CLAIMS:

1. An isolated artificially modified solanaceous Class II defensin polypeptide with a loop region (Loop 1B) between a first β-strand and an α-helix at its N-terminal end portion and having anti-fungal activity, and wherein said Loop 1B is replaced by an exogenous Loop 1B amino acid sequence, said polypeptide having at least 70% similarity to SEQ ID NO:52 after optimal alignment.

2. The isolated polypeptide of Claim 1 wherein said polypeptide comprises an amino acid sequence as set forth in SEQ ID NO:57 or an amino acid sequence having at least 70% similarity to SEQ ID NO:57 after optimal alignment.

3. The isolated polypeptide of Claim 1 or 2 wherein the polypeptide comprises a Loop1B selected from the list consisting of SEQ ID NOs:29 through 38.

4. The isolated polypeptide of Claim 1 or 2 wherein the polypeptide comprises a Loop 1B selected from the list consisting of SEQ ID NOs:67 through 79.

5. The isolated polypeptide of Claim 1 or 2 where the Loop 1B amino acid sequence comprises SEQ ID NO:29.

6. The isolated polypeptide of Claim 1 or 2 having at least 90% amino acid sequence similarity to a polypeptide selected from HXP4 (SEQ ID NO:39), HXP34 (SEQ ID NO:40) and HXP35 (SEQ ID NO:41).

7. The isolated polypeptide of Claim 6 wherein the polypeptide is selected from HXP4 (SEQ ID NO:39), HXP34 (SEQ ID NO:40) and HXP35 (SEQ ID NO:41).

8. The isolated polypeptide of Claim 1 or 2 wherein the fungal pathogen is selected from a plant fungal pathogen, a mammalian fungal pathogen and a rust.

9. The isolated polypeptide of Claim 8 wherein the fungus is selected from the list consisting of *Colletotrichum graminicola*, *Diplodia maydis*, *Fusarium graminearum*, *Fusarium verticilloides*, *Fusarium virgululiforme*, *Fusarium solani*, *Sclerotinia sclerotiorum*, *Fusarium oxysporum* and *Fusarium tucumaniae*.

10. The isolated polypeptide of Claim 8 wherein the fungus is selected from the list consisting of *Alternaeria* spp, *Aspergillus* spp, *Candida* spp, *Fusarium* spp, *Trychophyton* spp, *Cryptococcus* spp, *Microsporum* spp, *Penicillium* spp, *Trichosporon* spp, *Scedosporium* spp, *Paeciliomyces* spp, *Acremonium* spp and Dermatiaceous molds.

11. An isolated nucleic acid molecule encoding an isolated polypeptide of any one of Claims 1 to 10.

12. A genetically modified plant which produces the polypeptide of any one of Claims 1 to 10 or progeny of said plant which produces said polypeptide.

13. The genetically modified plant of Claim 12 selected from the list consisting of corn, soybean, cotton, sorghum, wheat, barley, maize, canola, abaca, alfalfa, almond, apple, asparagus, banana, bean-phaseolus, blackberry, broad bean, cashew, cassava, chick pea, citrus, coconut, coffee, fig, flax, grapes, groundnut, hemp, lavender, mushroom, olive, onion, pea, peanut, pear, pearl millet, potato, rapeseed, ryegrass, strawberry, sugar beet, sugarcane, sunflower, sweetpotato, taro, tea, tobacco, tomato, triticale, truffle and yam.

14. A method for generating a genetically modified plant or its progeny which exhibits anti-fungal activity as a result of the genetic modification, the method comprising creating a plant which comprises cells which express the nucleic acid encoding the polypeptide of any one of Claims 1 to 10, the level of expression in the plant or its progeny sufficient for the modified defensin to exhibit a protective effect against a plant fungal pathogen.

15. A method for generating a defensin comprising a backbone amino acid sequence from a Class II solanaceous defensin having a Loop 1B region between β-strand 1 and the α-helix on the N-terminal end portion of the Class II solanaceous defensin, the method comprising modifying the Loop 1B region by an amino acid substitution of the entire Loop 1B region for an exogenous Loop1B sequence to generate a defensin polypeptide with anti-fungal activity.

16. The method of Claim 15 wherein the Loop 1B on the Class II solanaceous defensin is modified to an amino acid sequence selected from SEQ ID NOs:29 through 38.

17. The method of Claim 15 wherein the Loop 1B on the Class II solanaceous defensin is modified to an amino acid sequence selected from SEQ ID NO:67 through 79.

18. An isolated defensin from *Nicotiana suaveolens* having an amino acid sequence as set forth in SEQ ID NO:49 [NsD1] or an amino acid sequence having at least 70% thereto after optimal alignment.

19. An isolated defensin from *Nicotiana suaveolens* having an amino acid sequence as set forth in SEQ ID NO:51 [NsD2] or an amino acid sequence having at least 70% thereto after optimal alignment.

20. An isolated nucleic acid molecule or comprising a sequence of nucleotides encoding the defensin of Claim 18 or 19.

21. The isolated nucleic acid molecule of Claim 18 comprising a nucleotide sequence selected from SEQ ID NO:48, SEQ ID NO:50, a nucleotide sequence capable of hybridizing to SEQ ID NO:48 or 50, under medium stringency conditions and a nucleotide sequence having at least 70% identity to SEQ ID NO:46 or 48 after optimal alignment.

CLAIMS:

1. An isolated artificially modified solanaceous Class II defensin polypeptide with a loop region (Loop 1B) between a first β-strand and an α-helix at its N-terminal end portion and having anti-fungal activity, and wherein said Loop 1B is replaced by an exogenous Loop 1B amino acid sequence, said polypeptide having at least 70% similarity to SEQ ID NO:52 after optimal alignment.

2. The isolated polypeptide of Claim 1 wherein said polypeptide comprises an amino acid sequence as set forth in SEQ ID NO:57 or an amino acid sequence having at least 70% similarity to SEQ ID NO:57 after optimal alignment.

3. The isolated polypeptide of Claim 1 or 2 wherein the polypeptide comprises a Loop1B selected from the list consisting of SEQ ID NOs:29 through 38.

4. The isolated polypeptide of Claim 1 or 2 wherein the polypeptide comprises a Loop 1B selected from the list consisting of SEQ ID NOs:67 through 79.

5. The isolated polypeptide of Claim 1 or 2 where the Loop 1B amino acid sequence comprises SEQ ID NO:29.

6. The isolated polypeptide of Claim 1 or 2 having at least 90% amino acid sequence similarity to a polypeptide selected from HXP4 (SEQ ID NO:39), HXP34 (SEQ ID NO:40) and HXP35 (SEQ ID NO:41).

7. The isolated polypeptide of Claim 6 wherein the polypeptide is selected from HXP4 (SEQ ID NO:39), HXP34 (SEQ ID NO:40) and HXP35 (SEQ ID NO:41).

8. The isolated polypeptide of Claim 1 or 2 wherein the fungal pathogen is selected from a plant fungal pathogen, a mammalian fungal pathogen and a rust.

9. The isolated polypeptide of Claim 8 wherein the fungus is selected from the list consisting of *Colletotrichum graminicola, Diplodia maydis, Fusarium graminearum, Fusarium verticilloides, Fusarium virgululiforme, Fusarium solani, Sclerotinia sclerotiorum, Fusarium oxysporum* and *Fusarium tucumaniae*.

10. The isolated polypeptide of Claim 8 wherein the fungus is selected from the list consisting of *Alternaeria* spp, *Aspergillus* spp, *Candida* spp, *Fusarium* spp, *Trychophyton* spp, *Cryptococcus* spp, *Microsporum* spp, *Penicillium* spp, *Trichosporon* spp, *Scedosporium* spp, *Paeciliomyces* spp, *Acremonium* spp and Dermatiaceous molds.

11. An isolated nucleic acid molecule encoding an isolated polypeptide of any one of Claims 1 to 10.

12. A genetically modified plant which produces the polypeptide of any one of Claims 1 to 10 or progeny of said plant which produces said polypeptide.

13. The genetically modified plant of Claim 12 selected from the list consisting of corn, soybean, cotton, sorghum, wheat, barley, maize, canola, abaca, alfalfa, almond, apple, asparagus, banana, bean-phaseolus, blackberry, broad bean, cashew, cassava, chick pea, citrus, coconut, coffee, fig, flax, grapes, groundnut, hemp, lavender, mushroom, olive, onion, pea, peanut, pear, pearl millet, potato, rapeseed, ryegrass, strawberry, sugar beet, sugarcane, sunflower, sweetpotato, taro, tea, tobacco, tomato, triticale, truffle and yam.

14. A method for generating a genetically modified plant or its progeny which exhibits anti-fungal activity as a result of the genetic modification, the method comprising creating a plant which comprises cells which express the nucleic acid encoding the polypeptide of any one of Claims 1 to 10, the level of expression in the plant or its progeny sufficient for the modified defensin to exhibit a protective effect against a plant fungal pathogen.

15. A method for generating a defensin comprising a backbone amino acid sequence from a Class II solanaceous defensin having a Loop 1B region between β-strand 1 and the α-helix on the N-terminal end portion of the Class II solanaceous defensin, the method comprising modifying the Loop 1B region by an amino acid substitution of the entire Loop 1B region for an exogenous Loop1B sequence to generate a defensin polypeptide with anti-fungal activity.

16. The method of Claim 15 wherein the Loop 1B on the Class II solanaceous defensin is modified to an amino acid sequence selected from SEQ ID NOs:29 through 38.

17. The method of Claim 15 wherein the Loop 1B on the Class II solanaceous defensin is modified to an amino acid sequence selected from SEQ ID NO:67 through 79.