Spider neurotoxins and method of producing the same

The present invention relates to a novel toxin, and a method of producing a toxin, particularly but not exclusively to an insect specific neurotoxin δ-Latroinsectotoxin (δ-LIT), and a method of producing same.

A family of high molecular weight neurotoxins has been found in the venom of the black widow spider (Latrodectus mactans Tredecimguttatus). Some of these toxins have been identified as being either vertebrate or invertebrate specific. α-Latrotoxin (α-LT) and α-Latroinsectotoxins (α-LIT) are two such neurotoxins that have been characterised as being vertebrate and invertebrate specific respectively. The primary structures of these proteins have been determined, but characterisation of the structural features of the cloned toxins has not been possible due to the inability to achieve functional expression of their genes.

It is an object of the present invention to provide a novel toxin and a method of producing a toxin usually naturally produced by post-translational modification of a precursor protein, using recombinant technology.

According to the present invention there is provided a polypeptide, such as a toxin, formed by expression of a truncated form of a gene sequence, or an

analogue thereof.

Preferably the polypeptide is a neurotoxin and preferably corresponds to a toxic derivative of a substantially non-toxic precursor polypeptide encoded by the gene sequence. The polypeptide may comprise an amino acid sequence that corresponds to a truncated form of the amino acid sequence of a substantially non-toxic precursor polypeptide. Preferably the amino acid sequence of the polypeptide corresponds to the amino acid sequence of the precursor polypeptide with truncation thereof principally at the carboxy (C) end, and desirably by about 150 to 200 amino acids. The polypeptide amino acid sequence may in addition correspond to the precursor polypeptide amino acid sequence truncated at the amino end (N) preferably by less than 50 amino acids, and desirably by 7 or 28 amino acids.

The amino acid sequence of the polypeptide may be homologous to the amino acid sequence of the insect specific neurotoxin δ-Latroinsectotoxin (δ-LIT) or an active derivative thereof, and preferably comprises an amino acid sequence as shown in SEQIDNO1 and SEQIDNO2 or an active derivative thereof. Preferably the toxin is expressed from a nucleotide construct or truncated form of the gene sequence comprising a sequence as shown in SEQIDNO1, or active variants thereof. Preferably the

toxin is expressed from a sequence substantially as provided in a microorganism deposited at The National Collections of Industrial and Marine Bacteria Limited, under Accession No. NCIMB 40632.

The invention also provides a protein for use as a toxin comprising an amino acid sequence substantially as shown in SEQIDNO1 and SEQIDNO2, or an active derivative thereof.

According to a further aspect of the present invention there is provided a nucleotide sequence comprising a truncated form of a gene sequence or an analogue thereof, for use in the expression of a polypeptide, such as a toxin.

Preferably the nucleotide sequence corresponds to a gene encoding for a precursor polypeptide and truncated at the 3' end thereof or an active derivative thereof. Preferably the nucleotide sequence corresponds to the gene truncated by about 400 to 650 nucleotide bases, and desirably between 550 to 600 nucleotide bases.

The nucleotide sequence may also correspond to the gene truncated at the 5' thereof, preferably by less than 100 nucleotide bases, and desirably by either 84 or 21 nucleotide bases.

Preferably the nucleotide sequence corresponds to part of a gene encoding for a neurotoxin in the venom of the Black Widow Spider (Latrodectus mactans Tredecimguttatus), or an active derivative thereof.

The nucleotide sequence may correspond to part of the gene encoding the precursor polypeptide of insect specific toxin δ-Lactoinsectotoxin (δ-LIT), or an active derivative thereof. The nucleotide sequence preferably codes for a polypeptide comprising a sequence of 991 amino acids.

Preferably the nucleotide sequence comprises a base sequence as shown in SEQIDNO1, or an active derivative thereof, and preferably as comprised in a microorganism deposited under Accession No. NCIMB 40632 at The National Collections of Industrial and Marine Bacteria Limited.

Preferably the nucleotide sequence codes for a polypeptide having an amino acid sequence as shown in SEQIDNO1 and SEQIDNO2, or an active derivative thereof.

The nucleotide sequence may be a cDNA derived from mRNA by the use of an enzyme such as reverse transcriptase. The nucleotide sequence may alternatively be an oligonucleotide DNA construct produced perhaps using the polymerase chain reaction (PCR).

According to a further aspect of the present invention there is provided a method of producing a polypeptide, the method comprising producing a recombinant DNA molecule comprising a truncated form of a gene, and expressing the truncated form in a host expression system, such as a viral or bacterial expression system, to produce the polypeptide.

Preferably the polypeptide produced is an active toxin and desirably a neurotoxin substantially as defined above. Preferably the truncated form comprises part of a gene which encodes for a non-toxic precursor polypeptide.

Preferably the truncated form comprises a nucleotide sequence substantially as defined above, and as shown in SEQIDNO1, or an active derivative thereof. Preferably the expression system comprises E.coli BL21 (DE3) bacterial cells transformed with pT7-7 vectors comprising the truncated form of the sequence, desirably substantially as deposited under Accession No. NCIMB 40632 at The National Collections of Industrial and Marine Bacteria Limited. The expression system may comprise a baculovirus system.

In a further aspect of the present invention there is provided a recombinant DNA molecule, such as a virus, and in particular a baculovirus comprising a truncated form of a gene encoding for a toxin generally

as defined above, and substantially as provided in the microorganism deposited under Accession No. NCIMB 40632.

A still further aspect of the present invention provides an expression vector comprising a truncated form of a gene, the truncated form encoding for a toxin generally as defined above.

The invention also provides a cell, such as a viral or bacterial cell transformed with a recombinant molecule as defined above.

There is also provided an insecticide comprising a toxin as defined above. The insecticide may be so as to be administered orally or topically. The insecticide may comprise a spray.

This invention also provides an insecticide system comprising means for expressing a truncated form of a gene to produce a toxin as described above in an insect to kill or incapacitate the insect. The insecticide system may comprise a viral expression system, and desirably a baculovirus expression system.

According to a further aspect there is provided a plant comprising a genetically modified cell containing a truncated form of a gene sequence substantially as defined above.

Still further according to the present invention

there is provided a non-human animal comprising a genetically modified cell containing a truncated form of a gene sequence substantially as defined above.

According to a further aspect of the present invention there is provided a toxin formed by processing of a substantially isolated non-toxic precursor polypeptide.

The toxin is preferably a neurotoxin and is preferably formed by truncation toward the carboxy (C) end of the precursor polypeptide, preferably by site-directed mutagenesis. Desirably the toxin amino acid sequence generally corresponds to the amino acid sequence of the precursor polypeptide, truncated by between 150 and 200 amino acids. The toxin amino acid sequence may also be formed by truncation toward the amino (N) end of the precursor polypeptide amino acid sequence, the fragment cleaved therefrom preferably being significantly smaller than the fragment cleaved from the carboxy end, and may comprise 7 or 28 amino acids.

Preferably the toxin has an amino acid sequence corresponding to polypeptide encoded by part of a gene of the Black Widow Spider (Latrodectus mactans Tredecimguttatus). The toxin may comprise or be an analogue of the insect specific neurotoxin δ-Latroinsectotoxin (δ-LIT), or an active derivative

thereof.

Preferably the toxin comprises an amino acid sequence as shown in SEQIDNO1 and SEQIDNO2 or an active derivative thereof.

In a further aspect of the present invention there is provided a method of producing an active polypeptide from an inactive precursor polypeptide, the method comprising truncating the isolated precursor polypeptide.

Preferably the isolated precursor polypeptide is truncated at the Carboxyl end, perhaps using proteolytic cleavage, and preferably by site directed mutagenesis. Truncation of the N terminus may also be provided. Preferably the active polypeptide is a toxin and is substantially as described above.

According to another aspect of the present invention there is provided an isolated nucleotide base sequence encoding for a toxin precursor polypeptide as defined above and preferably with an amino acid sequence as shown in SEQIDNO4 or an active derivative thereof. The base sequence preferably comprises the sequence shown in SEQIDNO3 or a derivative thereof. The nucleotide base sequence preferably encodes a precursor polypeptide of the neurotoxin δ-Latroinsectotoxin (δ-LIT). Preferably the base sequence is substantially

as provided in the microorganism deposited under Accession No. NCIMB 40633.

In a further aspect there is provided a recombinant DNA molecule such as a virus, and more particularly a baculovirus comprising a sequence as defined in the preceding paragraph.

In a still further aspect the invention provides a cell, such as a bacterial cell or viral cell, transformed with a recombinant DNA molecule as described in the preceding paragraph.

This invention also provides an insecticide system comprising means for expressing a gene as described above to produce a precursor polypeptide as described above and to process the precursor polypeptide to produce a toxin in an insect to kill or incapacitate the insect. The insecticide system may comprise a viral expression system, and desirably a baculovirus expression system.

According to a further aspect there is provided a plant comprising a genetically modified cell containing a gene as defined above.

Still further according to the present invention there is provided a non-human animal comprising a genetically modified cell containing a gene as defined above.

Preferred embodiments of the present invention will now be described by way of example only, with reference to the accompanying sequences, in which:-

SEQ ID NO. 1 shows the nucleotide base sequence and the corresponding amino acid sequence of a truncated form of a gene and a polypeptide encoded thereby, according to one aspect of the present invention;

SEQ ID NO. 2 shows the polypeptide sequence of SEQIDNO1;

SEQ ID NO. 3 shows the nucleotide base sequence and the corresponding amino acid sequence of a gene and a polypeptide encoded thereby, according to another aspect of the present invention; and

SEQ ID NO. 4 shows the polypeptide sequence of SEQIDNO3.

Referring to the sequences, a polypeptide such as a toxin as in SEQIDNO2 is formed by expression of a truncated form of a gene sequence (SEQIDNO1), or an analogue thereof.

A toxin from Black Widow Spider (Latrodectus mactans Tredecimguttatus) venom (BWSV),

δ-Latroinsectotoxin, (δ-LIT) has been purified and shown to possess insect specific toxicity. The δ-LIT structural gene has been cloned and sequenced and the N- and C terminii of the native (precursor) and functional protein toxin have been determined as described below. Site directed mutagenesis of δ-LIT cDNA enabled expression of the mature protein product (toxin) in bacteria, and this has been shown to be toxic to locusts.

Expression and production of this and other such toxins in bacterial expression systems has hitherto not been possible. The invention includes identification of the sites for cleavage of the precursor protein to produce the toxin, and the precise site of truncation of the gene sequence which has enabled the toxin to be expressed in bacterial, and indeed other suitable hosts.

Microorganism deposits have been made under the Budapest Treaty on 3rd May 1994, at the National Collections of Industrial and Marine Bacteria Limited, of 23 St. Machar Drive, Aberdeen, Scotland, United Kingdom. Escherichia coli (XL-1 Blue pT7.δM) cloned with the truncated form of the gene sequence is deposited under Accession No. 40632, and Escherichia coli (HMS 174 pT7.δFL) cloned with substantially the full gene sequence is deposited under Accession No. 40633).

In more detail, the cDNA cloning and sequencing was

conducted as follows. Poly(A+)-RNA was isolated from venom glands of the Black Widow Spider (Latrodectus mactans Tredecimguttatus) and a cDNA library constructed in the plasmid vector pSP65 (according to Kiyatkin et al, 1993). A library of $6x10^4$ clones was screened with an end-labelled 23-mer oligonucleotide probe based on the N-terminal sequence of δ-LIT (amino acid residues 1-8)- 5' GA(C/T)GA(A/G)GA(A/G)GA(C/T)GG(A/T)GAAATGAC 3' . Hybridization was performed. Positive clones were colony-purified and analysed by restriction mapping. The inserts were excised and fragmented by sonication as described (Sambrook et al, 1989) followed by cloning into the SmaI site of pBluescript II SK+ and SK- vectors (Stratagene, USA). Single-stranded templates for sequencing were obtained after infection with helper phage VCS (Stratagene). The DNA sequences were determined by the chain-termination method (Sanger et al, 1977) using Sequenase 2.0 version kit (USB Corporation) and T7 and T3 vector-specific primers (Stratagene). Each sequence was determined at least twice on both strands. Synthetic primers were used to sequence regions that were not covered by isolated subcloned fragments.

DNA and protein sequence analysis was performed using the computer software DNASTAR (Dnastar Inc) and PCGENE (IntelliGenetics Inc). This work benefitted from the GCG programme mounted on the SERC Daresbury SEQNET

facility (Devereux, Haeberli and Smithies, (1984), Nucleic Acids Research 12(1); 387-395).

The full-length cDNA construction was carried out as follows. Two sets of oligonucleotide primers were used to produce N- and C- overlapping parts of δ-LIT coding sequences by polymerase chain reaction. To facilitate subcloning into the expression vector the 5' sense primer (P1) (TTGGGATCCGATGAAGAAGATGGAGAA) and 3' antisense primer (P8) (CAATGGTCGACACAGAAGGAATGGTA) contained BamHI and SalI restriction enzyme sites. Two other primers -P9, sense (GTCTGAACCATTTACTGTCC) (position 1283-1302) and P3, antisense (GTAAGATTACCATCTGCAAC) (complementary to position 2253-2272) were chosen to produce overlapping fragments with an internal NcoI (2056) restriction site. An oligonucleotide was designed to terminate the protein sequence after amino acid 991- 5' CGTTTCGTCGACTCATTCCGGTAAAGTACGACGAAA 3' . The polymerase chain reaction was performed using 1 unit of Taq-polymerase (Promega) under standard conditions (30 cycles, 55°C for 1 min, 72°C for 3 min, 94°C for 1 min, with 100 pmol of each primer and 1-10 ng first-strand cDNA). In the first cycle the denaturation time was elongated to 5 min. The molecular mass of the amplified material was checked on an agarose gel. First-strand cDNA synthesis was carried out using First-strand cDNA Synthesis Kit (Pharmacia) with both random and specific

primers as recommended by the manufacturer. The PCR products were purified from agarose gel using GeneClean Kit (Bio 101 Inc.), digested with appropriate pairs of enzymes (BamHI and NdeI for the N-terminus part and SalI/NdeI for the C-terminus) and cloned into the pT7-7 vector restricted with the similar pairs of enzymes. The full-length cDNA was created as a result of three-way ligation between N-terminal BamHI/NdeI-fragment, C-terminal NdeI/SalI-fragment and pT7-7 BamHI/SalI-digested vector. The final construct had eight additional amino acid residues at the amino terminal end (MARIRARG). All plasmid constructs were verified by sequencing from both ends and through the junction region. The full length construct was designated pT7δ.FL a sample of which is deposited at the NCIMB, accession No 40633 and the truncated clone (1-991 amino acids) was designated pT7.δM. (NCIMB No 40632).

In order to verify the identity of the δ-LIT cDNA, this clone was expressed in the bacterial pT7-7 vector in E.coli BL21(DE3) cells. A full-length toxin cDNA (corresponding to Asp residue 29 to 1186) 1214 of SEQION04 was constructed and designated pT7.δFL. The first 28 amino acids are believed to be present in the precursor polypeptide in spider venom glands, but cleaved during N-terminal processing. The recombinant protein constitutes approximately 10% of the total bacterial

lysate protein. A polyclonal antibody specific was raised to δ-LIT purified from spider venom glands, and demonstrated to be specific for the δ toxin. This protein specifically detected a protein of 130 kDa in bacteria expressing recombinant full-length δ-LIT. Comparison of the molecular mass of the bacterially expressed full-length δ-LIT and the toxin purified from venom glands demonstrated a size difference of approximately 23kDa, in agreement with the calculated molecular mass. The full-length δ-LIT had no toxicity towards insects and is considered to be an inactive precursor form of the toxin.

δ -LIT purified from venom glands was analysed by mass spectrometry (on a Kratos Kompact MALDI 3 Mass Spectrometer, using sinapinic acid as a matrix. The nitrogen laser excitation was at 337nm, and the positive ion was detected in the linear mode) yielding a prominent molecular ion with a m/z+ ratio of 110916. This corresponds closely to the expected molecular mass of δ -LIT which is truncated at amino acid 991. By comparison, the bacterially expressed full length δ-LIT yielded a molecular ion with an m/z+ ratio of 133631 (VK, DRB, PNRU, Data not shown), within 100 Da of the calculated value. Site directed mutagenesis was used to create a novel δ-LIT cDNA clone (pT7δM), which was truncated after amino acid 991 of the δ -LIT sequence

(SEQIDNO2). This protein was expressed in bacteria, yielding a protein of similar molecular mass to the mature toxin isolated from spider venom.

E. coli BL21(DE3) cells transformed with pT7 clones were grown in LB medium containing 100mg ampicillin/ml at 30°C to an A_{600nm} of approximately 0.5. Then expression was induced by addition of IPTG (1mM) to the medium, and incubation continued for 1 hour. For functional studies, bacteria were washed and resuspended in 50 mM TrisHC1, 100mM NaCl, 10mM KCl, 0.4% Triton X-100, 12% (W/V) sucrose, 5mM DTT, 2 μg/ml aprotonin, 2mM EDTA, pH8, and sonicated on ice. Ammonium sulphate was added to the cleared supernatant to a final concentration of 20% of saturation, and the pellet was resuspended in buffer without DTT. These samples (5-15 μl) were used for thoracic injection into locusts (100-300 mg body weight); each test was performed on more than 4 locusts, and the locusts were examined for toxicity for 24 hours. Extracts from pT7-7 and pT7.δFL produced no effects on the locusts, but extracts from bacteria carrying pT7.δM caused rapid lethality. The time of death of the locusts varied from 5 minutes - 4 hours, depending on the potency of the batch of toxin.

Preliminary studies were undertaken on

neurally-excited and resting retractor unguis nerve-muscle preparations isolated from metathoracic legs of adult (male and female) locusts (Usherwood and Machili, 1968). δ-LIT was applied in standard locust saline (mM: NaCl, 180; KCl, 10; CaCl2, 2; Hepes, 10 (pH 6.8)). A few studies were undertaken using saline in which CaCl2 was omitted. Mechanical responses were recorded using a Grass strain guage connected to a Grass pen recorder. Recordings of miniature excitatory postsynaptic potentials were made from fibres of metathoracic extensor tibiae muscles of adult locusts (either sex) using intracellular microelectrodes (approximately 10mΩ resistance). δ-LIT was applied in either standard locust saline, saline in which CaCl2 was omitted or saline which contained MgCl2 substituted for NaCl. The miniature potentials were recorded on video tape and analysed on a MassComp computer using in-house software. Membrane bilayers were formed at the tips of patch pipettes (diam 1-2μm; fabricated from Clark Electromedical glass) from monolayers of either diphytanoyl phosphatidylcholine or a mixture of 9 parts isolectin and 1 part cholesterol using a pipette dipping technique (Montal and Muller, 198). Similar patch pipettes were used to excise membrane patches from locust metathoracic extensor tibiae muscle fibres (Huddie et al). In order to reduce the activities of endogenous potassium channels KCl was eliminated from the pipette

and bath salines.

The neurally-evoked twitch contraction of the locust retractor unguis muscle was reduced by approximately 40% by 10^{-11}M δ-LIT (applied in standard saline) and was abolished during application of 10^{-10}M toxin. Small spontaneous contractions sometimes occurred during δ-LIT application. The changes in twitch amplitude were accompanied by an irreversible muscle contracture. The appearance of the contracture was delayed and its amplitude was reduced when the concentration of δ-LIT was lowered. A muscle contracture also occured when toxin was applied when the muscle was not neurally stimulated. Twitch contractions do not occur in calcium-free saline and when 10^{-10}M toxin was applied to a preparation equilibrated in this saline a contracture did not occur even after 30 min application of the toxin.

When inside-out patches excised from locust muscle fibres were exposed to 10^{-11}M α-LIT in the patch pipette, channel opening, of maximum conductance approximately 40pS, were observed. Channel openings of this type were never seen in the absence of toxin. The channel current exhibited inward rectification when the patch pipette and bath contained identical salines (including 2mM CaCl2), and channel open times were longer at negative than at positive pipette potentials. When

there was a 10-fold Ca2+ gradient across a patch, the reversal potential of the channel current was +/- 15mV, the sign being dependent on the Ca2+ gradient.

In the artificial bilayer studies where 10^{-11}M ω-LIT was placed in the patch pipettes, single channel openings of approximately 30pS conductance were observed. These channels were not seen when toxin was omitted from the patch pipette. With identical salines (containing 2mM CaCl2) in the patch pipette and bath, the current-voltage characteristic of the ω-LITx channel was sigmoidal with a reversal potential at 0mV. The channel was shown to be Ca-selective by manipulating the ionic regimes of patch pipette and bath.

A cDNA library from venom gland cDNA was screened with a 23-bp oligonucleotide probe corresponding to the N-terminal sequence of ω-LIT (as described above). To reduce the number of nucleotide ambiguities the codon usage data available from the nucleotide sequences of ω-LT and ω-LIT cDNA (Kiyatkin et al, 1990, Kiyatkin et al 1993) was referred to. Five positive cDNA clones were colony-purified and sequenced. The longest clone (pDT-1) contained more than 2 (kb) of ω-LIT coding region. A PstI-3' fragment was used to rescreen the cDNA library to search for clones encoding the C-terminal part of the toxin. An additional cDNA clone, pDT-17, was isolated,

which covered the C-terminal coding region of the δ-LIT. Two overlapping clones, covering the entire open reading frame, have been sequenced in their entirety. The two clones have been demonstrated to be part of a single, continuous RNA from venom glands by polymerase chain reaction across the overlapping region, using two distinct sets of primers. The composite clones encode a cDNA with a frame of 3642 bp starting from the first in-frame Methionine and ending with TAA stop codon (SEQIDNO3).

The Met residue is preceded by an in-frame stop codon confirming the full length of the deduced sequence.

δ-LIT was purified to homogeneity from Black Widow Spider venom by three rounds of column chromatography according to (Krasnoperov et al, 1992). 23 amino acid residues of the N-terminal sequence of δ-LIT was sequenced. The pure toxin was digested with trypsin and seven individual peptides were isolated and partially sequenced.

Direct N-terminal sequence determination demonstrates that the mature protein starts from the sequence DEEDGEM..., so residue 1 in SEQIDNO1 and 2 is the first Asp of this sequence. The deduced polypeptide starting from Asp (+1) consists of 1186 amino acid (as

shown in SEQIDNO3^{+4}, Asp residue 29 to residue 1214) residues with a predicted molecular mass of 132671 Daltons and pI of 5.4. It contains all of the peptide sequences determined by amino acid sequencing analysis. There are two in-frame Met residues (-7 and -28) upstream of the N-terminus (as shown in SEQIDNO3) of the mature protein which can serve as translation initiation sites. The nucleotide sequence surrounding the ATG codon for Met (-7) correlates better with the classical Kozak consensus (Kozak, 1989), but the nucleotide arrangement for Met (-28) strongly corresponds to starting points for at least two other known proteins which have been isolated from arachnids: Major house dust mite allergen (AAAATGA) (Yuuki et al, 1991) and Low molecular weight protein co-purified with α-Latrotoxin (AAATGA) (Kiyatkin et al, 1992). In both cases, the deduced sequence preceding the N-terminus of the mature protein does not correspond to classical signal peptide structures. We conclude that post-translational modification of δ-LIT N-terminus is limited to removal of 7 or 28 amino acid residues. The existence of a cluster of positive amino acid residues Arg-X-Lys-Arg (-1-4) which can serve as a potential endopeptidase-cleavage site supports the hypothesis that post-translational processing occurs at the N-terminus.

Analysis of the deduced structure of δ-LIT with PEST (Rogers, S. et al, 1986) reveals the presence of an

amino acid sequence enriched in P, E, S and T, which has previously been correlated with rapid degradation of intracellular proteins (Gottesman & Maurizi, 1992). This region has the sequence EESGAPEGSFDSPSS, and is situated between residues 956-970. The presence of the PEST-region in the C-terminal part of δ-LIT is consistent with C-terminal processing of this protein.

Computer analysis of δ-LIT predicts three putative transmembrane helixes two of them situating in terminal regions (residues 39-67 and 221-240) and the third one of a minimal length (residues 580-595) being in the central region. The second putative transmembrane helix (residues 221-240) belongs to a very conservative region between all spider high molecular weight protein neurotoxins (Kiyatkin et al, 1993).

Dot-matrix analysis of the predicted δ-LIT amino acid sequence revealed the presence of a repeated motif in the central part of the protein molecule. 460 amino acid residues of the δ-LIT primary structure comprise tandemly arranged imperfect copies of the ankyrin-like repeats (Michaely & Bennett, 1992). Whereas αLT and α-LIT (Kiyatkin et al, 1990, Kiyatkin et al, 1993) have no less than 20 repeats, δ-LIT has been found to have only 13 successive repeated units. Their optimal alignment is with phasing originally suggested in (Lux et

al, 1990). The sequence of 13 amino acids which precede the first repeat can be viewed as a reduced repeated unit according to its good correlation with a consensus sequence. The majority of δ-LIT repeated units are 33-34 amino acids in length. but two repeats contain 35 (R1) and 36(R6) residues, respectively.

Analysis with the PCOMPARE programme showed the linear correlation between the repeated units of two insect-specific toxins. Strong linear correspondence has been found for δ-LIT repeats R2-R9 in comparison to the analogous repeats in α-LIT (Kiyatkin et al, 1993). The first repeat in δ-LIT does not correspond well to the first one in α-LIT and shows high similarity to R7 from α-LIT. δ-LIT repeat R10 is most similar to R19 from α-LIT: this repeat is unusual in having Ser and Gly residues at position 8 and 31, respectively. The next stretch of similarity is found between R11-R13 of δ-LIT and R10-R12 of α-LIT. We have noted that the R7, R2 and R9 repeats are the most highly conserved between the insectotoxins, suggesting a functional role in insectotoxicity. It has been shown that Erythrocyte Ankyrin repeats are not equivalent in respect of their functional ability to bind different proteins (Davis et al, 1991), and thus toxin repeats are also expected to make different contributions to their function.

Dot-matrix comparison of δ- and α-LIT shows that they share a similar overall organization, with the strong central diagonal broken once (between 900 and 1130 amino acid residues of δ-LIT) and restored for the last 160 amino acids of both toxins. The displacement of the central diagonal reflects the difference in toxin length; δ-LIT is 190 amino acids shorter than its insect-specific counterpart.

The mature protein can be divided into several structural domains: an N-terminus consisting of about 470 amino acid residues and possessing strong linear homology with α-LIT; the central domain of about 430 amino acids almost completely comprised of tandemly arranged ankyrin-like repeated units and a C-terminal domain of about 160 amino acids.

Alignment of the insectotoxin protein sequences shows that both the N- and C-terminal structural domains demonstrate the presence of high identity regions separated by rather dissimilar sequences, with a high level of identity (44.9% for the N-terminal domain and 37.1% for the C-terminus). The most dramatic changes in primary structure of the two insectotoxins are concentrated in C-terminal parts of the repeat containing domains. A stretch of homology is localized to 13 ankyrin repeat units of δ-LIT. This region is followed

by a sequence of about 110 amino acid residues that has no obvious homology either with α-LIT or αLT nor with any other proteins from NBRF-PIR database. Interestingly, this domain, which is absent from δ-LIT, forms a specific region in the primary structure of α-LIT that has an unusual clustering of Cys-residues and possesses homology with mammalian-specific αLT (Kiyatkin et al, 1993). So striking structural difference between the two insect-specific neurotoxins suggests that the C-terminal part of the ankyrin-like repeated domain plays a particular role in providing a structural basis for their different functional properties.

The high molecular weight protein toxins from the venom of the Black Widow Spider are a potent and specific class of toxins. These toxins offer a great potential for elucidating the function of neural proteins, and for providing insect specific toxins. However this potential has not previously been realised due to the inability to express these protein toxins with any function. The present invention provides for the cloning of a novel DNA transcript encoding for a novel insect-specific toxin, and functional expression of this toxin, and other polypeptides in bacteria.

The δ-LIT cDNA was cloned with an oligonucleotide based on the sequence of amino acids 1-23 of the toxin,

and its identity confirmed by additional peptide sequences, and immunochemical identity, using an antibody specific for the δ-LIT. The deduced primary structure of δ-LIT has considerable similarity to the mammalian specific αLT and the insect-specific α-LIT, suggesting that these toxins are part of a family with similar structure. The three proteins have a central domain which is composed of "ankyrin-like" repeats, with 13 repeats in δ-LIT. The ankyrin family of proteins couple spectrin to a variety of integral membrane proteins (Bennett, 1992), and it is believed that the "ankyrin repeat" domain of the ankyrins is responsible for specific binding to proteins (Davis and Bennett, 1990 J Biol Chem 265: 10589-10596; Davis et al (1991) J. Biol Chem 266: 11163-11169). This structural similarity with the ankyrin family is reflected in the known functional properties of the latrotoxins; α LT is known to bind to a receptor with high affinity (K_d $\tilde{}$ 10^{-9}M). It remains to be determined whether this specific binding to the α LT receptor is mediated via the ankyrin repeat region of the toxin.

Surprisingly, δ-LIT has no greater similarity to the insect-specific α-LIT (38%) than to the mammalian-specific αLT (37%). Whereas δ-LIT has only 13 repeats, the α LT and α-LIT have 19 and 20 ankyrin repeats, respectively. The latter 6/7 repeats have no counterpart

in the δ-LIT, and may be a structural unit, as the α-toxins both contain 6 cysteine residues in this region, with partially conserved spacing. However, in view of the differences in target toxicity of the αLT and α-LIT, it is not possible to identify this structural features with insect-specific toxicity.

δ-LIT exhibits a marked disparity between the molecular weight of the toxin, as deduced from the cDNA sequence, and the relative mobility of the pure toxin purified from venom. Whilst the N-terminus of the protein has been identified unambiguously by protein sequencing, the precise position of the C-terminus has been difficult to document. Expression of the full length δ-LIT cDNA in bacteria demonstrated that the calculated molecular mass is accurately reflected in the relative mobility of the protein on SDS-PAGE, and that the natural venom derives predominantly, if not wholly from proteolytic, C-terminal processing. The full-length recombinant protein was purified, but was not toxic to locusts under any conditions. The full-length protein is an inactive precursor of the functional toxin.

The precise site of the C-terminus of δ-LIT purified from venom was assessed by MALDI-mass spectrometry, which localised the site of cleavage to amino acid 991 of the protein. The cDNA was mutated to

produce a protein of 991 amino acids with a sequence as shown in SEQIDNO2, and expressed in bacteria. The mature recombinant protein was soluble and was lethal to locusts. Partial purification of the protein suggests that the toxin is highly toxic.

Expression of the mature toxin from using the truncated form of the full gene sequence as described above has considerable advantages. Firstly, the toxin can be produced relatively easily by functional expression of the truncated form in a bacterial system, thereby obviating the need to purify toxin from venom glands of spiders. This enables industrial production of the toxin and hence commercial exploitation, for example as the major component of an insecticide system.

Moreover, it presents possible administration systems for the toxin as an insecticide, beside conventional methods such as spraying. For example it may be possible to produce a modified plant cell or plant, such as a crop plant, containing a recombinant molecule incorporating the truncated sequence. Such a system comprises a recombinant baculovirus comprising the truncated form. Such viruses are highly infectious in vivo and resistant to inactivation in host cells, and are capable of high levels of expression of the inserted nucleotide sequence in host insect cells. This is expected to be harmless to the plant and indeed to

vertebrates. Upon ingestion of the plant tissue an insect will take in the recombinant molecule and/or toxin, resulting ultimately in the death of the insect. Since the toxin is insect specific, it is expected to have no detrimental effect to humans or animals upon consumption.

This is an example of one use of one embodiment of the invention to express a toxin that is usually produced by post-translational modification of a precursor protein in biological systems, in a bacterial expression system. It is to be appreciated that the truncated form of other genes coding for other proteins could be expressed in this way, and fall within the scope of the present invention.

The invention also provides toxin formed from the expression of a full, isolated gene to produce a precursor polypeptide which is then post-translationally modified. The precursor polypeptide has an amino acid sequence as shown in SEQIDNO4, and the toxin has a sequence as shown in SEQIDNO2.

The isolated gene (SEQIDNO3) (or an analogue) encoding for the precursor polypeptide of the toxin δ LIT can be cloned into a vector for expression of the precursor polypeptide. A baculovirus expression system

can be used. The precursor polypeptide thus produced can then be truncated at the sites indicated above, by site directed mutagenesis, to produce an active toxin. This enables the toxin αLIT or an active derivative thereof, to be produced independently of the Black Widow Spider, and thus on an industrial scale, for use as indicated as an insecticide.

Whilst endeavouring in the foregoing specification to draw attention to those features of the invention believed to be of particular importance it should be understood that the Applicant claims protection in respect of any patentable feature or combination of features hereinbefore referred to and/or shown in the drawings whether or not particular emphasis has been placed thereon.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: BRITISH TECHNOLOGY GROUP LIMITED
(B) STREET: 101 NEWINGTON CAUSEWAY
(C) CITY: LONDON
(E) COUNTRY: UNITED KINGDOM
(F) POSTAL CODE (ZIP): SE1 6BU

(ii) TITLE OF INVENTION: A NOVEL TOXIN AND A METHOD OF PRODUCING A TOXIN

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release £1.0, Version £1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2976 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PLASMID DNA"

(vi) ORIGINAL SOURCE:
(A) ORGANISM: LATRODECTUS MACTANS TREDECIMGUTTATUS

(vii) IMMEDIATE SOURCE:
(B) CLONE: pT7.deltaM

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:1..2976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GAT GAA GAA GAT GGA GAA ATG ACT CTA GAA GAA AGA CAA GCA CAA TGC        48
Asp Glu Glu Asp Gly Glu Met Thr Leu Glu Glu Arg Gln Ala Gln Cys
 1               5                  10                  15

AAA GCA ATA GAG TAC AGC AAT TCA GTT TTT GGG ATG ATC GCT GAT GTA        96
Lys Ala Ile Glu Tyr Ser Asn Ser Val Phe Gly Met Ile Ala Asp Val
            20                  25                  30

GCT AAC GAC ATC GGT TCC ATT CCT GTA ATT GGC GAA GTA GTT GGC ATT       144
Ala Asn Asp Ile Gly Ser Ile Pro Val Ile Gly Glu Val Val Gly Ile
        35                  40                  45

GTA ACT GCC CCA ATT GCC ATC GTA AGT CAC ATT ACT AGC GCA GGC TTG       192
Val Thr Ala Pro Ile Ala Ile Val Ser His Ile Thr Ser Ala Gly Leu
    50                  55                  60

GAT ATA GCT TCT ACG GCA TTA GAT TGT GAT GAT ATA CCT TTT GAT GAG       240
Asp Ile Ala Ser Thr Ala Leu Asp Cys Asp Asp Ile Pro Phe Asp Glu
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55 70 75 80

ATT AAG GAA ATA TTA GAA GAA AGA TTC AAT GAA ATA GAT AGA AAG TTG 288
Ile Lys Glu Ile Leu Glu Glu Arg Phe Asn Glu Ile Asp Arg Lys Leu
85 90 95

GAC AAG AAC ACA GCT GCT TTG GAA GAG GTC TCT AAA CTG GTA AGT AAA 336
Asp Lys Asn Thr Ala Ala Leu Glu Glu Val Ser Lys Leu Val Ser Lys
100 105 110

ACT TTT GTT ACG GTG GAA AAA ACA AGG AAT GAA ATG AAC GAA AAT TTT 384
Thr Phe Val Thr Val Glu Lys Thr Arg Asn Glu Met Asn Glu Asn Phe
115 120 125

AAG CTT GTT TTG GAA ACT ATA GAA AGC AAA GAA ATA AAA TCA ATT GTA 432
Lys Leu Val Leu Glu Thr Ile Glu Ser Lys Glu Ile Lys Ser Ile Val
130 135 140

TTC AAA ATA AAT GAT TTT AAA AAG TTT TTT GAA AAA GAA CGA CAA AGA 480
Phe Lys Ile Asn Asp Phe Lys Lys Phe Phe Glu Lys Glu Arg Gln Arg
145 150 155 160

ATT AAA GGT TTG CCT AAA GAT AGG TAT GTT GCT AAG CTT CTA GAA CAA 528
Ile Lys Gly Leu Pro Lys Asp Arg Tyr Val Ala Lys Leu Leu Glu Gln
165 170 175

AAA GGT ATT TTA GGT TCT TTA AAA GAA GTA AGA GAA CCA TCT GGA AAC 576
Lys Gly Ile Leu Gly Ser Leu Lys Glu Val Arg Glu Pro Ser Gly Asn
180 185 190

AGT CTG AGC TCC GCG TTA AAT GAA CTC TTA GAC AAA AAC AAC AAC TAT 624
Ser Leu Ser Ser Ala Leu Asn Glu Leu Leu Asp Lys Asn Asn Asn Tyr
195 200 205

GCC ATC CCA AAA GTG GTT GAT GAT AAT AAG GCC TTT CAG GCG CTG TAT 672
Ala Ile Pro Lys Val Val Asp Asp Asn Lys Ala Phe Gln Ala Leu Tyr
210 215 220

GCT TTA TTT TAT GGA ACT CAG ACT TAT GCA GCC GTT ATG TTT TTC TTA 720
Ala Leu Phe Tyr Gly Thr Gln Thr Tyr Ala Ala Val Met Phe Phe Leu
225 230 235 240

CTC GAA CAA CAT TCT TAT CTG GCT GAT TAT TAT TAC CAA AAA GGT GAT 768
Leu Glu Gln His Ser Tyr Leu Ala Asp Tyr Tyr Tyr Gln Lys Gly Asp
245 250 255

GAT GTA AAT TTT AAT GCA GAA TTT AAT AAT GTA GCA ATT ATT TTT GAT 816
Asp Val Asn Phe Asn Ala Glu Phe Asn Asn Val Ala Ile Ile Phe Asp
260 265 270

GAC TTT AAA TCA TCA CTA ACA GGA GGA GAT GAC GGA TTA ATA GAT AAT 864
Asp Phe Lys Ser Ser Leu Thr Gly Gly Asp Asp Gly Leu Ile Asp Asn
275 280 285

GTC ATT GAG GTT CTT AAC ACC GTG AAA GCA TTA CCA TTT ATA AAG AAC 912
Val Ile Glu Val Leu Asn Thr Val Lys Ala Leu Pro Phe Ile Lys Asn
290 295 300

GCC GAC AGT AAA CTA TAC AGA GAA TTA GTA ACT AGA ACA AAA GCT TTA 960
Ala Asp Ser Lys Leu Tyr Arg Glu Leu Val Thr Arg Thr Lys Ala Leu
305 310 315 320

GAG ACT CTT AAA AAT CAA ATC AAA ACG ACT GAT TTG CCT CTT ATA GAT 1008
Glu Thr Leu Lys Asn Gln Ile Lys Thr Thr Asp Leu Pro Leu Ile Asp
325 330 335

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GAT ATA CCC GAA ACT TTG TCT CAA GTG AAC TTT CCG AAT GAC GAA AAT      1056
Asp Ile Pro Glu Thr Leu Ser Gln Val Asn Phe Pro Asn Asp Glu Asn
            340                 345                 350

CAA TTG CCT ACA CCA ATA GGA AAT TGG GTT GAT GGC GTA GAA GTT AGG      1104
Gln Leu Pro Thr Pro Ile Gly Asn Trp Val Asp Gly Val Glu Val Arg
        355                 360                 365

TAC GCA GTA CAG TAT GAA AGT AAG GGC ATG TAT TCG AAA TTC AGT GAA      1152
Tyr Ala Val Gln Tyr Glu Ser Lys Gly Met Tyr Ser Lys Phe Ser Glu
    370                 375                 380

TGG TCT GAA CCA TTT ACT GTC CAA GGT AAC GCT TGT CCG ACT ATA AAA      1200
Trp Ser Glu Pro Phe Thr Val Gln Gly Asn Ala Cys Pro Thr Ile Lys
385                 390                 395                 400

GTT CGT GTT GAT CCG AAA AAG AGA AAT AGA CTT ATC TTT AGG AAG TTC      1248
Val Arg Val Asp Pro Lys Lys Arg Asn Arg Leu Ile Phe Arg Lys Phe
                405                 410                 415

AAC TCA GGA AAA CCT CAG TTT GCT GGA ACC ATG ACT CAT TCA CAA ACA      1296
Asn Ser Gly Lys Pro Gln Phe Ala Gly Thr Met Thr His Ser Gln Thr
            420                 425                 430

AAT TTT AAA GAT ATT CAT CGT GAT CTA TAC GAT GCA GCC TTA AAT ATT      1344
Asn Phe Lys Asp Ile His Arg Asp Leu Tyr Asp Ala Ala Leu Asn Ile
        435                 440                 445

AAT AAG TTG AAA GCA GTG GAT GAA GCT ACA ACT TTG ATT GAA AAG GGT      1392
Asn Lys Leu Lys Ala Val Asp Glu Ala Thr Thr Leu Ile Glu Lys Gly
    450                 455                 460

GCA GAC ATA GAA GCA AAA TTT GAC AAT GAC AGA AGT GCA ATG CAC GCA      1440
Ala Asp Ile Glu Ala Lys Phe Asp Asn Asp Arg Ser Ala Met His Ala
465                 470                 475                 480

GTT GCA TAT CGA GGA AAT AAC AAA ATA GCC TTA AGA TTT CTT TTG AAA      1488
Val Ala Tyr Arg Gly Asn Asn Lys Ile Ala Leu Arg Phe Leu Leu Lys
                485                 490                 495

AAT CAA TCC ATT GAC ATC GAG TTA AAA GAT AAA AAC GGC TTT ACT CCT      1536
Asn Gln Ser Ile Asp Ile Glu Leu Lys Asp Lys Asn Gly Phe Thr Pro
            500                 505                 510

CTA CAC ATC GCA GCT GAA GCA GGT CAG GCA GGA TTT GTT AAG TTA CTA      1584
Leu His Ile Ala Ala Glu Ala Gly Gln Ala Gly Phe Val Lys Leu Leu
        515                 520                 525

ATA AAT CAT GGA GCT GAT GTG AAT GCA AAA ACA AGT AAG ACA AAT TTG      1632
Ile Asn His Gly Ala Asp Val Asn Ala Lys Thr Ser Lys Thr Asn Leu
    530                 535                 540

ACA CCA TTA CAT CTT GCA ACA CGT AGT GGA TTT TCA AAA ACT GTA AGA      1680
Thr Pro Leu His Leu Ala Thr Arg Ser Gly Phe Ser Lys Thr Val Arg
545                 550                 555                 560

AAT TTA CTA GAA AGC CCA AAT ATT AAG GTA AAT GAA AAG GAG GAT GAC      1728
Asn Leu Leu Glu Ser Pro Asn Ile Lys Val Asn Glu Lys Glu Asp Asp
                565                 570                 575

GGA TTT ACA CCT TTG CAT ACT GCA GTA ATG AGT ACT TAT ATG GTT GTC      1776
Gly Phe Thr Pro Leu His Thr Ala Val Met Ser Thr Tyr Met Val Val
            580                 585                 590

GAT GCT TTG CTA AAT CAT CCA GAC ATT GAT AAA AAT GCG CAG TCT ACG      1824
Asp Ala Leu Leu Asn His Pro Asp Ile Asp Lys Asn Ala Gln Ser Thr
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595 600 605

TCA GGA TTG ACT CCT TTC CAT TTA GCA ATT ATT AAT GAA AGT CAA GAA 1872
Ser Gly Leu Thr Pro Phe His Leu Ala Ile Ile Asn Glu Ser Gln Glu
610 615 620

GTT GCA GAA TCT TTA GTG GAA AGT AAT GCT GAT CTA AAT ATT CAG GAT 1920
Val Ala Glu Ser Leu Val Glu Ser Asn Ala Asp Leu Asn Ile Gln Asp
625 630 635 640

GTT AAC CAT ATG GCT CCT ATT CAT TTT GCA GCT TCA ATG GGT AGT ATT 1968
Val Asn His Met Ala Pro Ile His Phe Ala Ala Ser Met Gly Ser Ile
645 650 655

AAA ATG CTT AGA TAT CTC ATT TCC ATA AAA GAT AAA GTT AGT ATT AAT 2016
Lys Met Leu Arg Tyr Leu Ile Ser Ile Lys Asp Lys Val Ser Ile Asn
660 665 670

TCT GTG ACT GAG AAT AAT AAC TGG ACA CCT TTA CAT TTT GCT ATA TAT 2064
Ser Val Thr Glu Asn Asn Asn Trp Thr Pro Leu His Phe Ala Ile Tyr
675 680 685

TTT AAA AAA GAA GAT GCT GCA AAA GAA TTG TTG AAA CAA GAT GAC ATA 2112
Phe Lys Lys Glu Asp Ala Ala Lys Glu Leu Leu Lys Gln Asp Asp Ile
690 695 700

AAT TTA ACA ATT GTT GCA GAT GGT AAT CTT ACC GTT TTA CAT CTT GCT 2160
Asn Leu Thr Ile Val Ala Asp Gly Asn Leu Thr Val Leu His Leu Ala
705 710 715 720

GTT TCG ACA GGA CAA ATA AAT ATA ATT AAA GAA TTA TTG AAG AGA GGC 2208
Val Ser Thr Gly Gln Ile Asn Ile Ile Lys Glu Leu Leu Lys Arg Gly
725 730 735

TCC AAT ATA GAA GAA AAA ACT GGA GAA GGA TAT ACA TCT CTC CAC ATC 2256
Ser Asn Ile Glu Glu Lys Thr Gly Glu Gly Tyr Thr Ser Leu His Ile
740 745 750

GCT GCG ATG CGA AAG GAG CCA GAG ATA GCT GTT GTT TTG ATT GAA AAC 2304
Ala Ala Met Arg Lys Glu Pro Glu Ile Ala Val Val Leu Ile Glu Asn
755 760 765

GGT GCT GAC ATA GAA GCT CGA TCA GCT GAT AAT TTA ACA CCT TTA CAT 2352
Gly Ala Asp Ile Glu Ala Arg Ser Ala Asp Asn Leu Thr Pro Leu His
770 775 780

TCT GCC GCA AAA ATA GGA AGG AAA TCT ACA GTA CTT TAC TTA TTA GAA 2400
Ser Ala Ala Lys Ile Gly Arg Lys Ser Thr Val Leu Tyr Leu Leu Glu
785 790 795 800

AAA GGA GCT GAC ATT GGA GCT AAA ACA GCA GAC GGT TCT ACT GCC TTG 2448
Lys Gly Ala Asp Ile Gly Ala Lys Thr Ala Asp Gly Ser Thr Ala Leu
805 810 815

CAT TTA GCT GTA TCT GGT CGT AAA ATG AAA ACT GTT GAA ACT CTA TTA 2496
His Leu Ala Val Ser Gly Arg Lys Met Lys Thr Val Glu Thr Leu Leu
820 825 830

AAT AAA GGA GCA AAT TTA AAA GAA TAC GAT AAC AAT AAA TAT TTG CCA 2544
Asn Lys Gly Ala Asn Leu Lys Glu Tyr Asp Asn Asn Lys Tyr Leu Pro
835 840 845

ATA CAT AAA GCT ATT ATT AAT GAT GAC CTT GAC ATG GTA CGT TTG TTT 2592
Ile His Lys Ala Ile Ile Asn Asp Asp Leu Asp Met Val Arg Leu Phe
850 855 860

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CTT GAA AAA GAT CCC AGT CTC AAA GAT GAT GAA ACA GAA GAG GGT AGA      2640
Leu Glu Lys Asp Pro Ser Leu Lys Asp Asp Glu Thr Glu Glu Gly Arg
865                 870                 875                 880

ACT TCA ATT ATG TTA ATT GTT CAG AAA TTG CTT CTT GAA TTA TAT AAC      2688
Thr Ser Ile Met Leu Ile Val Gln Lys Leu Leu Leu Glu Leu Tyr Asn
                885                 890                 895

TAT TTT ATA AAT AAT TAT GCT GAA ACT TTG GAT GAA GAA GCT TTA TTC      2736
Tyr Phe Ile Asn Asn Tyr Ala Glu Thr Leu Asp Glu Glu Ala Leu Phe
            900                 905                 910

AAC CGC TTA GAT GAA CAA GGG AAA TTA GAG CTT GCA TAT ATC TTC CAT      2784
Asn Arg Leu Asp Glu Gln Gly Lys Leu Glu Leu Ala Tyr Ile Phe His
        915                 920                 925

AAT AAA GAA GGT GAT GCA AAA GAG GCT GTT AAG CCA ACT ATC CTT GTT      2832
Asn Lys Glu Gly Asp Ala Lys Glu Ala Val Lys Pro Thr Ile Leu Val
    930                 935                 940

ACA ATT AAA CTT ATG GAA TAC TGC TTA AAA AAA CTT CGC GAA GAG TCT      2880
Thr Ile Lys Leu Met Glu Tyr Cys Leu Lys Lys Leu Arg Glu Glu Ser
945                 950                 955                 960

GGA GCT CCT GAA GGT AGT TTC GAT TCT CCA TCT TCA AAG CAA TGT ATT      2928
Gly Ala Pro Glu Gly Ser Phe Asp Ser Pro Ser Ser Lys Gln Cys Ile
                965                 970                 975

TCT ACC TTT TCA GAG GAT GAA ATG TTT CGT CGT ACT TTA CCG GAA TGA      2976
Ser Thr Phe Ser Glu Asp Glu Met Phe Arg Arg Thr Leu Pro Glu  *
            980                 985                 990
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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 992 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Asp Glu Glu Asp Gly Glu Met Thr Leu Glu Glu Arg Gln Ala Gln Cys
 1               5                  10                  15

Lys Ala Ile Glu Tyr Ser Asn Ser Val Phe Gly Met Ile Ala Asp Val
            20                  25                  30

Ala Asn Asp Ile Gly Ser Ile Pro Val Ile Gly Glu Val Val Gly Ile
        35                  40                  45

Val Thr Ala Pro Ile Ala Ile Val Ser His Ile Thr Ser Ala Gly Leu
    50                  55                  60

Asp Ile Ala Ser Thr Ala Leu Asp Cys Asp Asp Ile Pro Phe Asp Glu
65                  70                  75                  80

Ile Lys Glu Ile Leu Glu Glu Arg Phe Asn Glu Ile Asp Arg Lys Leu
                85                  90                  95

Asp Lys Asn Thr Ala Ala Leu Glu Glu Val Ser Lys Leu Val Ser Lys
            100                 105                 110

Thr Phe Val Thr Val Glu Lys Thr Arg Asn Glu Met Asn Glu Asn Phe
        115                 120                 125
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Lys Leu Val Leu Glu Thr Ile Glu Ser Lys Glu Ile Lys Ser Ile Val
130 135 140

Phe Lys Ile Asn Asp Phe Lys Lys Phe Phe Glu Lys Glu Arg Gln Arg
145 150 155 160

Ile Lys Gly Leu Pro Lys Asp Arg Tyr Val Ala Lys Leu Leu Glu Gln
165 170 175

Lys Gly Ile Leu Gly Ser Leu Lys Glu Val Arg Glu Pro Ser Gly Asn
180 185 190

Ser Leu Ser Ser Ala Leu Asn Glu Leu Leu Asp Lys Asn Asn Asn Tyr
195 200 205

Ala Ile Pro Lys Val Val Asp Asp Asn Lys Ala Phe Gln Ala Leu Tyr
210 215 220

Ala Leu Phe Tyr Gly Thr Gln Thr Tyr Ala Ala Val Met Phe Phe Leu
225 230 235 240

Leu Glu Gln His Ser Tyr Leu Ala Asp Tyr Tyr Tyr Gln Lys Gly Asp
245 250 255

Asp Val Asn Phe Asn Ala Glu Phe Asn Asn Val Ala Ile Ile Phe Asp
260 265 270

Asp Phe Lys Ser Ser Leu Thr Gly Gly Asp Asp Gly Leu Ile Asp Asn
275 280 285

Val Ile Glu Val Leu Asn Thr Val Lys Ala Leu Pro Phe Ile Lys Asn
290 295 300

Ala Asp Ser Lys Leu Tyr Arg Glu Leu Val Thr Arg Thr Lys Ala Leu
305 310 315 320

Glu Thr Leu Lys Asn Gln Ile Lys Thr Thr Asp Leu Pro Leu Ile Asp
325 330 335

Asp Ile Pro Glu Thr Leu Ser Gln Val Asn Phe Pro Asn Asp Glu Asn
340 345 350

Gln Leu Pro Thr Pro Ile Gly Asn Trp Val Asp Gly Val Glu Val Arg
355 360 365

Tyr Ala Val Gln Tyr Glu Ser Lys Gly Met Tyr Ser Lys Phe Ser Glu
370 375 380

Trp Ser Glu Pro Phe Thr Val Gln Gly Asn Ala Cys Pro Thr Ile Lys
385 390 395 400

Val Arg Val Asp Pro Lys Lys Arg Asn Arg Leu Ile Phe Arg Lys Phe
405 410 415

Asn Ser Gly Lys Pro Gln Phe Ala Gly Thr Met Thr His Ser Gln Thr
420 425 430

Asn Phe Lys Asp Ile His Arg Asp Leu Tyr Asp Ala Ala Leu Asn Ile
435 440 445

Asn Lys Leu Lys Ala Val Asp Glu Ala Thr Thr Leu Ile Glu Lys Gly
450 455 460

Ala Asp Ile Glu Ala Lys Phe Asp Asn Asp Arg Ser Ala Met His Ala
465 470 475 480

Val Ala Tyr Arg Gly Asn Asn Lys Ile Ala Leu Arg Phe Leu Leu Lys
485 490 495

Asn Gln Ser Ile Asp Ile Glu Leu Lys Asp Lys Asn Gly Phe Thr Pro
500 505 510

Leu His Ile Ala Ala Glu Ala Gly Gln Ala Gly Phe Val Lys Leu Leu
515 520 525

Ile Asn His Gly Ala Asp Val Asn Ala Lys Thr Ser Lys Thr Asn Leu
530 535 540

Thr Pro Leu His Leu Ala Thr Arg Ser Gly Phe Ser Lys Thr Val Arg
545 550 555 560

Asn Leu Leu Glu Ser Pro Asn Ile Lys Val Asn Glu Lys Glu Asp Asp
565 570 575

Gly Phe Thr Pro Leu His Thr Ala Val Met Ser Thr Tyr Met Val Val
580 585 590

Asp Ala Leu Leu Asn His Pro Asp Ile Asp Lys Asn Ala Gln Ser Thr
595 600 605

Ser Gly Leu Thr Pro Phe His Leu Ala Ile Ile Asn Glu Ser Gln Glu
610 615 620

Val Ala Glu Ser Leu Val Glu Ser Asn Ala Asp Leu Asn Ile Gln Asp
625 630 635 640

Val Asn His Met Ala Pro Ile His Phe Ala Ala Ser Met Gly Ser Ile
645 650 655

Lys Met Leu Arg Tyr Leu Ile Ser Ile Lys Asp Lys Val Ser Ile Asn
660 665 670

Ser Val Thr Glu Asn Asn Asn Trp Thr Pro Leu His Phe Ala Ile Tyr
675 680 685

Phe Lys Lys Glu Asp Ala Ala Lys Glu Leu Leu Lys Gln Asp Asp Ile
690 695 700

Asn Leu Thr Ile Val Ala Asp Gly Asn Leu Thr Val Leu His Leu Ala
705 710 715 720

Val Ser Thr Gly Gln Ile Asn Ile Ile Lys Glu Leu Leu Lys Arg Gly
725 730 735

Ser Asn Ile Glu Glu Lys Thr Gly Glu Gly Tyr Thr Ser Leu His Ile
740 745 750

Ala Ala Met Arg Lys Glu Pro Glu Ile Ala Val Val Leu Ile Glu Asn
755 760 765

Gly Ala Asp Ile Glu Ala Arg Ser Ala Asp Asn Leu Thr Pro Leu His
770 775 780

Ser Ala Ala Lys Ile Gly Arg Lys Ser Thr Val Leu Tyr Leu Leu Glu
785 790 795 800

Lys Gly Ala Asp Ile Gly Ala Lys Thr Ala Asp Gly Ser Thr Ala Leu
805 810 815

His Leu Ala Val Ser Gly Arg Lys Met Lys Thr Val Glu Thr Leu Leu
820 825 830

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Asn Lys Gly Ala Asn Leu Lys Glu Tyr Asp Asn Asn Lys Tyr Leu Pro
        835                 840                 845

Ile His Lys Ala Ile Ile Asn Asp Asp Leu Asp Met Val Arg Leu Phe
    850                 855                 860

Leu Glu Lys Asp Pro Ser Leu Lys Asp Asp Glu Thr Glu Glu Gly Arg
865                 870                 875                 880

Thr Ser Ile Met Leu Ile Val Gln Lys Leu Leu Leu Glu Leu Tyr Asn
                885                 890                 895

Tyr Phe Ile Asn Asn Tyr Ala Glu Thr Leu Asp Glu Glu Ala Leu Phe
            900                 905                 910

Asn Arg Leu Asp Glu Gln Gly Lys Leu Glu Leu Ala Tyr Ile Phe His
        915                 920                 925

Asn Lys Glu Gly Asp Ala Lys Glu Ala Val Lys Pro Thr Ile Leu Val
    930                 935                 940

Thr Ile Lys Leu Met Glu Tyr Cys Leu Lys Lys Leu Arg Glu Glu Ser
945                 950                 955                 960

Gly Ala Pro Glu Gly Ser Phe Asp Ser Pro Ser Ser Lys Gln Cys Ile
                965                 970                 975

Ser Thr Phe Ser Glu Asp Glu Met Phe Arg Arg Thr Leu Pro Glu  *
            980                 985                 990
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3706 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PLASMID DNA"

(vi) ORIGINAL SOURCE:
(A) ORGANISM: LATRODECTUS MACTANS TREDECIMGUTTATUS

(vii) IMMEDIATE SOURCE:
(B) CLONE: pT7.deltaFL

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:45..3686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
GGTCAATTGA AACTTTATGA TAGGATTCAC TTTCTTATAT AGAA ATG CAT TCC AAA      56
                                                 Met His Ser Lys
                                                 995

GAA TTA CAA ACT ATT TCA GCA GCG GTA GCA CGA AAA GCA GTA CCC AAT      104
Glu Leu Gln Thr Ile Ser Ala Ala Val Ala Arg Lys Ala Val Pro Asn
            1000                1005                1010

ACT ATG GTT ATT CGG TTG AAA AGA GAT GAA GAA GAT GGA GAA ATG ACT      152
Thr Met Val Ile Arg Leu Lys Arg Asp Glu Glu Asp Gly Glu Met Thr
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        1015                1020                1025

CTA GAA GAA AGA CAA GCA CAA TGC AAA GCA ATA GAG TAC AGC AAT TCA      200
Leu Glu Glu Arg Gln Ala Gln Cys Lys Ala Ile Glu Tyr Ser Asn Ser
    1030                1035                1040

GTT TTT GGG ATG ATC GCT GAT GTA GCT AAC GAC ATC GGT TCC ATT CCT      248
Val Phe Gly Met Ile Ala Asp Val Ala Asn Asp Ile Gly Ser Ile Pro
1045                1050                1055                1060

GTA ATT GGC GAA GTA GTT GGC ATT GTA ACT GCC CCA ATT GCC ATC GTA      296
Val Ile Gly Glu Val Val Gly Ile Val Thr Ala Pro Ile Ala Ile Val
                1065                1070                1075

AGT CAC ATT ACT AGC GCA GGC TTG GAT ATA GCT TCT ACG GCA TTA GAT      344
Ser His Ile Thr Ser Ala Gly Leu Asp Ile Ala Ser Thr Ala Leu Asp
            1080                1085                1090

TGT GAT GAT ATA CCT TTT GAT GAG ATT AAG GAA ATA TTA GAA GAA AGA      392
Cys Asp Asp Ile Pro Phe Asp Glu Ile Lys Glu Ile Leu Glu Glu Arg
        1095                1100                1105

TTC AAT GAA ATA GAT AGA AAG TTG GAC AAG AAC ACA GCT GCT TTG GAA      440
Phe Asn Glu Ile Asp Arg Lys Leu Asp Lys Asn Thr Ala Ala Leu Glu
    1110                1115                1120

GAG GTC TCT AAA CTG GTA AGT AAA ACT TTT GTT ACG GTG GAA AAA ACA      488
Glu Val Ser Lys Leu Val Ser Lys Thr Phe Val Thr Val Glu Lys Thr
1125                1130                1135                1140

AGG AAT GAA ATG AAC GAA AAT TTT AAG CTT GTT TTG GAA ACT ATA GAA      536
Arg Asn Glu Met Asn Glu Asn Phe Lys Leu Val Leu Glu Thr Ile Glu
                1145                1150                1155

AGC AAA GAA ATA AAA TCA ATT GTA TTC AAA ATA AAT GAT TTT AAA AAG      584
Ser Lys Glu Ile Lys Ser Ile Val Phe Lys Ile Asn Asp Phe Lys Lys
            1160                1165                1170

TTT TTT GAA AAA GAA CGA CAA AGA ATT AAA GGT TTG CCT AAA GAT AGG      632
Phe Phe Glu Lys Glu Arg Gln Arg Ile Lys Gly Leu Pro Lys Asp Arg
        1175                1180                1185

TAT GTT GCT AAG CTT CTA GAA CAA AAA GGT ATT TTA GGT TCT TTA AAA      680
Tyr Val Ala Lys Leu Leu Glu Gln Lys Gly Ile Leu Gly Ser Leu Lys
    1190                1195                1200

GAA GTA AGA GAA CCA TCT GGA AAC AGT CTG AGC TCC GCG TTA AAT GAA      728
Glu Val Arg Glu Pro Ser Gly Asn Ser Leu Ser Ser Ala Leu Asn Glu
1205                1210                1215                1220

CTC TTA GAC AAA AAC AAC AAC TAT GCC ATC CCA AAA GTG GTT GAT GAT      776
Leu Leu Asp Lys Asn Asn Asn Tyr Ala Ile Pro Lys Val Val Asp Asp
                1225                1230                1235

AAT AAG GCC TTT CAG GCG CTG TAT GCT TTA TTT TAT GGA ACT CAG ACT      824
Asn Lys Ala Phe Gln Ala Leu Tyr Ala Leu Phe Tyr Gly Thr Gln Thr
            1240                1245                1250

TAT GCA GCC GTT ATG TTT TTC TTA CTC GAA CAA CAT TCT TAT CTG GCT      872
Tyr Ala Ala Val Met Phe Phe Leu Leu Glu Gln His Ser Tyr Leu Ala
        1255                1260                1265

GAT TAT TAT TAC CAA AAA GGT GAT GAT GTA AAT TTT AAT GCA GAA TTT      920
Asp Tyr Tyr Tyr Gln Lys Gly Asp Asp Val Asn Phe Asn Ala Glu Phe
    1270                1275                1280
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AAT AAT GTA GCA ATT ATT TTT GAT GAC TTT AAA TCA TCA CTA ACA GGA 968
Asn Asn Val Ala Ile Ile Phe Asp Asp Phe Lys Ser Ser Leu Thr Gly
1285 1290 1295 1300

GGA GAT GAC GGA TTA ATA GAT AAT GTC ATT GAG GTT CTT AAC ACC GTG 1016
Gly Asp Asp Gly Leu Ile Asp Asn Val Ile Glu Val Leu Asn Thr Val
1305 1310 1315

AAA GCA TTA CCA TTT ATA AAG AAC GCC GAC AGT AAA CTA TAC AGA GAA 1064
Lys Ala Leu Pro Phe Ile Lys Asn Ala Asp Ser Lys Leu Tyr Arg Glu
1320 1325 1330

TTA GTA ACT AGA ACA AAA GCT TTA GAG ACT CTT AAA AAT CAA ATC AAA 1112
Leu Val Thr Arg Thr Lys Ala Leu Glu Thr Leu Lys Asn Gln Ile Lys
1335 1340 1345

ACG ACT GAT TTG CCT CTT ATA GAT GAT ATA CCC GAA ACT TTG TCT CAA 1160
Thr Thr Asp Leu Pro Leu Ile Asp Asp Ile Pro Glu Thr Leu Ser Gln
1350 1355 1360

GTG AAC TTT CCG AAT GAC GAA AAT CAA TTG CCT ACA CCA ATA GGA AAT 1208
Val Asn Phe Pro Asn Asp Glu Asn Gln Leu Pro Thr Pro Ile Gly Asn
1365 1370 1375 1380

TGG GTT GAT GGC GTA GAA GTT AGG TAC GCA GTA CAG TAT GAA AGT AAG 1256
Trp Val Asp Gly Val Glu Val Arg Tyr Ala Val Gln Tyr Glu Ser Lys
1385 1390 1395

GGC ATG TAT TCG AAA TTC AGT GAA TGG TCT GAA CCA TTT ACT GTC CAA 1304
Gly Met Tyr Ser Lys Phe Ser Glu Trp Ser Glu Pro Phe Thr Val Gln
1400 1405 1410

GGT AAC GCT TGT CCG ACT ATA AAA GTT CGT GTT GAT CCG AAA AAG AGA 1352
Gly Asn Ala Cys Pro Thr Ile Lys Val Arg Val Asp Pro Lys Lys Arg
1415 1420 1425

AAT AGA CTT ATC TTT AGG AAG TTC AAC TCA GGA AAA CCT CAG TTT GCT 1400
Asn Arg Leu Ile Phe Arg Lys Phe Asn Ser Gly Lys Pro Gln Phe Ala
1430 1435 1440

GGA ACC ATG ACT CAT TCA CAA ACA AAT TTT AAA GAT ATT CAT CGT GAT 1448
Gly Thr Met Thr His Ser Gln Thr Asn Phe Lys Asp Ile His Arg Asp
1445 1450 1455 1460

CTA TAC GAT GCA GCC TTA AAT ATT AAT AAG TTG AAA GCA GTG GAT GAA 1496
Leu Tyr Asp Ala Ala Leu Asn Ile Asn Lys Leu Lys Ala Val Asp Glu
1465 1470 1475

GCT ACA ACT TTG ATT GAA AAG GGT GCA GAC ATA GAA GCA AAA TTT GAC 1544
Ala Thr Thr Leu Ile Glu Lys Gly Ala Asp Ile Glu Ala Lys Phe Asp
1480 1485 1490

AAT GAC AGA AGT GCA ATG CAC GCA GTT GCA TAT CGA GGA AAT AAC AAA 1592
Asn Asp Arg Ser Ala Met His Ala Val Ala Tyr Arg Gly Asn Asn Lys
1495 1500 1505

ATA GCC TTA AGA TTT CTT TTG AAA AAT CAA TCC ATT GAC ATC GAG TTA 1640
Ile Ala Leu Arg Phe Leu Leu Lys Asn Gln Ser Ile Asp Ile Glu Leu
1510 1515 1520

AAA GAT AAA AAC GGC TTT ACT CCT CTA CAC ATC GCA GCT GAA GCA GGT 1688
Lys Asp Lys Asn Gly Phe Thr Pro Leu His Ile Ala Ala Glu Ala Gly
1525 1530 1535 1540

CAG GCA GGA TTT GTT AAG TTA CTA ATA AAT CAT GGA GCT GAT GTG AAT 1736
Gln Ala Gly Phe Val Lys Leu Leu Ile Asn His Gly Ala Asp Val Asn

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                1545                1550                1555

GCA AAA ACA AGT AAG ACA AAT TTG ACA CCA TTA CAT CTT GCA ACA CGT   1784
Ala Lys Thr Ser Lys Thr Asn Leu Thr Pro Leu His Leu Ala Thr Arg
          1560                1565                1570

AGT GGA TTT TCA AAA ACT GTA AGA AAT TTA CTA GAA AGC CCA AAT ATT   1832
Ser Gly Phe Ser Lys Thr Val Arg Asn Leu Leu Glu Ser Pro Asn Ile
     1575                1580                1585

AAG GTA AAT GAA AAG GAG GAT GAC GGA TTT ACA CCT TTG CAT ACT GCA   1880
Lys Val Asn Glu Lys Glu Asp Asp Gly Phe Thr Pro Leu His Thr Ala
1590                1595                1600

GTA ATG AGT ACT TAT ATG GTT GTC GAT GCT TTG CTA AAT CAT CCA GAC   1928
Val Met Ser Thr Tyr Met Val Val Asp Ala Leu Leu Asn His Pro Asp
1605                1610                1615                1620

ATT GAT AAA AAT GCG CAG TCT ACG TCA GGA TTG ACT CCT TTC CAT TTA   1976
Ile Asp Lys Asn Ala Gln Ser Thr Ser Gly Leu Thr Pro Phe His Leu
                1625                1630                1635

GCA ATT ATT AAT GAA AGT CAA GAA GTT GCA GAA TCT TTA GTG GAA AGT   2024
Ala Ile Ile Asn Glu Ser Gln Glu Val Ala Glu Ser Leu Val Glu Ser
          1640                1645                1650

AAT GCT GAT CTA AAT ATT CAG GAT GTT AAC CAT ATG GCT CCT ATT CAT   2072
Asn Ala Asp Leu Asn Ile Gln Asp Val Asn His Met Ala Pro Ile His
     1655                1660                1665

TTT GCA GCT TCA ATG GGT AGT ATT AAA ATG CTT AGA TAT CTC ATT TCC   2120
Phe Ala Ala Ser Met Gly Ser Ile Lys Met Leu Arg Tyr Leu Ile Ser
1670                1675                1680

ATA AAA GAT AAA GTT AGT ATT AAT TCT GTG ACT GAG AAT AAT AAC TGG   2168
Ile Lys Asp Lys Val Ser Ile Asn Ser Val Thr Glu Asn Asn Asn Trp
1685                1690                1695                1700

ACA CCT TTA CAT TTT GCT ATA TAT TTT AAA AAA GAA GAT GCT GCA AAA   2216
Thr Pro Leu His Phe Ala Ile Tyr Phe Lys Lys Glu Asp Ala Ala Lys
                1705                1710                1715

GAA TTG TTG AAA CAA GAT GAC ATA AAT TTA ACA ATT GTT GCA GAT GGT   2264
Glu Leu Leu Lys Gln Asp Asp Ile Asn Leu Thr Ile Val Ala Asp Gly
          1720                1725                1730

AAT CTT ACC GTT TTA CAT CTT GCT GTT TCG ACA GGA CAA ATA AAT ATA   2312
Asn Leu Thr Val Leu His Leu Ala Val Ser Thr Gly Gln Ile Asn Ile
     1735                1740                1745

ATT AAA GAA TTA TTG AAG AGA GGC TCC AAT ATA GAA GAA AAA ACT GGA   2360
Ile Lys Glu Leu Leu Lys Arg Gly Ser Asn Ile Glu Glu Lys Thr Gly
1750                1755                1760

GAA GGA TAT ACA TCT CTC CAC ATC GCT GCG ATG CGA AAG GAG CCA GAG   2408
Glu Gly Tyr Thr Ser Leu His Ile Ala Ala Met Arg Lys Glu Pro Glu
1765                1770                1775                1780

ATA GCT GTT GTT TTG ATT GAA AAC GGT GCT GAC ATA GAA GCT CGA TCA   2456
Ile Ala Val Val Leu Ile Glu Asn Gly Ala Asp Ile Glu Ala Arg Ser
                1785                1790                1795

GCT GAT AAT TTA ACA CCT TTA CAT TCT GCC GCA AAA ATA GGA AGG AAA   2504
Ala Asp Asn Leu Thr Pro Leu His Ser Ala Ala Lys Ile Gly Arg Lys
          1800                1805                1810
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TCT ACA GTA CTT TAC TTA TTA GAA AAA GGA GCT GAC ATT GGA GCT AAA          2552
Ser Thr Val Leu Tyr Leu Leu Glu Lys Gly Ala Asp Ile Gly Ala Lys
        1815                1820                1825

ACA GCA GAC GGT TCT ACT GCC TTG CAT TTA GCT GTA TCT GGT CGT AAA          2600
Thr Ala Asp Gly Ser Thr Ala Leu His Leu Ala Val Ser Gly Arg Lys
    1830                1835                1840

ATG AAA ACT GTT GAA ACT CTA TTA AAT AAA GGA GCA AAT TTA AAA GAA          2648
Met Lys Thr Val Glu Thr Leu Leu Asn Lys Gly Ala Asn Leu Lys Glu
1845                1850                1855                1860

TAC GAT AAC AAT AAA TAT TTG CCA ATA CAT AAA GCT ATT ATT AAT GAT          2696
Tyr Asp Asn Asn Lys Tyr Leu Pro Ile His Lys Ala Ile Ile Asn Asp
                1865                1870                1875

GAC CTT GAC ATG GTA CGT TTG TTT CTT GAA AAA GAT CCC AGT CTC AAA          2744
Asp Leu Asp Met Val Arg Leu Phe Leu Glu Lys Asp Pro Ser Leu Lys
            1880                1885                1890

GAT GAT GAA ACA GAA GAG GGT AGA ACT TCA ATT ATG TTA ATT GTT CAG          2792
Asp Asp Glu Thr Glu Glu Gly Arg Thr Ser Ile Met Leu Ile Val Gln
        1895                1900                1905

AAA TTG CTT CTT GAA TTA TAT AAC TAT TTT ATA AAT AAT TAT GCT GAA          2840
Lys Leu Leu Leu Glu Leu Tyr Asn Tyr Phe Ile Asn Asn Tyr Ala Glu
    1910                1915                1920

ACT TTG GAT GAA GAA GCT TTA TTC AAC CGC TTA GAT GAA CAA GGG AAA          2888
Thr Leu Asp Glu Glu Ala Leu Phe Asn Arg Leu Asp Glu Gln Gly Lys
1925                1930                1935                1940

TTA GAG CTT GCA TAT ATC TTC CAT AAT AAA GAA GGT GAT GCA AAA GAG          2936
Leu Glu Leu Ala Tyr Ile Phe His Asn Lys Glu Gly Asp Ala Lys Glu
                1945                1950                1955

GCT GTT AAG CCA ACT ATC CTT GTT ACA ATT AAA CTT ATG GAA TAC TGC          2984
Ala Val Lys Pro Thr Ile Leu Val Thr Ile Lys Leu Met Glu Tyr Cys
            1960                1965                1970

TTA AAA AAA CTT CGC GAA GAG TCT GGA GCT CCT GAA GGT AGT TTC GAT          3032
Leu Lys Lys Leu Arg Glu Glu Ser Gly Ala Pro Glu Gly Ser Phe Asp
        1975                1980                1985

TCT CCA TCT TCA AAG CAA TGT ATT TCT ACC TTT TCA GAG GAT GAA ATG          3080
Ser Pro Ser Ser Lys Gln Cys Ile Ser Thr Phe Ser Glu Asp Glu Met
    1990                1995                2000

TTT CGT CGT ACT TTA CCG GAA ATT GTA AAA GAA ACG AAC AGC AGA TAT          3128
Phe Arg Arg Thr Leu Pro Glu Ile Val Lys Glu Thr Asn Ser Arg Tyr
2005                2010                2015                2020

TTA CCA CTA AAG GGC TTT TCT CGC AGC CTA AAT AAG TTT CTC CCT TCT          3176
Leu Pro Leu Lys Gly Phe Ser Arg Ser Leu Asn Lys Phe Leu Pro Ser
                2025                2030                2035

CTA AAA TTT GCC GAA AGT AAG AAT AGC TAC AGA TCT GAA AAT TTT GTT          3224
Leu Lys Phe Ala Glu Ser Lys Asn Ser Tyr Arg Ser Glu Asn Phe Val
            2040                2045                2050

AGC AAT ATT GAT TCC AAC GGA GCA TTA CTT TTA CTC GAT GTA TTT ATC          3272
Ser Asn Ile Asp Ser Asn Gly Ala Leu Leu Leu Leu Asp Val Phe Ile
        2055                2060                2065

AGA AAG TTT ACT AAT GAG AAA TAC AAT TTG ACT GGA AAA GAA GCT GTA          3320
Arg Lys Phe Thr Asn Glu Lys Tyr Asn Leu Thr Gly Lys Glu Ala Val
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2070                2075                2080

CCC TAT CTG GAA GCA AAG GCT TCA TCA TTA CGT ATC GCT TCT AAA TTT      3368
Pro Tyr Leu Glu Ala Lys Ala Ser Ser Leu Arg Ile Ala Ser Lys Phe
2085                2090                2095                2100

GAA GAA CTT CTA ACT GAA GTT AAA GGT ATT CCG GCT GGA GAG CTA ATT      3416
Glu Glu Leu Leu Thr Glu Val Lys Gly Ile Pro Ala Gly Glu Leu Ile
                2105                2110                2115

AAT ATG GCC GAA GTG AGT TCC AAC ATA CAT AAG GCA ATT GCA AGT GGT      3464
Asn Met Ala Glu Val Ser Ser Asn Ile His Lys Ala Ile Ala Ser Gly
            2120                2125                2130

AAG CCT GTA TCA AAA GTC TTA TGT TCG TAT TTG GAT ACC TTT TCT GAA      3512
Lys Pro Val Ser Lys Val Leu Cys Ser Tyr Leu Asp Thr Phe Ser Glu
        2135                2140                2145

TTA AAT TCT CAA CAA ATG GAA GAA TTA GTT AAC ACA TAC TTA TCC ACC      3560
Leu Asn Ser Gln Gln Met Glu Glu Leu Val Asn Thr Tyr Leu Ser Thr
    2150                2155                2160

AAA CCT TCT GTA ATT ACG TCA GCA TCT GCA GAT TAC CAG AAA CTT CCT      3608
Lys Pro Ser Val Ile Thr Ser Ala Ser Ala Asp Tyr Gln Lys Leu Pro
2165                2170                2175                2180

AAT TTG TTA ACT GCA ACT TGC TTA GAA CCA GAA AGA ATG GCT CAA CTT      3656
Asn Leu Leu Thr Ala Thr Cys Leu Glu Pro Glu Arg Met Ala Gln Leu
                2185                2190                2195

ATA GAT GTG CAT CAA AAG ATG TTT TTA CGT TAAAATACCA TTCCTTCTGT       3706
Ile Asp Val His Gln Lys Met Phe Leu Arg
            2200                2205
```

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1214 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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Met His Ser Lys Glu Leu Gln Thr Ile Ser Ala Ala Val Ala Arg Lys
 1               5                  10                  15

Ala Val Pro Asn Thr Met Val Ile Arg Leu Lys Arg Asp Glu Glu Asp
            20                  25                  30

Gly Glu Met Thr Leu Glu Glu Arg Gln Ala Gln Cys Lys Ala Ile Glu
        35                  40                  45

Tyr Ser Asn Ser Val Phe Gly Met Ile Ala Asp Val Ala Asn Asp Ile
    50                  55                  60

Gly Ser Ile Pro Val Ile Gly Glu Val Val Gly Ile Val Thr Ala Pro
65                  70                  75                  80

Ile Ala Ile Val Ser His Ile Thr Ser Ala Gly Leu Asp Ile Ala Ser
                85                  90                  95

Thr Ala Leu Asp Cys Asp Asp Ile Pro Phe Asp Glu Ile Lys Glu Ile
            100                 105                 110
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Leu Glu Glu Arg Phe Asn Glu Ile Asp Arg Lys Leu Asp Lys Asn Thr
115 120 125

Ala Ala Leu Glu Glu Val Ser Lys Leu Val Ser Lys Thr Phe Val Thr
130 135 140

Val Glu Lys Thr Arg Asn Glu Met Asn Glu Asn Phe Lys Leu Val Leu
145 150 155 160

Glu Thr Ile Glu Ser Lys Glu Ile Lys Ser Ile Val Phe Lys Ile Asn
165 170 175

Asp Phe Lys Lys Phe Phe Glu Lys Glu Arg Gln Arg Ile Lys Gly Leu
180 185 190

Pro Lys Asp Arg Tyr Val Ala Lys Leu Leu Glu Gln Lys Gly Ile Leu
195 200 205

Gly Ser Leu Lys Glu Val Arg Glu Pro Ser Gly Asn Ser Leu Ser Ser
210 215 220

Ala Leu Asn Glu Leu Leu Asp Lys Asn Asn Asn Tyr Ala Ile Pro Lys
225 230 235 240

Val Val Asp Asp Asn Lys Ala Phe Gln Ala Leu Tyr Ala Leu Phe Tyr
245 250 255

Gly Thr Gln Thr Tyr Ala Ala Val Met Phe Phe Leu Leu Glu Gln His
260 265 270

Ser Tyr Leu Ala Asp Tyr Tyr Tyr Gln Lys Gly Asp Asp Val Asn Phe
275 280 285

Asn Ala Glu Phe Asn Asn Val Ala Ile Ile Phe Asp Asp Phe Lys Ser
290 295 300

Ser Leu Thr Gly Gly Asp Asp Gly Leu Ile Asp Asn Val Ile Glu Val
305 310 315 320

Leu Asn Thr Val Lys Ala Leu Pro Phe Ile Lys Asn Ala Asp Ser Lys
325 330 335

Leu Tyr Arg Glu Leu Val Thr Arg Thr Lys Ala Leu Glu Thr Leu Lys
340 345 350

Asn Gln Ile Lys Thr Thr Asp Leu Pro Leu Ile Asp Asp Ile Pro Glu
355 360 365

Thr Leu Ser Gln Val Asn Phe Pro Asn Asp Glu Asn Gln Leu Pro Thr
370 375 380

Pro Ile Gly Asn Trp Val Asp Gly Val Glu Val Arg Tyr Ala Val Gln
385 390 395 400

Tyr Glu Ser Lys Gly Met Tyr Ser Lys Phe Ser Glu Trp Ser Glu Pro
405 410 415

Phe Thr Val Gln Gly Asn Ala Cys Pro Thr Ile Lys Val Arg Val Asp
420 425 430

Pro Lys Lys Arg Asn Arg Leu Ile Phe Arg Lys Phe Asn Ser Gly Lys
435 440 445

Pro Gln Phe Ala Gly Thr Met Thr His Ser Gln Thr Asn Phe Lys Asp
450 455 460

Ile His Arg Asp Leu Tyr Asp Ala Ala Leu Asn Ile Asn Lys Leu Lys
465 470 475 480

Ala Val Asp Glu Ala Thr Thr Leu Ile Glu Lys Gly Ala Asp Ile Glu
485 490 495

Ala Lys Phe Asp Asn Asp Arg Ser Ala Met His Ala Val Ala Tyr Arg
500 505 510

Gly Asn Asn Lys Ile Ala Leu Arg Phe Leu Leu Lys Asn Gln Ser Ile
515 520 525

Asp Ile Glu Leu Lys Asp Lys Asn Gly Phe Thr Pro Leu His Ile Ala
530 535 540

Ala Glu Ala Gly Gln Ala Gly Phe Val Lys Leu Leu Ile Asn His Gly
545 550 555 560

Ala Asp Val Asn Ala Lys Thr Ser Lys Thr Asn Leu Thr Pro Leu His
565 570 575

Leu Ala Thr Arg Ser Gly Phe Ser Lys Thr Val Arg Asn Leu Leu Glu
580 585 590

Ser Pro Asn Ile Lys Val Asn Glu Lys Glu Asp Asp Gly Phe Thr Pro
595 600 605

Leu His Thr Ala Val Met Ser Thr Tyr Met Val Val Asp Ala Leu Leu
610 615 620

Asn His Pro Asp Ile Asp Lys Asn Ala Gln Ser Thr Ser Gly Leu Thr
625 630 635 640

Pro Phe His Leu Ala Ile Ile Asn Glu Ser Gln Glu Val Ala Glu Ser
645 650 655

Leu Val Glu Ser Asn Ala Asp Leu Asn Ile Gln Asp Val Asn His Met
660 665 670

Ala Pro Ile His Phe Ala Ala Ser Met Gly Ser Ile Lys Met Leu Arg
675 680 685

Tyr Leu Ile Ser Ile Lys Asp Lys Val Ser Ile Asn Ser Val Thr Glu
690 695 700

Asn Asn Asn Trp Thr Pro Leu His Phe Ala Ile Tyr Phe Lys Lys Glu
705 710 715 720

Asp Ala Ala Lys Glu Leu Leu Lys Gln Asp Asp Ile Asn Leu Thr Ile
725 730 735

Val Ala Asp Gly Asn Leu Thr Val Leu His Leu Ala Val Ser Thr Gly
740 745 750

Gln Ile Asn Ile Ile Lys Glu Leu Leu Lys Arg Gly Ser Asn Ile Glu
755 760 765

Glu Lys Thr Gly Glu Gly Tyr Thr Ser Leu His Ile Ala Ala Met Arg
770 775 780

Lys Glu Pro Glu Ile Ala Val Val Leu Ile Glu Asn Gly Ala Asp Ile
785 790 795 800

Glu Ala Arg Ser Ala Asp Asn Leu Thr Pro Leu His Ser Ala Ala Lys
805 810 815

Ile Gly Arg Lys Ser Thr Val Leu Tyr Leu Leu Glu Lys Gly Ala Asp
820 825 830

Ile Gly Ala Lys Thr Ala Asp Gly Ser Thr Ala Leu His Leu Ala Val
835 840 845

Ser Gly Arg Lys Met Lys Thr Val Glu Thr Leu Leu Asn Lys Gly Ala
850 855 860

Asn Leu Lys Glu Tyr Asp Asn Asn Lys Tyr Leu Pro Ile His Lys Ala
865 870 875 880

Ile Ile Asn Asp Asp Leu Asp Met Val Arg Leu Phe Leu Glu Lys Asp
885 890 895

Pro Ser Leu Lys Asp Asp Glu Thr Glu Glu Gly Arg Thr Ser Ile Met
900 905 910

Leu Ile Val Gln Lys Leu Leu Leu Glu Leu Tyr Asn Tyr Phe Ile Asn
915 920 925

Asn Tyr Ala Glu Thr Leu Asp Glu Glu Ala Leu Phe Asn Arg Leu Asp
930 935 940

Glu Gln Gly Lys Leu Glu Leu Ala Tyr Ile Phe His Asn Lys Glu Gly
945 950 955 960

Asp Ala Lys Glu Ala Val Lys Pro Thr Ile Leu Val Thr Ile Lys Leu
965 970 975

Met Glu Tyr Cys Leu Lys Lys Leu Arg Glu Glu Ser Gly Ala Pro Glu
980 985 990

Gly Ser Phe Asp Ser Pro Ser Ser Lys Gln Cys Ile Ser Thr Phe Ser
995 1000 1005

Glu Asp Glu Met Phe Arg Arg Thr Leu Pro Glu Ile Val Lys Glu Thr
1010 1015 1020

Asn Ser Arg Tyr Leu Pro Leu Lys Gly Phe Ser Arg Ser Leu Asn Lys
1025 1030 1035 1040

Phe Leu Pro Ser Leu Lys Phe Ala Glu Ser Lys Asn Ser Tyr Arg Ser
1045 1050 1055

Glu Asn Phe Val Ser Asn Ile Asp Ser Asn Gly Ala Leu Leu Leu Leu
1060 1065 1070

Asp Val Phe Ile Arg Lys Phe Thr Asn Glu Lys Tyr Asn Leu Thr Gly
1075 1080 1085

Lys Glu Ala Val Pro Tyr Leu Glu Ala Lys Ala Ser Ser Leu Arg Ile
1090 1095 1100

Ala Ser Lys Phe Glu Glu Leu Leu Thr Glu Val Lys Gly Ile Pro Ala
1105 1110 1115 1120

Gly Glu Leu Ile Asn Met Ala Glu Val Ser Ser Asn Ile His Lys Ala
1125 1130 1135

Ile Ala Ser Gly Lys Pro Val Ser Lys Val Leu Cys Ser Tyr Leu Asp
1140 1145 1150

Thr Phe Ser Glu Leu Asn Ser Gln Gln Met Glu Glu Leu Val Asn Thr
1155 1160 1165

Tyr Leu Ser Thr Lys Pro Ser Val Ile Thr Ser Ala Ser Ala Asp Tyr
1170 1175 1180

Gln Lys Leu Pro Asn Leu Leu Thr Ala Thr Cys Leu Glu Pro Glu Arg
1185 1190 1195 1200

Met Ala Gln Leu Ile Asp Val His Gln Lys Met Phe Leu Arg
1205 1210

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CLAIMS

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1. A polypeptide, such as a toxin, formed by expression of a truncated form of a gene sequence, or an analogue thereof.

2. A polypeptide as claimed in claim 1, in which the polypeptide is a neurotoxin.

3. A polypeptide as claimed in any preceding claim, in which the polypeptide corresponds to a toxic derivative of a substantially non-toxic precursor polypeptide encoded by the gene sequence.

4. A polypeptide as claimed in any preceding claim, in which the polypeptide comprises an amino acid sequence that corresponds to a truncated form of the amino acid sequence of a substantially non-toxic precursor polypeptide.

5. A polypeptide as claimed in claim 4, in which the amino acid sequence of the polypeptide corresponds to the amino acid sequence of the precursor polypeptide with truncation thereof principally at the carboxy (C) end.

6. A polypeptide as claimed in claim 5, in which truncation is by about 150 to 200 amino acids.

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7. A polypeptide as claimed in any of claims 4 to 6, in which the polypeptide amino acid sequence in addition corresponds to the precursor polypeptide amino acid sequence truncated at the amino end (N).

8. A polypeptide as claimed in claim 7, in which the truncation is by less than 50 amino acids, and desirably by 7 or 28 amino acids.

9. A polypeptide as claimed in any preceding claim, in which the amino acid sequence of the polypeptide is homologous to the amino acid sequence of the insect specific neurotoxin δ-Latroinsectotoxin (δ-LIT) or an active derivative thereof.

10. A polypeptide as claimed in any preceding claim, in which the polypeptide comprises an amino acid sequence as shown in SEQIDNO1 and SEQIDNO2 or an active derivative thereof.

11. A polypeptide as claimed in any preceding claim, in which the toxin is expressed from a nucleotide construct or truncated form of a gene sequence comprising a sequence as shown in SEQIDNO1, or active variants thereof.

12. A polypeptide as claimed in any preceding claim, in

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which the polypeptide is expressed from a sequence substantially as provided in a microorganism deposited at The National Collections of Industrial and Marine Bacteria Limited, under Accession No. NCIMB 40632.

13. A protein for use as a toxin comprising an amino acid sequence substantially as shown in SEQIDNO1 and SEQIDNO2, or an active derivative thereof.

14. A nucleotide sequence comprising a truncated form of a gene sequence or an analogue thereof, for use in the expression of a polypeptide, such as a toxin.

15. A nucleotide sequence as claimed in claim 14, in which the nucleotide sequence corresponds to a gene encoding for a precursor polypeptide and truncated at the 3' end thereof, or an active derivative thereof.

16. A nucleotide sequence as claimed in claim 15, in which the nucleotide sequence corresponds to the gene truncated by about 400 to 650 nucleotide bases, and desirably between 550 to 600 nucleotide bases.

17. A nucleotide sequence as claimed in any of claims 14 to 16, in which the nucleotide sequence corresponds to the gene truncated at the 5' thereof.

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18. A nucleotide sequence as claimed in claim 17, in which the truncation is by less than 100 nucleotide bases, and desirably by either 84 or 21 nucleotide bases.

19. A nucleotide sequence as claimed in any of claims 14 to 18, in which the nucleotide sequence corresponds to part of a gene encoding for a neurotoxin in the venom of the Black Widow Spider (Latrodectus mactans Tredecimguttatus), or an active derivative thereof.

20. A nucleotide sequence as claimed in claim 19, in which the nucleotide sequence corresponds to part of the gene encoding the precursor polypeptide of insect specific toxin δ-Lactoinsectotoxin (δ-LIT), or an active derivative thereof.

21. A nucleotide sequence as claimed in any of claims 14 to 20, in which the nucleotide sequence codes for a polypeptide comprising a sequence of 991 amino acids.

22. A nucleotide sequence as claimed in any of claims 14 to 21, in which the nucleotide sequence comprises a base sequence as shown in SEQIDNO1, or an active derivative thereof.

23. A nucleotide sequence as claimed in any of claims 14 to 22, in which the nucleotide sequences comprises a

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base sequence substantially as comprised in a micro-organism deposited under Accession No. NCIMB 40632 at The National Collections of Industrial and Marine Bacteria Limited.

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24. A nucleotide sequence as claimed in any of claims 14 to 23, in which the nucleotide sequence codes for a polypeptide having an amino acid sequence as shown in SEQIDNO1 and SEQIDNO2, or an active derivative thereof.

25. A nucleotide sequence as claimed in any of claims 14 to 24, in which the nucleotide sequence is a cDNA derived from mRNA by the use of an enzyme such as reverse transcriptase.

26. A nucleotide sequence as claimed in any of claims 14 to 25, in which the nucleotide sequence is an oligonucleotide DNA construct produced perhaps using the polymerase chain reaction (PCR).

27. A method of producing a polypeptide, the method comprising producing a recombinant DNA molecule comprising a truncated form of a gene, and expressing the truncated form in a host expression system, such as a viral or bacterial expression system, to produce the polypeptide.

28. A method as claimed in claim 27, in which the

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polypeptide produced is an active toxin substantially as claimed in any preceding claim.

29. A method as claimed in claim 27 or claim 28, in which the truncated form comprises part of a gene which encodes for a non-toxic precursor polypeptide.

30. A method as claimed in any of claims 27 to 29, in which the truncated form comprises a nucleotide sequence substantially as claimed in any of claims 14 to 26.

31. A method as claimed in any of claims 27 to 30, in which the expression system comprises E.coli BL21 (DE3) bacterial cells transformed with pT7-7 vectors comprising the truncated form of the sequence.

32. A method as claimed in any of claims 27 to 31, in which the expression system comprises a baculovirus system.

33. A recombinant DNA molecule comprising a truncated form of a gene encoding for a toxin generally as claimed in any preceding claim.

34. A recombinant DNA molecule as claimed in claim 33, in which the molecule comprises a virus.

35. A recombinant DNA molecule as claimed in claim 34,

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in which the molecule comprises a baculovirus.

36. A recombinant DNA molecule substantially as provided in the microorganism deposited under Accession No. NCIMB 40632.

37. An expression vector comprising a truncated form of a gene generally as claimed in any of claims 14 to 26.

38. A cell, such as a viral or bacterial cell transformed with a recombinant molecule substantially as claimed in any of claims 33 to 37.

39. An insecticide comprising a toxin substantially as claimed in any of claims 1 to 13.

40. An insecticide as claimed in claim 39, in which the insecticide is so as to be administered orally or topically.

41. An insecticide as claimed in claim 39 or claim 40, in which the insecticide comprises a spray.

42. An insecticide system comprising means for expressing a truncated form of a gene to produce a toxin substantially as claimed in any preceding claim in an insect to kill or incapacitate the insect.

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43. An insecticide system as claimed in claim 42, in which the insecticide system comprises a viral expression system.

44. An insecticide system as claimed in claim 43, in which the viral expression system comprises a baculovirus expression system.

45. A plant comprising a genetically modified cell containing a truncated form of a gene sequence substantially as claimed in any of claims 14 to 26.

46. A non-human animal comprising a genetically modified cell containing a truncated form of a gene sequence substantially as claimed in any of claims 14 to 26.

47. A toxin formed by processing of a substantially isolated non-toxic precursor polypeptide.

48. A toxin as claimed in claim 47, in which the toxin is formed by truncation toward the carboxy (C) end of the precursor polypeptide.

49. A toxin as claimed in claim 48, in which the toxin amino acid sequence generally corresponds to the amino acid sequence of the precursor polypeptide, truncated by between 150 and 200 amino acids.

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50. A toxin as claimed in any of claims 47 to 49, in which the toxin amino acid sequence is formed by truncation toward the amino (N) end of the precursor polypeptide amino acid sequence.

51. A toxin as claimed in claim 50, in which the fragment cleaved from the amino end is significantly smaller than the fragment cleaved from the carboxy end.

52. A toxin as claimed in claim 50 or claim 51, in which the fragment cleaved off comprises 7 or 28 amino acids.

53. A toxin as claimed in any of claims 47 to 52, in which the toxin has an amino acid sequence corresponding to a polypeptide encoded by part of a gene of the Black Widow Spider (Latrodectus mactans Tredecimguttatus).

54. A toxin as claimed in any of claims 47 to 53, in which the toxin comprises or is an analogue of the insect specific neurotoxin δ-Latroinsectotoxin (δ-LIT), or an active derivative thereof.

55. A toxin as claimed in any of claims 47 to 54, in which the toxin comprises an amino acid sequence as shown in SEQIDNO1 and SEQIDNO2 or an active derivative thereof.

56. A method of producing an active polypeptide from an

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isolated inactive precursor polypeptide, the method comprising truncating the isolated precursor polypeptide.

57. A method as claimed in claim 56, in which the isolated precursor polypeptide is truncated at the Carboxyl end.

58. A method as claimed in claim 56 or claim 57, in which the truncation is effected using proteolytic cleavage, and preferably by site directed mutagenesis.

59. A method as claimed in any of claims 56 to 58, in which truncation of the N terminus may be provided.

60. A method as claimed in claims 56 to 59, in which the active polypeptide is a toxin and is substantially as claimed in any of claims 1 to 13, 47 to 55.

61. An isolated nucleotide base sequence encoding for a toxin precursor polypeptide with an amino acid sequence as shown in SEQIDNO4 or a derivative thereof.

62. An isolated base sequence comprising a base sequence as shown in SEQIDNO3 or a derivative thereof.

63. An isolated base sequence as claimed in any of claims 61 or 62, in which the nucleotide base sequence encodes a precursor polypeptide of the neurotoxin

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δ-Latroinsectotoxin (δ-LIT).

64. An isolated base sequence substantially as provided in the microorganism deposited under Accession No. NCIMB 40633.

65. A recombinant DNA molecule comprising a sequence substantially as claimed in any of claims 61 to 64.

66. A recombinant molecule as claimed in claim 65, in which the molecule comprises a virus.

67. A recombinant molecule as claimed in claim 66, in which the virus comprises a baculovirus.

68. A cell, such as a bacterial or viral cell, transformed with a recombinant DNA molecule substantially as claimed in any of claims 65 to 67.

69. An insecticide system comprising means for expressing a base sequence substantially as claimed in any of claims 61 to 64 to produce a precursor polypeptide and to process the precursor polypeptide to produce a toxin in an insect to kill or incapacitate the insect.

70. An insecticide system as claimed in claim 69, in which the system comprises a viral expression system.

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71. An insecticide system as claimed in claim 69, in which the viral expression system comprises baculovirus.

72. A plant comprising a genetically modified cell containing a nucleotide sequence substantially as claimed in any of claims 61 to 64.

73. A non-human animal comprising a genetically modified cell containing a nucleotide sequence substantially as claimed in any of claims 61 to 64.

74. A novel toxin substantially as hereinbefore described with reference to SEQIDNO1 and SEQIDNO2.

75. A nucleotide sequence substantially as hereinbefore described with reference to SEQIDNO1.

76. An isolated polypeptide substantially as hereinbefore described with reference to SEQIDNO3 and SEQIDNO4.

77. An isolated nucleotide sequence substantially as hereinbefore described with reference to SEQIDNO3.

78. Any novel subject matter or combination including novel subject matter disclosed, whether or not within the scope of or relating to the same invention as any of the preceding claims.

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AMENDED CLAIMS

[Received by the International Bureau on 14 September 1995 (14.09.95); original claims 1-78 replaced by amended claims 1-74 (9 pages)]

1. An active insect specific neurotoxin polypeptide, formed by expression of a truncated form of a gene sequence corresponding to part of a gene encoding for an insect specific neurotoxin present in the venom of the Black Widow Spider (Latrodectus mactans Tredecimguttatus), or an analogue thereof.

2. A polypeptide as claimed in any preceding claim, in which the polypeptide corresponds to a toxic derivative of a substantially non-toxic precursor polypeptide encoded by the gene sequence.

3. A polypeptide as claimed in any preceding claim, in which the polypeptide comprises an amino acid sequence that corresponds to a truncated form of the amino acid sequence of a substantially non-toxic precursor polypeptide.

4. A polypeptide as claimed in claim 3, in which the amino acid sequence of the polypeptide corresponds to the amino acid sequence of the precursor polypeptide with truncation thereof principally at the carboxy (C) end.

5. A polypeptide as claimed in claim 4, in which truncation is by about 150 to 200 amino acids.

6. A polypeptide as claimed in any of claims 3 to 5, in which the polypeptide amino acid sequence in addition corresponds to the precursor polypeptide amino acid sequence truncated at the amino end (N).

7. A polypeptide as claimed in claim 6, in which the truncation is by less than 50 amino acids and desirably by 7 or 28 amino acids.

8. A polypeptide as claimed in any preceding claim, in which the amino acid sequence of the polypeptide is homologous to the amino acid sequence of the insect specific neurotoxin δ-Latroinsectotoxin (δ-LIT) or an active derivative thereof.

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9. A polypeptide as claimed in any preceding claim, in which the polypeptide comprises an amino acid sequence as shown in SEQIDN01 and SEQIDN02 or an active derivative thereof.

10. A polypeptide as claimed in any preceding claim, in which the toxin is expressed from a nucleotide construct or truncated form of a gene sequence comprising a sequence as shown in SEQIDN01, or active variants thereof.

11. A polypeptide as claimed in any preceding claim, in which the polypeptide is expressed from a sequence substantially as provided in a microorganism deposited at The National Collections of Industrial and Marine Bacteria Limited, under Accession No. NCIMB 40632.

12. A protein for use as a toxin comprising an amino acid sequence substantially as shown in SEQIDN01 and SEQIDN02, or an active derivative thereof.

13. A nucleotide sequence comprising a truncated form of a gene sequence corresponding to part of a gene encoding for an insect specific neurotoxin present in the venom of the Black Widow Spider (Latrodectus mactans Tredecimguttatus) or an analogue thereof, for use in the expression of an active insect specific neurotoxin polypeptide.

14. A nucleotide sequence as claimed in claim 13, in which the nucleotide sequence corresponds to a gene encoding for a precursor polypeptide and truncated at the 3' end thereof, or an active derivative thereof.

15. A nucleotide sequence as claimed in claim 14, in which the nucleotide sequence corresponds to the gene truncated by about 400 to 650 nucleotide bases, and desirably between 550 to 600 nucleotide bases.

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16. A nucleotide sequence as claimed in any of claims 13 to 15, in which the nucleotide sequence corresponds to the gene truncated at the 5' thereof.

17. A nucleotide sequence as claimed in claim 16, in which the truncation is by less than 100 nucleotide bases, and desirably by either 84 or 21 nucleotide bases.

18. A nucleotide sequence as claimed in any one of claims 13 to 17, in which the nucleotide sequence corresponds to part of the gene encoding the precursor polypeptide of insect specific toxin δ-Lactoinsectotoxin (δ-LIT), or an active derivative thereof.

19. A nucleotide sequence as claimed in any of claims 13 to 18, in which the nucleotide sequence codes for a polypeptide comprising a sequence of 991 amino acids.

20. A nucleotide sequence as claimed in any of claims 13 to 19, in which the nucleotide sequence comprises a base sequence as shown in SEQIDN01, or an active derivative thereof.

21. A nucleotide sequence as claimed in any of claims 13 to 20, in which the nucleotide sequence comprises a base sequence substantially as comprised in a microorganism deposited under Accession No. NCIMB 40632 at The National Collections of Industrial and Marine Bacteria Limited.

22. A nucleotide sequence as claimed in any of claims 13 to 21, in which the nucleotide sequence codes for a polypeptide having an amino acid sequence as shown in SEQIDN01 and SEQIDN02, or an active derivative thereof.

23. A nucleotide sequence as claimed in any of claims 13 to 22, in which the nucleotide sequence is a cDNA derived from mRNA by the use of an enzyme such as reverse transcriptase.

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24. A nucleotide sequence as claimed in any of claims 13 to 23, in which the nucleotide sequence is an oligonucleotide DNA construct produced perhaps using the polymerase chain reaction (PCR).

25. A method of producing a polypeptide as claimed in claim 1, the method comprising producing a recombinant DNA molecule comprising a truncated form of a gene as claimed in claim 13, and expressing the truncated form in a host expression system, such as a bacterial expression system, to produce the polypeptide.

26. A method as claimed in claim 25, in which the polypeptide produced is an active toxin substantially as claimed in any preceding claim.

27. A method as claimed in claim 25 or claim 26, in which the truncated form comprises part of a gene which encodes for a non-toxic precursor polypeptide.

28. A method as claimed in any of claims 25 to 27, in which the truncated form comprises a nucleotide sequence substantially as claimed in any of claims 14 to 24.

29. A method as claimed in any of claims 25 to 28, in which the expression system comprises E. coli BL21 (DE3) bacterial cells transformed with pT7-7 vectors comprising the truncated form of the sequence.

30. A method as claimed in any of claims 25 to 29, in which the expression system comprises a baculovirus system.

31. A recombinant DNA molecule comprising a truncated form of a gene encoding for a toxin generally as claimed in any preceding claim.

32. A recombinant DNA molecule as claimed in claim 31, in which the molecule comprises a virus.

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33. A recombinant DNA molecule as claimed in claim 32, in which the molecule comprises a baculovirus.

34. A recombinant DNA molecule substantially as provided in the microorganism deposited under Accession No. NCIMB 40632.

35. An expression vector comprising a truncated form of a gene generally as claimed in any of claims 14 to 24.

36. A cell, such as a viral or bacterial cell transformed with a recombinant molecule substantially as claimed in any of claims 31 or 35.

37. An insecticide comprising a toxin substantially as claimed in any of claims 1 to 12.

38. An insecticide as claimed in claim 37, in which the insecticide is so as to be administered orally or topically.

39. An insecticide as claimed in claim 37 or claim 38, in which the insecticide comprises a spray.

40. An insecticide system comprising means for expressing a truncated form of a gene as claimed in any one of claims 13 to 24 to produce a toxin substantially as claimed in any preceding claim in an insect to kill or incapacitate the insect.

41. An insecticide system as claimed in claim 40, in which the insecticide system comprises a viral expression system.

42. An insecticide system as claimed in claim 41, in which the viral expression system comprises a baculovirus expression system.

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43. A plant comprising a genetically modified cell containing a truncated form of a gene sequence substantially as claimed in any of claims 13 to 24.

44. A non-human animal comprising a genetically modified cell containing a truncated form of a gene sequence substantially as claimed in any of claims 13 to 24.

45. A toxin formed by processing of a substantially isolated non-toxic precursor polypeptide having an amino acid sequence corresponding to that of an insect specific neurotoxin present in the venom of the Black Widow Spider (Latrodectus mactans Tredecimguttatus).

46. A toxin as claimed in claim 45, in which the toxin is formed by truncation toward the carboxy (C) end of the precursor polypeptide.

47. A toxin as claimed in claim 46, in which the toxin amino acid sequence generally corresponds to the amino acid sequence of the precursor polypeptide, truncated by between 150 and 200 amino acids.

48. A toxin as claimed in any of claims 45 to 47, in which the toxin amino acid sequence is formed by truncation toward the amino (N) end of the precursor polypeptide amino acid sequence.

49. A toxin as claimed in claim 48, in which the fragment cleaved from the amino end is significantly smaller than the fragment cleaved from the carboxy end.

50. A toxin as claimed in claim 48 or claim 49, in which the fragment cleaved off comprises 7 or 28 amino acids.

51. A toxin as claimed in any of claims 45 to 50, in which the toxin comprises or is an analogue of the insect specific neurotoxin δ-Latroinsectotoxin (δ-LIT), or an active derivative thereof.

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52. A toxin as claimed in any of claims 45 to 51, in which the toxin comprises an amino acid sequence as shown in SEQIDN01 and SEQIDN02 or an active derivative thereof.

53. A method of producing an active insect specific neurotoxin polypeptide from an isolated inactive precursor polypeptide having an amino acid sequence corresponding to that of an insect specific neurotoxin present in the venom of the Black Widow Spider (Latrodectus mactans Tredecimguttatus), the method comprising truncating the isolated precursor polypeptide.

54. A method as claimed in claim 53, in which the isolated precursor polypeptide is truncated at the Carboxyl end.

55. A method as claimed in claim 53 or claim 54, in which the truncation is effected using proteolytic cleavage, and preferably by site directed mutagenesis.

56. A method as claimed in any of claims 53 to 55, in which truncation of the N terminus is provided.

57. A method as claimed in claims 53 to 56, in which the active polypeptide is a toxin and is substantially as claimed in any of claims 1 to 12, 45 to 52.

58. An isolated nucleotide base sequence encoding for a toxin precursor polypeptide with an amino acid sequence as shown in SEQIDN04 or a derivative thereof.

59. An isolated base sequence comprising a base sequence as shown in SEQIDN03 or a derivative thereof.

60. An isolated base sequence as claimed in any of claims 58 or 59, in which the nucleotide base sequence encodes a precursor polypeptide of the neurotoxin δ-Latroinsectotoxin (δ-LIT).

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61. An isolated base sequence substantially as provided in the microorganism deposited under Accession No. NCIMB 40633.

62. A recombinant DNA molecule comprising a sequence substantially as claimed in any of claims 58 to 61.

63. A recombinant molecule as claimed in claim 62, in which the molecule comprises a virus.

64. A recombinant molecule as claimed in claim 63, in which the virus comprises a baculovirus.

65. A cell, such as a bacterial or viral cell, transformed with a recombinant DNA molecule substantially as claimed in any of claims 62 to 64.

66. An insecticide system comprising means for expressing a base sequence substantially as claimed in any of claims 58 to 61 to produce a precursor polypeptide and to process the precursor polypeptide to produce a toxin in an insect to kill or incapacitate the insect.

67. An insecticide system as claimed in claim 66, in which the system comprises a viral expression system.

68. An insecticide system as claimed in claim 67, in which the viral expression system comprises baculovirus.

69. A plant comprising a genetically modified cell containing a nucleotide sequence substantially as claimed in any of claims 58 to 61.

70. A non-human animal comprising a genetically modified cell containing a nucleotide sequence substantially as claimed in any of claims 58 to 61.

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71. A novel toxin substantially as hereinbefore described with reference to SEQIDN01 and SEQIDN02.

72. A nucleotide sequence substantially as hereinbefore described with reference to SEQIDN01.

73. An isolated polypeptide substantially as hereinbefore described with reference to SEQIDN03 and SEQIDN04.

74. An isolated nucleotide sequence substantially as hereinbefore described with reference to SEQIDN03.

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