCGGCAGCCAGCAG
TACCGCGCCCTCACCGTGCCCGAACTCACCCAGCAGATGTTTCGACGCTAAGAACATGATG
GCGGCGTGCGACCCGCGTCACGGCCGCTACCTCACCGTCGCCGCCATCTTCCGTGGTTCG
25 ATGTCCATGAAGGAGGTCGACGAGCAGATGCTCAACATCCAGAACAAGAACTCGTCGTAC
TTCGTTGAATGGATCCCCAACACGTGAAGACCGCCGTGTGCGACATCCCGCCCCGTGGT
CTCAAGATGTCGGCCACTTTCATCGGCAACTCCACCGCTATCCAGGAGCTGTTCAAGCGC
ATCTCTGAACAGTTCACCGCTATGTTTCAGGCGCAAGGCTTCTTGCAATTGGTACACCGGC
GAGGGCATGGACGAGATGGAGTTCACCGAGGCCGAGAGCAACATGAACGACCTGGTGTCC
30 GAGTACCAACAGTACCAGGAGGCCACCGCCGACGAGGACGCCGAGTTCGACGAGGAGCAA
GAGCAGGAGATCG

[0298] > *P. xylostella*- Peptidoglycan recognition protein 2 (PxPGRP2);
ACB32179.1(SEQ ID NO: 120)

CCCCGATACAGTTGGAGTACCTGCCCCGGCCCCTGGGGCTGGTGGTGGTCCAGCACACCGC
CACCCCCGCGTGTGACACTGACGCCGCGTGTGTGGAGCTGGTGCAGAACATACAGACCAA
5 TCATATGGATGTGCTGAAGTTTTGGGATATTGGACCGAACTTCCTGATTGGTGGGAACGG
CAAGGTGTACGAGGGCCCTGGTTGGCTGCACGTCGGCGCCACACTTACGGCTACAACAG
GAAGTCTATCGGGATCTCTTTCATTAGGAATTTTAATGCTAAGACCCCAACAAAAGCAGC
GTTGAATGCGGCTGAAGCATTGCTGAAGTGTGGAGTGAGAGAAGGACACCTGTCTCACTC
ATACGCAGTGGTCGGCCATAGACAACCTGATCGCAACAGAGAGCCCAGGCAGGAAACTGTA
10 CCAAATCATCAGGCGCTGG

[0299] > *P. xylostella*- Immune Deficiency Protein (PxIMD); Px003008 (SEQ
ID NO: 121)

TCCCGAAGCCACCTAGAGAACCGGTAGAGACTACAGAGACATCACAAAATAATACCGAAA
15 ATCAACCTTACAATGTCGAAGAAGAGGAAATACCCGAACCAGAAAAGCCTAAGAAAGAAA
AAAAGAATCCCAAGCCTACCAAAAAAACTTTCTTTAATCGTGACAAAATAACAAACACG
ACGATACCCGCAAACATACAAAATCCGGAAAGGACCAGACATCAATTAATACTCAAGGTA
ACTTGAAAATTATACTTCCTGTAACTTAAACGGCCCCGTTGACCCCAGTTTACCTTTCGCC
TTTCTTGATATATTTTTGTAATCCAGCCTTACTTTGGTAATACATACTTGCCCCACTTGT
20 ATTTAGTTAATGGTGGCACTAGCTAGATAGTAATGTTAAATGATGATAAGCAGTAGTGAT
TCATCATTCAAATGTATCATTGTCCTTTAATGTTAAGCGCAAATAGATTTTCATTGTTCT
CCCATGTGCTTCATGTTTTATGTATTTATAGGTAGGTACTTAATGTTTTATAAATATTTT
TTTGTTAATTGGGAATCCCCAGTCCCCATTGTCTGGACCAGTTTATATATAATTGAACTA
ACAAGAGTGTGCTTTAAATACTATTCTCTGCAATTATGATAATTAAACAACATGAATTTT
25 TCTTCACTTCCCTTCTCTTATTTAAATAATATTGTAGGAACTGTAATAACTAATACAAG
ATTATAAATTTCACTTAGCAACTGGTGATGTAATCCATGTGGTAAATTCCAAAGATGTG
CAGGTTCGGCCATCAGTATGTGTACAACATGGGAACTCCCGGAGCTAACTCACAGAAGAAT
AACCCATTTGATGATGAAGAAACAGTAGAAAAGACAAATCTAATAACTCTGGTCATGGAA
GCAAAAATTATGGTAATAACACATTTTTAACTAGGCATAAGGTCATAATTTAGCCAGAAT
30 CATCAGCTTGT

[0300] > *P. xylostella*- Cactus (PxCac); Px016665 (SEQ ID NO: 122)

CAATGCTGCGGAGGGTCTATGCGGGTGGACACCTCTACACGTAGCGGCGGCGGAGGCGA
CGTCGACACGGCTCGCTACTTGCTCGAGAAGTGCGCTGGCGTCGATCCCTCTGCCCTGGA
CTACGCCGGTTCGTACGGCCAGGAACTGGCGTTGAAGAATAAAGCGGCCGCCCTGTTTGA
5 CGGCAGTGAGGGCAGCGAGGAGGAGGATAGTGACAGTGAGGATGAGATGCTTCTGGAAAG
CGACCAGAGTCTGTTTCGACCGGATCCGTGACGGTATGAACGCCATCAACGTCGCCTGA

[0301] > *P. xylostella*- Dorsal (PxDor); Px000110 (SEQ ID NO: 123)

TAACCTGTGCCAGCAACCAATGGCTCCTATGGCGCAGCAGCTGATGGACCCGTCCCCCAG
10 CGACCCACCCCTCCATCACGGGGCTGCTGATGGATCGCCCGGACCAGCCCTACTCCGGGGA
GCTGTCTGGACTCTCCGCCCTGCTGGCTGAGGCAGCCCCCGCAGAGATGCTCAGCGATAG
CCTCAACAGACTGTCTACGGGGGACTTGTTGAGACAAGTTGATATGTGA

**[0302] > *P. xylostella*- Beta 1-3 glucan recognition protein 2 (PxβGRP2);
15 Q8MU95.1 (SEQ ID NO: 124)**

GAAGGATTGAAGTGAGCGCCAGAATGCCGCGCGGTGATTGGTTGATTCCAGATATTCTGC
TGGAGCCGAAAGAAAACCTTTACGGAGTACGCAATTACGCGTCAGGTCTACTCAGCATAG
CCTCAGTCAGAGGAAACACTGCTTACTCGAAGACCCTCAAAGGAGGCCCCATACTGTGTG
ACAAGGAACCGCAGAGAAGTGCCAAGTTGAGCGAAAAAGTTGGATATGACCATTGGAATA
20 AAGCCTTCCATAACTACACCATGATTTGGGCACCAAGTGGCATCACCATGCTGGTGGACG
GCGAGCAGTACGGGGACATCCGTCCCGGCGACGGCTTCAGCCAGGACCCGGCGGTGAGCA
GCGTGGTGGCCGCGCCGAGTGGCTGAAGGGCACCAGCATGGCGCCCTTTGATGTTATGT
TCTACATATCCCTTGGTCTCCGCGTGGGCGGAGTGAACGACTTCCCCGACACTCCTGAGA
AGCCGTGGAAGAACAAGGCCACTAAAGCCATGCTGAATTTCTGGAACGCCCGGGAACAGT
25 GGCAGAGCAGCTGGTTTGAGGACACCACTGCACTCCTCATAGACTATGTCAGGGTTTATG
CGCTGTGA

**[0303] > *P. xylostella*- Chitin synthase 1 (PxCHS1); KX420688.1 (SEQ ID NO:
125)**

CGTATCTCGCACGACCTGAAAGAGCTGCGAAACTCATCCGTCTTTTCCTTCTTTATGATC
30 AATGCCCTCTTTGTTCTCATCGTATTCTTGCTGCAACTGAACAAGGACAACCTCCACATA
AAGTGGCCCTTCGGAGTCAAACTAACATTACGTATGATGAGGTGACGCAAGAGGTGCTG
ATCTCCAAGGATACCTGCAACTAGAGCCTATTGGTCTGGTGTTCGTGTTCTTTTCGCAT

TGATTTTAGTCATCCAGTTCCTGACCATGTTGTTCCATCGATTCCGGAACCTTTGTGCGCATA
 TATTATCGTCTACGGAAGTGAAGTGGTCTGCAATAAGAAGGCGGAAGACTTATCTCAAG
 ACGCACTGCTAGATAAGAATGCGATAGCAATAGTGAAGGATCTCCAGAACTAAACGGGC
 TCGATGACGGGTATGACAATGACTCGGGGTCTGGGCCCCGACAATGTGGGAAGGAGAAAGA
 5 CGATACACAACCTGGAGAAAGCGAGACAGAAGAAGAGGAACATAGGAACGCTCGACGTCTG
 CTTTCAAGAAGCGATTCTTCAACATGAACGCTAATGAAGGACCAGGAACACCAGTTCTGA
 ACCGCAAGATGACGTTGCGAAGAGAGACGTTGAAGGCGTTGGAAACGAGGAGGAATTCTG
 TGATGGCCGAACGAAGGAAGTTCGCAATGCAAACTTGGAGCTAACAACGAATATGGAG
 TCACTGGAATCTTAAACAACAACCCAGCGGTGATGCCGCGCCACCGGCCGTCGACAGCCA
 10 ACATTTTCGGTCAAGGACGTCTTCGCGGAACCCACGGGGGACAAGTGAACCGAGGGTACG
 AGACCACGCACGGCGACGAGGGAGACGGCAACTCCATCAGACTGCAGCCGAGAACCAACC
 AGGTCTCCTTCCAGGGGAGATACCAATAA

[0304] > *P. xylostella*- Beta tubulin (Px β TUB); KX420688.1 (SEQ ID NO: 126)
 15 GAAGGAGGTCGACGAGCAAATGTTGAACATCCAGAACAAGAACAGCAGCTACTTCGTCTGA
 ATGGATCCCGAACAACGTCAAAACGGCCGTGTGCGACATACCGCCTCGTGGACTGAAGAT
 GTCTGCCACCTTTATCGGGAACACGACAGCAATCCAAGAGCTCTTCAAGAGGATTTCTGA
 GCAGTTCACTGCTATGTTTCAGGAGGGAAGCGTTCCTCCACTGGTATACTGGTGAAGGCAT
 GGACGAGATGGAGTTCACAGAGGCGGAGAGCAACATGAACGACCTGGTCTCCGAGTACCA
 20 GCAGTACCAGGACGCCACGGCTGAAGACGAGGGAGAATTCGACGAGGATATTGAAGACGA
 GTGA

[0305] > *S. frugiperda*-Peptidoglycan recognition protein 1 (SfPGRP1);
 rep_c7951 (SEQ ID NO: 127)
 25 CCTGATTGGTGGAAACGGGAGAGTTTATGAAGGAGCCGGCTGGCATCACGTTGGGGCCCA
 TACTTTGGGATACAATGCAAGATCTGTGGGGATCTCCTTCATTGGCGATTTTAGAACAAA
 ATTACCAACACCCGAAGCACTGAAAGCCTTCAACAGTCTCCTGGAATGTGGAGTCACGAA
 CAATTATCTGTCAAAGGACTATCACCTGGTGGCCCATAGTCAGCTCTCTATGACTGACAG
 TCCYGGAGACATGYTGAGGAAGCAGGTGGAATCGTGGCCTCMTTGGCTGGATAATGCCAA
 30 AGACATACTTAAGTAGAARAAGACTAAACGCCGTACTTTGAGCCATTTAATGGTTACTTA
 ACCCAGTCCTTAGCAATTTGATACAAGGCCAATGTCTCTAAGGGCGGCAGTAAAGGTCAA
 AACACATTTAATGAGTGTGTTTAAGATTTTGCTAGTGAAAATTGTTTTGAAGTACGTATT

TGATGTAAGTGATGATATCAGTACCCTTAGTATGAGTTTGCTTTACGTTCCACGAGATGG
AAACGAGAGCGCGTTTCGGCGCTCTGATTGGTTCGTTTCATTCATGCCGGCC

[0306] > *S. frugiperda*-Attacin (SfAtta); rep_c9395 (SEQ ID NO: 128)

5 GCCAGACATCTACCACAGGACCACTCAACGTACGACCAAGTACAACCTCCTCGGGTTCGAC
GAAGATGGACGACCAGTGTTTGAGCACGAAGACTTACTCCCAGAAGTAGAGGAGTCCTAC
CAGCCAGAGCACCTGGCGAGGACTCGCAGACAGGCGCAGGGCAGCGTCACCCTCAACTCC
GACGGCGGCATAGGCCTGGGCGCTAAGATCCCGCTCGCACACAACGACAAGAATGTGGTG
AGCGCCATCGGCTCCATGGACTTCAACAACAAGTTGCAGCCTGCTTCCAAGGGCTTCGGT
10 CTGGCTCTGGACAACGTCAACGGGCACGACTGACGGTGATGAAGGAAAGTATCCCCGGG
TTCGGGGACAGGCTGTCGGGCGCTGGCAAGCTGAACGTGTTCCACAACGACAACCACAAC
GTGGCCGTGACCGGCTCTCTCGCCAGGAACATGCCCAGCATCCCGAACGTGCCCCAATTTC
AACACGTACGGCGGGGGCGTCGACTACATGTACAAGAACAAGGTGGGAGCGTCTCTGGGC
ATGGCCAGTACTCCGTTCTTGGACCGCAAGGACTACTCCGCGATGGGCAACCTGAACCTG
15 TTCCGCAGCCCGACCACTACCGTGGACTTCAGCGCGGCTTTAAGAAGTTCGAATCTCCC
TTCATGAGCAGCGGCTGGAAGCCTAACTTCGGCCTTACTTTCGGCAGATCTTTCTAGATA
TATTTTGTAAATCTAAATTTAACTTTAACTTTGTTGTATAATATTTTGTGAATTAAGATC
AGTATTGTTCTACTAATAATTATATTATCAGTGTTTCTTATAAATTAA

20 [0307] > *S. frugiperda*-Hemolymph proteinase 10 (SfHP10); c12881 (SEQ ID NO: 129)

CAAGGCTCGTACCTTGACAGTTGAACCGACAATCTATTCCCTAAAGCCTTTTTAAGGTCAGG
AAAAATAGTTCCTACATCTAAATGCAGTAGAATTTGCGAAACGAATTTAAATAAAAAATGG
CGTCGATTGTGTTTGTGATTTTGTGTGTTACCGTCGCTGCGGTGAAAAGCGCGATTTTAA
25 ACCCGTGGAGTAAAGTTGAGGCCAACAAATGTGGTGTAGAAGCCAGTACTAACTTGGTCC
ATCACAATCCATGGTTGGTCTACATCGAGTATTGGCGTGGAACTCAGATACTGAGATCC
GATGCGCCGGTACTTTAATCGACAGCAAACATGTCGTACACAGCTGCCCCACTGCGTTAGGA
CTCTGAAGTTTAGTCATTTGATCGCCCGTCTTGGCGAATACGACGTAAATTCTAAGGAGG
ACTGCGTTCAGGGCGTGTGTGCCGATCCCATCGTCAGAATCAAGGTGGCTGAGATCATCG
30 TGCATCCTAACTACAGCAACCGGGAACA

[0308] > *S. frugiperda*-Trypsin like serine protease (SfTSP); rep_c48453
(SEQ ID NO: 130)

AGCAACAAAATGCGTGTCTCGCTTGCTTGGCCCTTCTCTTAGCTGTGGTAGCAGCCGTC
CCCTCCAATCCCCAGAGGATTGTGGGTGGTTTCGGTCACCACCATTGACCGGTACCCACCC
5 ATTGCATCCCTGCTGTACTCGTGGAACCTTGAGTTCTTACTGGCAGGCGTGCGGTGGTTCC
ATCTTGAACAACCGTGCCATCCTTACTGCTGCCCCTGCACAGTTGGTGACGCCGCCAAC
AGATGGAGAATCCGTCTTGGCTCCACCTGGGCCAACAGCGGTGGTGTGCTTCACAACGTC
AACACTAACATCGTCCACCCCTCATACTGCAACTTTGAACAACGACATCGCTATC
CTCCGCTCCGCCACCACCTTCTCCTTCAACAACAATGTTTCAGGCTGCCTCCATTGCTGGT
10 GCCAACTACTTGCCCGGTGACAACACCGCCGCCTGGGCCGCTGGATGGGGAACCTACCTCC
GCTGGTGGCTCTAGCTCTGAGCAGCTCCATCACGTTGAGCTGCGCATCATCAACCAGGCT
ACTTGCAAAAACAATTACGCTACCCGCGGTATCACCATCACCTACAACATGTTGTGCTCT
GGCTGGCCACCGGTGGTTCGCGACCAGTGCCAGGGTGACTCTGGTGGTCTCTCTACCAC
AACGGCATCGTTGTTGGTGTCTGCTCTTTCGGTATTGGCTGTGCTCAG
15

[0309] >*S. frugiperda*- C Type Lectin 6 (SfCTL6); Joint2_ rep_c448 (SEQ ID
NO: 131)

AACAGTTTTCTATTGGCAGTCAAAGACTTCAGTCGAAAAATAATCCTCATCAGAGTCGTG
AAGCAAGGTGCCCAAAATATAATGTAACCTAGATACCTATTAATAAATTATTTGTCAACC
20 AAAACGTTACGTTCAAAGTCCTTAAAATCAAATATCTTATGATTAGTTTTGATTTAAAA
ATAGAGGTTGAAATCGCCAACCCAAATAGGTTTAGTTTACGATTCAGGAAAAATCCTAA
CGTAGGGAAACATTATTTTACAAGACTTTTGGCTTAAAAACTTTGAGAACCAATGTCAAA
TTTGATAATAACTAATGAGGTATAAAAGCTTGATCCTATTAGGACTTATTTTCATAACAC
CATCGAGTTTGTATTTAATRRAGACGTGKGTAACTAACAACATGAAGACCGGTGTAAAA
25 TATTCTGTTMTTGGATATTCTCTCTATTYTGTATATAGAGGCAACATTTTCGTTGTGAC
TACACGTACAGCAAGGAAGCGAAGGGCTGGTTCAAACATGTGGTGATAACCAGCTACTTGG
GCTGACGCACGWCTGCACTGCACGTTGGAAGGTGCAACGCTGGCTTCTCCACTCAACCAG
GCTATMAGTAATGAGATGCAGTCCMTCTGGCRAACCTCTCGGCGCTGCAATCAGAAGTC
TTCACTGGAATTCACRCGACTKTTTCACGRMRCAACTTATATCATACYATYGAAGGTATA
30 CCTCTTAGTAAATTCATTAGATTGGGCAACAAATGAGCCAAATGGTGGGAGAGATGAA
AACTGTATCACGTTTAACTCCGATGGCCAAGCGGCAGACAGATCCTGTAARGAGACTCGA
CCTTACATCTGCTACCGACACACWACTAAAGTGACTGTGKCCAATGAATGTGGGACTGTA

GATCCTGAATACAATTTGGATAAAAGAACGGGCKCYTGCTATAAGTTCCACACRGTACCT
CGCACGTTTCGAGCGTGCCAACTTCGCGTGTTCTGCTGAAGGTG

[0310] > *S. frugiperda*- Cecropin (SfCec); rep_c42380 (SEQ ID NO: 132)

5 TTCGTGTCGTATCACTAGAGTTCGAAATACAAAATAATAACATTTATTATTTTGCCAT
AATTAATAATAAAGTTATTTTATTTTCATAATAATAATGAATTTACAAAGATATTTTGT
TGTTTTTGTCTTGCTTTGTTTTGATGGCGACCGTGTGAGGAGCTCCTGAACCGAGGTGGA
AATTCTTCAAGAAAGTGGAGAAGTTGGGCCAAAACATCCGCKATGGTATCATAAAGGCAG
GACCCGCAGTGGCCGTGGTGGGATCAGCRGCAGCCATWGGAAAGTGAKCCCTACGACCTG
10 AGACATGAAGACTAATATCCAYTAAAATAASAATATTGAGGCKTATAATATTAATTTATT
RTRTTTGTAATTAAATTATTTGTAAGATAA

[0311] > *S. frugiperda*- Beta 1, 3 glucanase recognition protein (SfβGRP2); EF641300 (SEQ ID NO: 133)

15 GCAACAATCGCACCAACTCTTTTCGTGCGCAGTGGAAGTTTGTTCATCCGTCCCTCTCTAA
CATCAGACGAGTTCGGAGAAGCTTTCCTCTCATCTGGACACTGGAACGTCGAGGGTGGTG
CTCCTGCTGATAGATGCACAAATCCACAATGGTGGGGTTGCGAGAGAACAGGCACGCCGA
CCAACATTTTGAACCCAATCAAGAGTGCTCGTGTCCGTACCGTCAATTCCTTCAGCTTCC
GTTACGGACGCCTCGAAGTCCGCGCTAAAATGCCCGCCGGAGATTGGATTTGGCCAGCTA
20 TCTGGTTGATGCCTGCGTACAACACTTACGGTACTTGGCCCGCATCAGGAGAGATTGACT
TAGTTGAGTCCCGAGGCAACCGTAACATGTTCCACAATGGTGTCCATATCGGTACACAGG
AAGCAGGCTCGACCTTGCACTACGGACCTTACCCAGCGATGAACGGTTGGGAGCGCGCCC
ATTGGGTCAGAAGGAACCCT

25 [0312] > *S. frugiperda*- joint2_rep_c16438 (Sfrc16438); Un-annotated (SEQ ID NO: 134)

TCGTTCTCCTCGTCGCTTTCTTGGGGACCTCATGGTTTACGGGAGATGTTTCTGCGAGTC
CGCGGCCGCAAGAGCCGCGTGTGGATCAAATCCGAATCAGGTGTCACCTTATGGAGGGT
CCGGGTACCACGCACCTCCGCAGTACCAACCGCAGTACCAACCACAGCCGTACTACCCAC
30 AGCCGCAGTACTACCCACAGCCGTACTACCCACCTCCTCAGTATTACCCACCGCAGCCAC
AAACACCTGAGAATGCTCCACTCATAAACACATGGAATGGTTTCCACGACTGGGCTCAGA
ATATCGTTCAAAGTGCTTTGGGGCAGAAATTCCCGAAAGGTAGACAGTAACTTTTAAATT
GTCAATTGAAGATAAGGCCCATTTACCAACTGCTGTTTAATTTAAGGAGCTCCTAAAC

TAACATAGGTGACACTTAGCGATATTCTGGATTTTTTGTGAACGTATAAATAATATCCAA
ATGTAAAAGATAAGAGGCCAAGAA

[0313] > *S. frugiperda*- Chitin synthase B (SfChsB);AY52599) (SEQ ID NO:
5 135)

GAATTTAGGAGCAGCGTGCGGGCGCATCCATCCTGTGGGCTCAGGCTTCATGGCATGGTA
TCAAATGTTTCGAGTACGCTATTGGTCATTGGCTGCAAAAGGCGACTGAACACATGATTGG
CTGTGTACTCTGTAGCCCTGGATGCTTCTCCCTCTTCAGAGGAAAGGCTTTGATGGACGA
CAACGTTATGAAGAAATATACCTTAACCTCCACGAGGCACGACACTATGTGCAATACGA
10 TCAAGGCGAGGACCGTTGGTGCACGCTACTGCTGCAGCGCGGTACCGCGTGGAGTACAG
CGCGGTGTTCGGACGCGTACACGCACTGCCCCGAGCACTTCGACGAGTTCTTCAACCAGCG
CCGCCGCTGGGTGCCCTCCACGCTCGCCAACATCTTCGACCTGCTCGGCAGCGCCAAGCT
CACCGTCAAGTCCAACGACAACATCTCCACCCTCTATATAGTCTATCAGTTCATGTTGAT
AGTGGGTACGGTGTGGGTCCCGGCACGATCTTCCTGATGATGGGGGAGCCATGAACGC
15 CATCATTCAGATCAGCAACGCGTACGCGATGATGTTGAACCTCGTACCACTCGTCATCTT
CCTTATAGTCTGTATGACTTGTTCAGTCAAAGACGCAGCTCTTCCTCGCTAACCTCATAAC
ATGCGCATACGCAATGGTGATGATGATCGTGATAGTGGGGATAGTTCTGCAGATAGTGGA
GGATGGATGGCTGGCTCCGTCCAGTATGTTACAGCTTTAATATTCGGTACATTCTTCGT
CACCGCGGCACTACACCCGCAAGAGATCAAATGTTTGTGTTTCATAGCAGTGACTATGT
20 AACCATCCCTAGTATGTACATGTTGTTGATCATATACTCCATCTGTAATCTCAACAACGT
ATCCTGGGGTACCAGGGAGACACCGCAGAAGAAAAGTCTAAGGAAATG

[0314] > *T. castaneum*- Peptidoglycan recognition protein 2 (TcPGRP2);
XM_965754.3 (SEQ ID NO:136)

25 ATGAGTGGCAGTGACCCTTTAACAAATACCCAACAATCCGATCAAGATTATTACCATCCA
CTCTGTTATTCAATTCAAGTGGACGACGAAAATGAACAATCAGCTCTCCTGCCCGCATTT
CATCAAAGGAAAAGTTTTCGAGTTCAGGATAAAATCTTTATTGTATTTTATTTTCAATT
CTAATTACCGGACTAGCCATTGGCCTCTATCTCCTTGCAACTGAGGGACACGAATGGAAA
GCTGCAGGAGTCTATAATATTACAGTTCGGGAACAGTGGCAAGCTCACGTCCCTTCATCA
30 ACAATGCCAAAGTTGGAACCTCCCGTAAGAAGAGTTTTATTTCTCCTGCAAATACCACT
AGCTGCGGCAGCAAATCCCACTGTGCCAAAGTCTCCAGGAACACAAATTACAGCATATG
CTGCAGTGGAAAGAACCTGACATCTCCTACAATTTTATAATGACTGCAGATGGCAGAATT
TTCGAGGGGAGAGGATGGGACTTTGAAACTTCTGTTCAAAATTGTACGGTTAATGATACT

GTGACAGTTGCTTTTTTGGACGAATTAGATGCGAAAGCACCGACGTTTAGACAAGCTGAA
GCGGCCAAAAATGTTTCCTGGAAGT

[0315] > *T. castaneum*- Beta 1-3 glucan binding protein (TcβGRP2);

5 XM_966587.4 (SEQ ID NO:137)

ACATTACAACGTTCCGCGACCCCTCAATCCAAGCATTTCAGGCCCCGTGGCTTCAAAGTGAG
CATCCCTCATACTGAAGGCATCCAATTATTCGCCTTTCATGGAAATATTAATAAACCCCT
GCACGGTCTCGAGGCCGGACAATTTTCCCAAGACGTCTCCAAAGGGAGGGAGACGAGTG
GGTGTTCOAAGACTCCAGTGCCAAATTAAACGTGGGAGATAAAATCTATTATTGGCTCTT
10 TATCATTTAAAGAAGACCTGGGCTACAGATACGATCACGGCGAGTACGAAGTGAAAAGTTTT
AGCCACCCGTGACTTCGATTCTCCTCAAACAACCTCTGTGACGCCGAATCTTGCCCCCAA
TCTCGGCATTTGCGAAAAGGTGATGGTAAATCTCACGCGGAAGCTGCTCGATTTGCAGCA
AGAAATTGAGTCCCTTAGGGAGACGAACGATATTTTGGAGGATATGGTTCAGAAGCACAC
TGATACGGCGACTACTCTCACTTTGGACGGCTTGATGATAAAGGATGACGACGAACCTTGT
15 TTCGGTGATTCAAGCAATTATTAAAGATAAACTTGGAATAAAAAGCAGGATTCAAAATGT
GACGAGGCAGGAGAATGGAATGGTCAAGTTTCAAGTGGCGAGTTTGAGAGAAAAGTTGGA
GGTTGTCAAAGCGGCCAAAAGAAAACCTCAAGTCGTGAGCTTTACGATCACGTATTAA

[0316] > *T. castaneum*- midgut protein (TcMDGP); XM_971351 (SEQ ID NO:

20 138)

CCGTTGAAGAGGATGCCCAGTGAAGAAATCAGTATCAGTGATCTGCCTAGCGAAATGAAA
GAAGTTTTACTAGAAATTAGCCCGAAGCTTTGATGAAAATCTGAAACGGGCTTTCAGGAAC
GAAGGAGTGAGGCTGCAGAGAGTGCAGAACAATGGACGATTTATTCATCAGCTGGACGAC
GTTCTCTTATCCATAGACGATACCAAAATCGAGTTACGCAACCTGAAATTCCCCTGGATC
25 CCCGACTTCCGCATCGTGGACTTGTCCAGCGACCTGCCCATGTCATGCCTCGACCTAAAC
CTAAACCTGGGCAATTTGCGAATTGAGGGCGAGTACGAAGCCAACAACACCACACTCAGG
CGATGGCTCCCGGTATCTCACATTGGTTCGAATCGTGATCGGTTTTAACAACGTCCGAGCG
AACGGAAAAGTCGGACTCGTGCTCGAGCAGGATTCTTTCGTTCCGCAGAATTATGATATT
AGATATGAGCCGACGGATGTTGTTATTAGGGTTAGCTATCACGTGGATGGCGAGAATGAG
30 GTGCAAAAATGAGATTAGCAATTCAGATATTGAGGCCACGCTAGGCAAGACCGTGTGGGTG
CAGTTGACTGAGATATTGTCCAACCTGTTGCATAGGCAATTGGGCGAGGTTGTAGTGGAG
T

[0317] > *T. castaneum*- Chitin synthase 2 (TcCHS2); EFA 10719.1 (SEQ ID NO: 139)

ATGGCGGCGCGTCATCGCTTTGCCACAGGGAGCCCTGAGGAAACAGAGCCCCTGTATTCTG
TCGACGCAAATGCCCCGAAAAAGTCCGGGAAAAATGGAACGTCTTCGACGACCCCCCAAGA
5 GAGCCCCTTCGGTTCCGAAGTCAAAAGAACCTACATCGAGTGGGGGGTGAAGTTTTTGA
AAGTTGTGACAATCATAACTGTGTTTTTTGTGGTCCTTGGTGCTGCAGTGGTTTCGAAAG
GGACAACCTTGTTCATGACGTCACAAATAAAAAAGAATGTGACAAGGGCTTATTGCAACA
AAAAGATAGACCGCAACCTCCAATTCGTCGTCTCCCTCCCCGAAGTGGAGCGCGTGCAAT
GGATCTGGCTCCTCATTTTCGCTTACTTGATCCCCGAAGTGGGTACCTGGATCCGCGCCG
10 TCCGCAAAATGCCTCTACAAGCTCTGAAAAATGCCCTCCCTCTCCGAATTCTCTCCCTCT
TCGGCACGGAACGTGCCCCGCCATCGGAAGCGCAATTTTGATATTTCGTGCTCCTCCCCG
AGCTGGACGTCGTCAAAGGGGCGATGCTCACAACGCGGTTTGTTCGTGCCCCGAGTTG
TGGCAATGTTCTCGCGCAAACCGTGCTCCATAAACGAGAACCTGAAAATGGGGCTGGACA
TCGCCAGCATAACTGCACAGGCGTCAAGCTTCGTGGTGTGGCCCTTGGTTGAAAAATAACC
15 CGACCTTGTACCTAATCCCCGTTTCCGTGATTTTGATTTTCGGTGGGT

[0318] The breadth and scope of the present disclosure should not be limited by any of the above-described exemplary embodiments, but should be defined only in accordance with the following claims and their equivalents.

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CLAIMS

What is claimed is:

1. An isolated double stranded RNA (dsRNA) molecule comprising a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of a target gene sequence,
wherein the target gene is a MIGGS-IRTG involved in gut microbe clearance and/or containment induced by microbes ingested during feeding and/or active feeding ,
wherein the target gene sequence includes at least one of the protein coding region, the 5' UTR region, the 3' UTR region, and any combination thereof, of a target gene, and
wherein the double stranded RNA molecule silences the target gene when ingested by an insect.
2. The isolated dsRNA molecule of claim 2, wherein the dsRNA molecule comprises two annealed complementary RNA strands.
3. The isolated dsRNA molecule of claim 3, wherein the dsRNA molecule comprises a single RNA strand comprising an inversely repeated sequence with a spacer in between and wherein the single RNA strand can anneal to itself to form a hairpin loop structure.
4. The isolated dsRNA molecule of any one of claims 1 to 3, comprising a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of the protein coding region of the target gene sequence.

5. The isolated dsRNA molecule of any one of claims 1 to 3, comprising a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of the 5' UTR region or the 3' UTR region of the target gene sequence.
6. The isolated dsRNA molecule of any one of claims 1 to 5, comprising a nucleic acid sequence complementary to a contiguous region comprising at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% of the length of the target gene sequence protein coding region, 5' UTR region, or 3' UTR region.
7. The isolated dsRNA molecule of any one of claims 1 to 6, comprising a nucleic acid sequence complementary to about 200 to 650 contiguous nucleotides of a target gene sequence.
8. The isolated dsRNA molecule of any one of claim 1 to 7, wherein the target gene is a type 1 MIGGS RNAi target or a type 2 MIGGS RNAi target.
9. The isolated dsRNA molecule of any one of claims 1 to 8, wherein the target gene is a pattern recognition receptor (PRR) class gene or an insect midgut structural component gene.
10. The isolated dsRNA molecule of any one of claims 1 to 9, wherein the target gene is expressed abundantly in a midgut specific manner during active feeding.
11. The isolated dsRNA molecule of any one of claims 1 to 10, wherein the target gene is selected from the group consisting of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine

proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-**Beta-1, 3-glycan-recognition protein 2 (MsβGRP2)**, *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsReIF), *M. sexta*-Cdc42 (MsCdc42), *M. sexta*-Dsor1 (MsDsor1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13 (MsAtg13), *M. sexta*-IAP1 (MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*-**Beta-1 tubulin (MsβTub)**, *M. sexta*-Beta fructofuranosidase 1 (MsSuc1), and orthologs thereof.

12. The isolated dsRNA molecule of any one of claims 1 to 11, wherein the target gene is selected from the group consisting of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-**Beta-1, 3-glycan-recognition protein 2 (MsβGRP2)**, *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsReIF), *M. sexta*-

Cdc42 (MsCdc42), *M. sexta*-Dsor1 (MsDsor1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13 (MsAtg13), *M. sexta*-IAP1 (MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*-**Beta-1 tubulin (Ms β Tub) and *M. sexta*- Beta fructofuranosidase 1 (MsSuc1).**

13. An isolated double stranded RNA (dsRNA) molecule comprising a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of a target gene sequence, wherein the target gene comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110, wherein the target gene sequence includes at least one of the protein coding region, the 5' UTR region, the 3' UTR region, and any combination thereof, of a target gene, and wherein the double stranded RNA molecule silences the target gene when ingested by an insect.
14. The isolated dsRNA molecule of claim 13, wherein the target gene sequence selected from the group consisting of:
- i) SEQ ID NOs: 1-9, 11, 14, 31, 39, 43, 44, and 71-75;
 - ii) SEQ ID NOs: 3, 4, and 43, wherein the dsRNA molecule causes impeded growth, developmental progression, and/or mortality and the like of TH, DMB, and FAW in an orthologous manner;
 - iii) SEQ ID NOs: 76, 77, 80, 81, 85, 87, and 88, wherein the dsRNA molecule causes impeded growth, developmental progression, and/or mortality and the like of DBM, optionally wherein the DBM is a Bt resistant strain;

- iv) SEQ ID NOs: 89, 92, 96, 101, 103, and 105, wherein the dsRNA molecule causes impeded growth, developmental progression, and/or mortality and the like of FAW; and
 - v) SEQ ID NOs: 107-110, wherein the dsRNA molecule caused impeded growth, developmental progression, and/or mortality and the like of RFB.
15. The isolated dsRNA molecule of claim 13 or 14, wherein the dsRNA molecule comprises two annealed complementary RNA stands.
16. The isolated dsRNA molecule of claim 15, wherein the dsRNA molecule comprises a single RNA strand comprising an inversely repeated sequence with a spacer in between and where the single RNA strand can anneal to itself to form a hairpin loop structure.
17. The isolated dsRNA molecule of any one of claims 13 to 16, comprising a nucleic acid sequence complementary to about 200 to 1000 contiguous nucleotides of the protein coding region of the target gene sequence.
18. The isolated dsRNA molecule of any one of claims 13 to 17, comprising a nucleic acid sequence complementary to a contiguous region comprising at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% of the length of a sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110.
19. The isolated dsRNA molecule of claim 18, comprising a nucleic acid sequence complementary to a contiguous region comprising at least about 50%, 60%, 70%, 80%,

90%, 95%, 98%, 99%, or 100% of the length of the target gene sequence protein coding region, 5' UTR region, or 3' UTR region.

20. The isolated dsRNA molecule of claim 1, comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 111-119, 120-126, 127-135, and 136-139, or a fragment of at least about 200 nucleotides thereof; optionally, wherein:

- i) the isolated dsRNA molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 110-119, or the fragment thereof, causes impeded growth, developmental progression, and/or mortality and the like of TH;
- ii) the isolated dsRNA molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 120-126, or the fragment thereof, causes impeded growth, developmental progression, and/or mortality and the like of DBM;
- iii) the isolated dsRNA molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 127-135, or the fragment thereof, causes impeded growth, developmental progression, and/or mortality and the like of FAW; or
- iv) the isolated dsRNA molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 136-139, or the fragment thereof, causes impeded growth, developmental progression, and/or mortality and the like of RFB.

21. The isolated dsRNA molecule of any one of claims 1 to 20, wherein the dsRNA molecule can form siRNA.

22. An isolated siRNA molecule derived from the processing of the dsRNA molecule of any one of claims 1 to 21.

23. An insecticidal composition comprising the isolated dsRNA molecule of any one of claims 1 to 21 or the siRNA molecule of claim 21 and a synthetic carrier or microbial conduit that can be a microorganism that has a natural capacity or is engineered to produce and/or deliver dsRNA to increase its bioavailability and/or biostability for causing RNA interference including but not restricted to plant growth promoting organisms, normal commensal and/or symbiotic microorganisms associated with the target insect pest or parasites and/or natural enemies of the target pest or pest target host or host cultivation range etc. from an insect or parasite and/or natural enemies of the target pest engineered or identified from natural populations containing microbial conduit to produce and/or deliver dsRNA and/or drive the transmission of such microbial conduits into natural populations of insect pests as a control option.
24. The insecticidal composition of claim 23, wherein the dsRNA molecule is conjugated with the synthetic carrier.
25. A recombinant DNA construct encoding a dsRNA molecule of any one of claims 1 to 21.
26. A recombinant DNA construct comprising a gene silencing sequence comprising about 200 to 1000 contiguous nucleotides of a target gene sequence,
wherein the target gene is a MIGGS-IRTG involved in gut microbe clearance and/or containment induced by microbes ingested during feeding and/or active feeding ,
and

wherein the target gene sequence includes at least one of the protein coding region, the 5' UTR region, the 3' UTR region, and any combination thereof, of a target gene.

27. The recombinant DNA construct of claim 26, wherein the gene silencing sequence comprises about 200 to 1000 contiguous nucleotides of the protein coding region of the target gene sequence.
28. The recombinant DNA construct of claim 25, wherein the gene silencing sequence comprises about 200 to 1000 contiguous nucleotides of the 5' UTR region or the 3' UTR region of the target gene sequence.
29. The recombinant DNA construct of any one of claims 25 to 28, wherein the gene silencing sequence comprises at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% contiguously of the length of target gene sequence protein coding region, 5' UTR region, or 3' UTR region.
30. The recombinant DNA construct of any one of claims 25 to 29, wherein the gene silencing sequence comprises about 200 to 650 contiguous nucleotides of the target gene sequence.
31. The recombinant DNA construct of any one of claims 25 to 30, wherein the target gene is a type I MIGGS RNAi target or a type 2 MIGGS RNAi target.

32. The recombinant DNA construct of any one of claims 25 to 31, wherein the target gene is a pattern recognition receptor (PRR) class gene or an insect midgut structural component gene.
33. The recombinant DNA construct of any one of claims 25 to 32, wherein the target gene is expressed abundantly in a midgut specific manner during active feeding.
34. The recombinant DNA construct of any one of claims 25 to 33, wherein the target gene is selected from the group consisting of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-**Beta-1, 3-glycan-recognition protein 2 (MsβGRP2)**, *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsRelF), *M. sexta*-Cdc42 (MsCdc42), *M. sexta*-Dsor1 (MsDsor1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13 (MsAtg13), *M. sexta*-IAP1 (MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*-**Beta-1 tubulin (MsβTub)**, *M. sexta*-Beta fructofuranosidase 1 (MsSuc1), and orthologs thereof.

35. The recombinant DNA construct of any one of claims 25 to 33, wherein the target gene is selected from the group consisting of *M. sexta*-Hemolin (MsHEM), *M. sexta*-Serine proteinase homolog 3 (MsSPH-3), *M. sexta*-Peptidoglycan recognition protein 2 (MsPGRP2), *M. sexta*-**Beta-1, 3-glycan-recognition protein 2 (Ms β GRP2)**, *M. sexta*-Relish family protein 2A (MsREL2A), *M. sexta*-Dorsal (MsDor), *M. sexta*-Spätzle (MsSPZ1A), *M. sexta*-Toll receptor (MsTOLL), *M. sexta*-Scolexin A (MsSCA1), *M. sexta*-Hemolymph proteinase 18 (MsHP18), *M. sexta*-Transferrin (MsTRN), *M. sexta*-Arylphorin beta subunit (MsARP), *M. sexta*-Chymotrypsinogen-like protein 1 (MsCTL1), *M. sexta*-Valine Rich Midgut Protein (MsVMP1), *M. sexta*-Imd (MsImd), *M. sexta*-FADD (MsFADD), *M. sexta*-Dredd (MsDRD), *M. sexta*-Relish F (MsRelF), *M. sexta*-Cdc42 (MsCdc42), *M. sexta*-Dsor1 (MsDsor1), *M. sexta*-Fos (MsFos), *M. sexta*-Jra (MsJra), *M. sexta*-Caudal (MsCAD1), *M. sexta*-Atg8 (MsAtg8), *M. sexta*-Atg13 (MsAtg13), *M. sexta*-IAP1 (MsIAP1), *M. sexta*-Chitin synthase 2 (MsChs2), *M. sexta*-**Beta-1 tubulin (Ms β Tub)** and *M. sexta*-Beta fructofuranosidase 1 (MsSuc1).
36. A recombinant DNA construct comprising a gene silencing sequence comprising about 200 to 1000 contiguous nucleotides of a target gene sequence,
- wherein the target gene comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110,
- wherein the target gene sequence includes at least one of the protein coding region, the 5' UTR region, the 3' UTR region, and any combination thereof, of a target gene.

37. The recombinant DNA construct of claim 36, wherein the target gene sequence is selected

from the group consisting of:

- i) SEQ ID NOs: 1-9, 11, 14, 31, 39, 43, 44, and 71-75;
- ii) SEQ ID NOs: 3, 4, and 43;
- iii) SEQ ID NOs: 76, 77, 80, 81, 85, 87, and 88;
- iv) SEQ ID NOs: 89, 92, 96, 101, 103, and 105; and
- v) SEQ ID NOs: 107-109, and 110.

38. The recombinant DNA construct of claim 36 or 37, wherein the gene silencing sequence

comprises about 200 to 1000 contiguous nucleotides of a sequence selected from the

group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-110.

39. The recombinant DNA construct of claim 36 or 37, wherein the gene silencing sequence

comprises at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or 100% contiguously of

a sequence selected from the group consisting of SEQ ID Nos: 1-14, 16-29, 31-70, 71-75,

76-88, 89-105, and 106-110.

40. The recombinant DNA construct of any one of claims 36 to 39, wherein the gene silencing

sequence comprises about 200 to 650 contiguous nucleotides of a sequence selected from

the group consisting of SEQ ID NOs: 1-14, 16-29, 31-70, 71-75, 76-88, 89-105, and 106-

110.

41. The recombinant DNA construct of any one of claims 25 to 40, wherein the gene silencing sequence is operably linked to one or more promoters for the expression of a dsRNA molecule that silences the target gene when ingested by an insect.
42. The recombinant DNA construct of any one of claims 25 to 41 wherein the construct is an expression vector.
43. The recombinant DNA construct of claim 42, wherein the expression vector can target single or multiple insect RNAi target genes or chimeric RNAi target genes.
44. A host cell comprising the dsRNA molecule of any one of claim 1 to 21, the siRNA molecule of claim 20, a polynucleotide encoding the dsRNA molecule of any one of claim 1 to 21, and/or the construct or a dsRNA encoding segment thereof of any one of claims 25 to 43.
45. The host cell of claim 44, wherein the cell is a bacterial or plant cell or organelle; optionally wherein the organelle is a plastid.
46. The host cell of claim of 44 or 45, wherein the cell is a transgenic and/or transplastomic plant cell.
47. The host cell of any one of claims 44 to 46, wherein said cell expresses the dsRNA of any one of claims 1 to 21 and/or produces the siRNA of claim 22.

48. A transgenic and/or transplastomic plant comprising the dsRNA molecule of any one of claim 1 to 21, the siRNA molecule of claim 22, a polynucleotide encoding the dsRNA of any one of claim 1 to 21, and/or the construct or a dsRNA encoding segment thereof of any one of claims 25 to 43.
49. The transgenic and/or transplastomic plant of claim 48, wherein at least one cell of the plant expresses the dsRNA molecule of any one of claim 1 to 21 and/or produces the siRNA molecule of claim 22.
50. A seed, part, tissue, cell, or organelle of the plant of claim 48 or 49, wherein said seed, part, tissue, cell, or organelle comprises a dsRNA molecule according to any one of claims 1 to 21 and/or the siRNA molecule of claim 22; optionally wherein the organelle is a plastid.
51. A method of silencing: (i) an insect immune response gene and/or (ii) an insect gene encoding for structural components of the insect midgut,
the method comprising providing for ingesting the isolated dsRNA molecule of any one of claims 1 to 21, the siRNA molecule of claim 22, the insecticidal composition of claim 23 or 24, the host cell of any one of claims 44 to 47, the transgenic and/or transplastomic plant of claim 48 or 49, and/or the seed, part, tissue, cell, or organelle of claim 50, to an insect.
52. A method of protecting a plant from an insect pest of the plant, the method comprising topically applying to the plant the isolated dsRNA molecule of any one of claims 1 to 21,

the siRNA molecule of claim 2, and/or the insecticidal composition of claim 23 or 24, and providing the plant in the diet of the insect pest.

53. The method of claim 52, wherein said dsRNA is topically applied by expressing the dsRNA in a microbe and topically applying the microbe onto the plant.
54. A method of producing a plant resistance to a pest insect of said plant, the method comprising transforming the plant with a polynucleotide encoding the dsRNA molecule of any one of claims 1 to 21 and/or the construct or a dsRNA encoding segment thereof of any one of claims 25 to 43, wherein the plant expresses the dsRNA molecule of any one of claim 1 to 21 and/or produces the siRNA of claim 21.
55. A method of improving crop yield, the method comprising growing a population of crop plants transformed with a polynucleotide encoding the dsRNA molecule of any one of claims 1 to 21 and/or the construct or a dsRNA encoding segment thereof of any one of claims 25 to 43 wherein the plant expresses the dsRNA molecule of any one of claim 1 to 21 and/or produces the siRNA molecule of claim 22, and wherein the population of transformed plants produces higher yields in the presence of pest insect infestation than a control population of untransformed plants.
56. A method for producing a plant resistant against a pest insect of said plant, the method comprising:

a) transforming a plant cell and/or organelle with a polynucleotide encoding the dsRNA molecule of any one of claim 1 to 21 and/or the construct or a dsRNA encoding segment thereof of any one of claims 25 to 43;

b) regenerating a plant from the transformed plant cell and/or organelle; and

c) growing the transformed plant under conditions suitable for the expression of said double stranded RNA molecule,

wherein said transformed plant of (c) is resistant to the plant pest insect compared to an untransformed plant.

57. The method of any one of claims 51 to 56, wherein the dsRNA is ingested by the actively feeding stage of the insect.

58. The method of any one of claims 51 to 57, wherein ingestion of the dsRNA induces a melanotic response in the insect larvae.

59. The method of any one of claims 51 to 58, wherein the ingestion of the dsRNA results in perturbation of gut microbial homeostasis.

60. The method of any one of claims 51 to 59, wherein the ingestion of the dsRNA results in defective clearance of opportunistic microbes.

61. The method of any one of claims 51 to 60, wherein the ingestion of the dsRNA results in defective containment of gut microbes.

62. The isolated dsRNA molecule of any one of claims 1 to 21, the siRNA molecule of claim 22, the insecticidal composition of claim 23 or 24, the construct or a dsRNA encoding segment thereof of any one of claims 25 to 43, the host cell of any one of claims 44 to 47, the transgenic and/or transplastomic plant of claim 48 or 49, the seed, part, tissue, cell, or organelle of claim 50, or the method of any one of claims 51 to 60, wherein the silencing of the target gene results in reduced appetite and/or developmental defects resulting in incomplete development and/or mortality and/or decrease the reproductive success of the insect.
63. The isolated dsRNA molecule, the siRNA, the insecticidal composition, the construct or a dsRNA encoding segment thereof, the host cell, the transgenic and/or transplastomic plant, the seed, part, tissue, cell, organelle, or the method of any of the above claims, wherein the reduced appetite and/or developmental defects and/or mortality and/or reduced reproductive fitness of the insect is observed after sustained feeding for at least 72 hours.
64. The isolated dsRNA molecule, the siRNA, the insecticidal composition, the construct or a dsRNA encoding segment thereof, the host cell, the transgenic and/or transplastomic plant, the seed, part, tissue, cell, or organelle, or the method of any of the above claims, wherein the insect is of the order Lepidoptera, Coleoptera, Hemiptera, Blattodea, or Diptera.
65. The isolated dsRNA molecule, the siRNA, the insecticidal composition, the construct or a dsRNA encoding segment thereof, the host cell, the transgenic and/or transplastomic

plant, the seed, part, tissue, cell, or organelle, or the method of any of the above claims, wherein the insect is *Manduca sexta* (*M. sexta*) (tobacco hornworm), *Spodoptera frugiperda* (fall armyworm), *Ostrinia nubilalis* (European corn borer), *Plutella xylostella* (Diamondback moth), *Leptinotarsa decemlineata* Say (Colorado potato beetle), *Diabrotica* spp. (Corn rootworm complex), *Tribolium castaneum* (Red flour beetle), *Popillia japonica* (Japanese beetle), *Agilus planipennis* (Emerald ash borer), *Diaphorina citri* (Asian citrus psyllid), *Cimex lectularius* (Bed bug), a cockroach or termite, or insect pests such as mosquitoes and flies.

66. The isolated dsRNA molecule, the siRNA, the insecticidal composition, the construct or a dsRNA encoding segment thereof, the host cell, the transgenic and/or transplastomic plant, the seed, part, tissue, cell, or organelle, or the method of any of the above claims, wherein the plant host is selected from the group consisting of *Zea mays* L (corn), *Sorghum bicolor* (sorghum), *Setaria italica* (fox tail millet), *Pennisetum glaucum* (Pearl millet), *Solanum tuberosum* (potato), *Oryza sativa* (rice), *Lycopersicon esculentum* (tomato), *Solanum melongena* (eggplant), cultivars of the *Brassica oleracea* family, *Citrus sinensis* (Orange), trees of the *Oleaceae* family, and crops of *Rosaceae*.