CLAIMS

1. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a pharmaceutically acceptable salt thereof.

2. The TVP of claim 1, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110, or a pharmaceutically acceptable salt thereof.

3. The TVP of claim 1, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51, or a pharmaceutically acceptable salt thereof.

4. The TVP of claim 1, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

5. The TVP of claim 1, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

6. The TVP of claim 1, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable linker or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

7. The TVP of claim 6, wherein the cleavable linker or non-cleavable linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

8. The TVP of any one of claims 1-7, wherein if Z_1 is T or S, then the TVP is glycosylated.

9. A composition consisting of a TVP, and one or more excipients; wherein the TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a pharmaceutically acceptable salt thereof; and at least one excipient.

10. The composition of claim 9, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

11. The composition of claim 9, wherein the TVP comprises an amino sequence as set forth in 9 SEQ ID NO: 51.

12. The composition of claim 9, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

13. The composition of claim 9, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

14. The composition of claim 9, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable linker or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

15. The TVP of claim 14, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

16. The composition of any one of claims 9-15, wherein if Z_1 is T or S, then the TVP is glycosylated.

17. The composition of any one of claims 9-16, wherein the at least one excipient is selected from the group consisting of: trehalose; maltodextrin; potassium phosphate dibasic anhydrous (K_2HPO_4); potassium phosphate monobasic (KH_2PO_4); BIT; and fermentation solids.

18. A composition consisting of a TVP, and a plurality of excipients; wherein the TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a pharmaceutically acceptable salt thereof; wherein the composition consists of an amount of TVP that is 8.5% w/w of the total weight of the composition; and wherein the plurality of excipients consists of the following: an amount of trehalose that is 25% w/w; an amount of BIT that is 0.05% w/w; an amount of maltodextrin that is 36.3% w/w; an amount of potassium phosphate dibasic anhydrous (K_2HPO_4) that is 2.6% w/w; an amount of potassium phosphate monobasic (KH_2PO_4) that is 0.4% w/w; and an amount of fermentation solids that is 26.85% w/w, of the total weight of the composition.

19. The composition of claim 18, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

20. The composition of claim 18, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51.

21. The composition of claim 18, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

22. The composition of claim 18, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

23. The composition of claim 18, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

24. The composition of claim 23, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

25. The composition of any one of claims 18-24, wherein if Z_1 is T or S, then the TVP is glycosylated.

26. A polynucleotide encoding a TVP, said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the TVP comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or

A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent; or a complementary nucleotide sequence thereof.

27. The polynucleotide of claim 26, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

28. The polynucleotide of claim 26, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51.

29. The polynucleotide of claim 26, wherein the polynucleotide sequence has a sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

30. The polynucleotide of any one of claims 26-29, wherein if Z_1 is T or S, then the TVP is glycosylated.

31. A method of producing a TVP, the method comprising:

(a) preparing a vector comprising a first expression cassette comprising a polynucleotide operable to encode a TVP, or complementary nucleotide sequence thereof, said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent;

(b) introducing the vector into a host cell; and

(c) growing the host cell in a growth medium under conditions operable to enable expression of the TVP and secretion into the growth medium.

32. The method of claim 31, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

33. The method of claim 31, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51.

34. The method of claim 31, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

35. The method of claim 31, wherein the vector is a plasmid comprising an alpha-MF signal.

36. The method of claim 35, wherein the alpha-MF signal is operable to express an alpha-MF signal peptide.

37. The method of claim 36, wherein the vector is transformed into a host cell.

38. The method of claim 37, wherein the host cell is a eukaryotic cell or a prokaryotic cell.

39. The method of claim 38, wherein the eukaryotic cell is a yeast cell, selected from any species belonging to the genera: *Saccharomyces*, *Pichia*, *Kluyveromyces*, *Hansenula*, *Yarrowia*, or *Schizosaccharomyces*.

40. The method of claim 39, wherein the yeast cell is *Kluyveromyces lactis* or *Kluyveromyces marxianus*.

41. The method of any one of claims 31-40 wherein if Z_1 is T or S, then the TVP is glycosylated.

42. A method of using the TVP of claim 1, or the composition of claim 9 to control insects, the method comprising, providing the TVP of claim 1 or the composition of claim 9 to the locus of an insect.

43. A method of protecting a plant from insects comprising, providing a plant which expresses a TVP, or polynucleotide encoding the same.

44. The method of claim 43, wherein said TVP comprises an amino acid sequence that is at least 90% identical to the amino acid sequence according to Formula (I): E-P-D-E-I-C-R-X_1-X_2-M-X_3-N-K-E-F-T-Y-X_4-S-N-V-C-N-N-C-G-D-Q-V-A-A-C-E-A-E-C-F-X_5-N-D-V-Y-Z_1-A-C-H-E-A-Q-X_6-X_7, wherein the polypeptide comprises at least one amino acid substitution relative to the wild-type sequence of U1-agatoxin-Ta1b as set forth in SEQ ID NO:1, and wherein X_1 is A, S, or N; X_2 is R, Q, N, A, G, N, L, D, V, M, I, C, E, T, or S; X_3 is T or P; X_4 is K or A; X_5 is R or A; Z_1 is T, S, A, F, P, Y, K, W, H, A, G, N, L, V, M, I, Q, C, E, or R; X_6 is K or absent; and X_7 is G or absent.

45. The method of claim 44, wherein the TVP comprises an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

46. The method of claim 44, wherein the TVP comprises an amino sequence as set forth in SEQ ID NO: 51.

47. The method of claim 44, wherein the TVP is encoded by a polynucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

48. The method of claim 44, wherein the TVP further comprises a homopolymer or heteropolymer of two or more TVPs, wherein the amino acid sequence of each TVP is the same or different.

49. The method of claim 44, wherein the TVP is a fused protein comprising two or more TVPs separated by a cleavable or non-cleavable linker, and wherein the amino acid sequence of each TVP may be the same or different.

50. The method of claim 49, wherein the linker has an amino acid sequence as set forth in any one of SEQ ID NOs: 61-70.

51. A method of combating, controlling, or inhibiting a pest comprising, applying a pesticidally effective amount of the TVP of claim 1, or the composition of claim 9, to the locus of the pest, or to a plant or animal susceptible to an attack by the pest.

52. The method of any one of claims 42-51, wherein the insect or pest is selected from the group consisting of: *Eumorpha achemon*; *Colias eurytheme*; *Caudra cautella*; *Amorbia humerosana*; *Pseudaletia unipuncta*; *Platyptilia carduidactyla*; *Datana major*; *Thyridopteryx ephemeraeformis*; *Hypercompe scribonia*; *Erionota thrax*; *Acleris gloverana*; *Phryganidia californica*; *Paleacrita merriccata*; *Grapholita packardi*; *Nymphula stagnata*; *Xylomyges curialis*; *Cydia pomonella*; *Acrobasis vaccinii*; *Evergestis rimosalis*; *Noctuid* species; *Agrotis ipsilon*; *Orgyia pseudotsugata*; *Erinnyis ello*; *Ennomos subsignaria*; *Lobesia botrana*; *Thymelicus lineola*; *Melissopus latiferreanus*; *Archips rosanus*; *Archips argyrospilia*; *Paralobesia viteana*; *Platynota stultana*; *Harrisina americana*; *Plathypena scabra*; *Dryocampa rubicunda*; *Batrachedra comosae*; *Lymantria dispar*; *Lambdina fiscellaria*; *Manduca quinquemaculata*; *Manduca sexta*; *Pieris rapae*; *Automeris io*; *Choristoneura pinus*; *Epiphyas postvittana*; *Diaphania hyalinata*; *Homadaula anisocentra*; *Choristoneura rosaceana*; *Syntomeida epilais*; *Playnota stultana*; *Sabulodes aegrotata*; *Papilio cresphontes*; *Argyrotaenia citrana*; *Grapholita molesta*; *Anarsia lineatella*; *Neophasia menapia*; *Argyrotaenia velutinana*; *Schizura concinna*; *Sibine stimulea*; *Heterocampa guttivitta*; *Estigmene acrea*; *Crambus* sp.; *Ennomos subsignaria*; *Alsophila pometaria*; *Choristoneura fumiferana*; *Lasiocampidae* sp.; *Thecla basilides*; *Ephestia elutella*; *Platynota idaeusalis*; *Anarsia lineatella*; *Peridroma saucia*; *Platynota flavedana*; *Anticarsia gemmatalis*; *Datana integerrima*; *Hyphantria cunea*; *Orgyia vetusta*; Southern *Diatraea crambidoides*; *Cylas formicarius*; *Anthonomus eugenii*; *Diaprepes abbreviatus*; *Otiorhynchus ovatus*; *Curculio caryae*; *Curculio occidentis*; *Lissorhoptrus*

oryzophilus; *Hypera postica*; *Hypera zoilus*; *Euwallacea fornicatus*; *Euetheola humilis*; *Hypothenemus hampei*; *Listronotus maculicollis*; *Maladera castanea*; *Rhizotroqus majalis*; *Cotinis nitida*; *Popillia japonica*; *Phyllophaga* sp.; *Cyclocephala borealis*; *Anomala orientalis*; *Cyclocephala lurida*; *Sphenophorus parvulus*; *Sphenophorus apicalis*; *Sphenophorus cariosus*; *Sphenophorus inaequalis*; *Sphenophorus minimus*; *Aedes aegypti*; *Busseola fusca*; *Chilo suppressalis*; *Culex pipiens*; *Culex quinquefasciatus*; *Diabrotica virgifera*; *Diatraea saccharalis*; *Helicoverpa armigera*; *Helicoverpa zea*; *Heliothis virescens*; *Leptinotarsa decemlineata*; *Ostrinia furnacalis*; *Ostrinia nubilalis*; *Pectinophora gossypiella*; *Plodia interpunctella*; *Plutella xylostella*; *Pseudoplusia includens*; *Spodoptera exigua*; *Spodoptera frugiperda*; *Spodoptera littoralis*; *Trichoplusia ni*; and *Xanthogaleruca luteola*

53. A vector comprising a polynucleotide operable to encode a TVP having an amino acid sequence with 90% similarity to a sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

54. The vector of claim 53, wherein the polynucleotide has a nucleotide sequence as set forth in any one of SEQ ID NOs: 17-30, 54-58, or 117-150, or a complementary nucleotide sequence thereof.

55. A yeast strain comprising: a TVP comprising an amino sequence as set forth in any one of SEQ ID NOs: 2-15, 49-53, or 77-110.

56. The yeast strain of claim 55, wherein the yeast cell is selected from any species belonging to the genera *Saccharomyces*, *Pichia*, *Kluyveromyces*, *Hansenula*, *Yarrowia* or *Schizosaccharomyces*.

57. The yeast strain of claim 56, wherein the yeast cell is selected from the group consisting of *Kluyveromyces lactis*, *Kluyveromyces marxianus, Saccharomyces cerevisiae*, and *Pichia pastoris*.

58. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence set forth in any one of SEQ ID NOs: 2, 49, or 51; or a pharmaceutically acceptable salt thereof.

59. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence set forth in any one of SEQ ID NOs: 2, 49, or 51; or a pharmaceutically acceptable salt thereof.

60. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP consisting of an amino acid sequence set forth in any one of SEQ ID NOs: 2, 49, or 51; or a pharmaceutically acceptable salt thereof.

61. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence that is at least 90% identical to the amino acid sequence set forth in SEQ ID NO 51, or a pharmaceutically acceptable salt thereof.

62. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP comprising an amino acid sequence set forth in SEQ ID NO: 51, or a pharmaceutically acceptable salt thereof.

63. An insecticidal U_1-agatoxin-Ta1b variant polypeptide (TVP), said TVP consisting of an amino acid sequence set forth in SEQ ID NO: 51, or a pharmaceutically acceptable salt thereof.