CLAIMS

1. A host cell comprising:

(a) a double stranded RNA (dsRNA) molecule comprising a nucleic acid sequence complementary to about 21 to 2000 contiguous nucleotides of a target gene sequence, wherein the target gene sequence includes at least one of the protein coding region, the 5' untranslated region (UTR), the 3' UTR, and any combination thereof, of a target gene and wherein the double stranded RNA molecule silences the target gene when ingested by an insect, and wherein the target gene is a microbe-induced gut specific gene-insect RNA target gene (MIGGS-IRTG) involved in gut microbe recognition, clearance and/or containment induced by microbes ingested during feeding and/or active feeding, and 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;

(b) an siRNA molecule derived from the processing of the dsRNA molecule; and/or

(c) a polynucleotide, construct or dsRNA encoding segment encoding the dsRNA molecule;

wherein the cell is a bacterial cell, a yeast cell, a fungal cell, or a plant cell.

2. The host cell of claim 1, wherein the cell expresses the dsRNA or produces the siRNA.

3. A transgenic and/or transplastomic plant comprising (a) a double stranded RNA (dsRNA) molecule comprising a nucleic acid sequence complementary to about 21 to 2000 contiguous nucleotides of a target gene sequence, wherein the target gene sequence includes at least one of the protein coding region, the 5' untranslated region (UTR), the 3' UTR, and any combination thereof, of a target gene and wherein the double stranded RNA molecule silences the target gene when ingested by an insect, and wherein the target gene is a microbe-induced gut specific gene-insect RNA target gene (MIGGS-IRTG) involved in gut microbe recognition, clearance and/or containment

induced by microbes ingested during feeding and/or active feeding, and 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; (b) an siRNA molecule derived from the processing of the dsRNA molecule; and/or (c) polynucleotide, a construct or a dsRNA encoding segment encoding the dsRNA molecule, or a seed, part, tissue, cell, or organelle thereof wherein said seed, part, tissue, cell or organelle comprises the dsRNA molecule and/or the siRNA molecule,

optionally wherein at least one cell of the plant expresses the dsRNA molecule and/or produces the siRNA.

4. A microbial conduit comprising a microorganism that has a natural capacity or is engineered to produce and/or deliver a dsRNA to increase its bioavailability and/or biostability for causing RNA interference, wherein the dsRNA comprises a nucleic acid sequence complementary to about 21 to 2000 contiguous nucleotides of a target gene sequence, wherein the target gene sequence includes at least one of the protein coding region, the 5' untranslated region (UTR), the 3' UTR, and any combination thereof, of a target gene and wherein the double stranded RNA molecule silences the target gene when ingested by an insect, and wherein: (i) the target gene is a microbe-induced gut specific gene-insect RNA target gene (MIGGS-IRTG) involved in gut microbe recognition, clearance and/or containment induced by microbes ingested during feeding and/or active feeding, and (ii) 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.

5. The microbial conduit of claim 4 comprising 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.

6. An ingestible insecticidal composition comprising:

(a) a double stranded RNA (dsRNA) molecule comprising a nucleic acid sequence complementary to about 21 to 2000 contiguous nucleotides of a target gene sequence, wherein the target gene sequence includes at least one of the protein coding region, the 5' untranslated region (UTR), the 3' UTR, and any combination thereof, of a target gene and wherein the double stranded RNA molecule silences the target gene when ingested by an insect, and wherein

(i) the target gene is a microbe-induced gut specific gene-insect RNA target gene (MIGGS-IRTG) involved in gut microbe recognition, clearance and/or containment induced by microbes ingested during feeding and/or active feeding, and

(ii) 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; and

(b) a synthetic carrier.

7. The ingestible insecticidal composition of claim 6, wherein the dsRNA molecule is bound to the synthetic carrier.

8. The ingestible insecticidal composition of claim 6 or 7, wherein the synthetic carrier comprises chitosan, liposomes, carbon quantum dots, biodegradable particles of plant, or soil.

9. The host cell of claim 1 or 2, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof of claim 3, the microbial conduit of claim 4 or 5, or the ingestible insecticidal composition of any one of claims 6 to 8, wherein the target gene is: (a) a type 1 MIGGS RNAi target or a type 2 MIGGS RNAi target; or (b) a pattern recognition receptor (PRR) class gene or an insect midgut structural component gene; and optionally wherein the target gene is expressed abundantly in a midgut specific manner during active feeding.

10. The host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof, the microbial conduit, or the ingestible insecticidal composition of claim 9, wherein the target gene is selected from the group consisting of, *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.

11. The host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof, the microbial conduit, or the ingestible insecticidal composition of any one of claims 9 or 10, 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, wherein the dsRNA molecule causes impeded growth, developmental progression, and/or mortality and the like of tobacco hornworm (TH), Diamondback moth (DMB), and fall armyworm (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 causes impeded growth, developmental progression, and/or mortality and the like of Red Flour Beetle (RFB).

12. The host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof, the microbial conduit, or the ingestible insecticidal composition of claims 9 to 11, comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 110-139, or a fragment of at least about 21 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.

13. The host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof, the microbial conduit, or the ingestible insecticidal composition of any one of claims 9 to 12, 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; or wherein the dsRNA molecule comprises two separate complementary RNA stands annealed together.

14. The host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof, the microbial conduit, or the ingestible insecticidal composition of any one of claims 9 to 13, wherein the construct encoding the dsRNA comprises 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, optionally wherein the recombinant DNA construct further comprises an additional transcription regulatory region or an additional transcriptional regulatory element.

15. The host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or

organelle thereof, the microbial conduit, or the ingestible insecticidal composition of claim 14, wherein the construct encoding the dsRNA is an expression vector and the expression vector can target single or multiple insect RNAi target genes or chimeric RNAi target genes.

16. A method of producing the transgenic and/or transplastomic plant of any one of claims 3 and 9 to 15, the method comprising transforming the plant with a polynucleotide encoding the dsRNA molecule, and/or the construct or a dsRNA encoding segment, wherein the plant expresses the dsRNA molecule and/or produces the siRNA, and wherein the plant has resistance to an insect pest of the plant.

17. A method for producing the transgenic or transplastomic plant of any one of claims 3 and 9 to 15, the method comprising:

a) transforming a plant cell and/or organelle with a polynucleotide encoding the dsRNA molecule and/or a construct or a dsRNA encoding segment thereof;

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 a plant pest insect compared to an untransformed plant.

18. A method of improving crop yield, the method comprising growing a population of transgenic or transplastomic plants of any one of claims 3 and 9 to 15, wherein the population of transformed plants produces higher yields in the presence of pest insect infestation than a control population of untransformed plants

19. 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 host cell of any one of claims 1 to 2 and 9 to 15, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof of any one of claims 3 and 9 to 15, the microbial conduit of claim 4 or 5, or the ingestible insecticidal composition of any one of claims 6 to 15 to an insect, wherein the dsRNA is ingested by the actively feeding stage of the insect and (a) ingestion of the dsRNA induces a melanotic response; and/or (b) ingestion of the dsRNA results in perturbation of gut microbial homeostasis; and/or (c) ingestion of the dsRNA results in defective clearance of opportunistic microbes; and/or (d) ingestion of the dsRNA results in defective containment of gut microbes.

20. A method of protecting a plant from an insect pest of the plant, the method comprising topically applying to the plant the host cell of any one of claims 1 to 2 and 9 to 15, the microbial conduit of any one of claims 4, 5 and 9 to 15, or the insecticidal composition of any one of claims 6 to 15, and providing the plant in the diet of the insect pest, optionally wherein the dsRNA is ingested by the actively feeding stage of the insect and (a) ingestion of the dsRNA induces a melanotic response; and/or (b) ingestion of the dsRNA results in perturbation of gut microbial homeostasis; and/or (c) ingestion of the dsRNA results in defective clearance of opportunistic microbes; and/or (d) ingestion of the dsRNA results in defective containment of gut microbes.

21. The host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof, the microbial conduit, the ingestible insecticidal composition, or the method of any of the above claims, wherein the silencing of the target gene results in reduced appetite and/or developmental defects resulting in incomplete development and/or mortality and/or decreased reproductive success of the insect, optionally 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 24 hours.

22. The insecticidal composition, the host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof, or the method of any of the above claims, wherein the insect is of the order *Lepidoptera*, *Coleoptera*, *Hemiptera*, *Blattodea*, or *Diptera*.

23. The host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof, the microbial conduit, the ingestible insecticidal composition, 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), *Agrilus planipennis* (Emerald ash borer), *Diaphorinacitri* (Asian citrus psyllid), *Cimex lectularius* (Bed bug), a cockroach or termite, or insect pests such as mosquitoes and flies.

24. The host cell, the transgenic and/or transplastomic plant or seed, part, tissue, cell, or organelle thereof, the microbial conduit, the ingestible insecticidal composition, or the method of any of the above claims, wherein the plant 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*.